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(54) Title: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS

(57) Abstract: The invention relates to plant transcription factor polypeptides, polynucleotides that encode them, homologs from a variety of plant species, and methods of using the polynucleotides and polypeptides to produce transgenic plants having advantageous properties compared to a reference plant. Sequence information related to these polynucleotides and polypeptides can also be used in bioinformatic search methods and is also disclosed.

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POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS**RELATIONSHIP TO COPENDING APPLICATIONS**

5 This application claims the benefit of copending US Provisional Application No. 60/411,837, filed September 18, 2002, US Provisional Application No. 60/434,166, filed December 17, 2002, and US Provisional Application No. 60/465,809, filed April 24, 2003, the entire contents of which are hereby incorporated by reference.

TECHNICAL FIELD

10 This invention relates to the field of plant biology, and to compositions and methods for modifying the phenotype of a plant.

BACKGROUND OF THE INVENTION

15 A plant's traits, such as its biochemical, developmental, or phenotypic characteristics, may be controlled through a number of cellular processes. One important way to manipulate that control is through transcription factors - proteins that influence the expression of a particular gene or sets of genes. Transformed and transgenic plants comprise cells having altered levels of at least one selected transcription factor, and may possess advantageous or desirable traits. Strategies for manipulating traits by altering a plant cell's transcription factor content can therefore result in plants and crops with new and/or improved commercially valuable properties.

20 Transcription factors can modulate gene expression, either increasing or decreasing (inducing or repressing) the rate of transcription. This modulation results in differential levels of gene expression at various developmental stages, in different tissues and cell types, and in response to different exogenous (e.g., environmental) and endogenous stimuli throughout the life cycle of the organism.

25 Because transcription factors are key controlling elements of biological pathways, altering the expression levels of one or more transcription factors can change entire biological pathways in an organism. For example, manipulation of the levels of selected transcription factors may result in increased expression of economically useful proteins or biomolecules in plants or improvement in other agriculturally relevant characteristics. Conversely, blocked or reduced expression of a transcription factor may reduce biosynthesis of unwanted compounds or remove an undesirable trait. Therefore, manipulating transcription factor levels in a plant offers tremendous potential in agricultural biotechnology for modifying a plant's traits. A number of the agriculturally relevant characteristics of

plants, and desirable traits that may be imbued by modified transcription factor gene expression, are listed below.

Chilling tolerance

5 The term "chilling sensitivity" has been used to describe many types of physiological damage produced at low, but above freezing, temperatures. Most crops of tropical origins such as soybean, rice, maize and cotton are easily damaged by chilling. Typical chilling damage includes wilting, necrosis, chlorosis or leakage of ions from cell membranes. The underlying mechanisms of chilling sensitivity are not completely understood yet, but probably involve the level of membrane saturation and other
10 physiological deficiencies. For example, photoinhibition of photosynthesis (disruption of photosynthesis due to high light intensities) often occurs under clear atmospheric conditions subsequent to cold late summer/autumn nights. By some estimates, chilling accounts for monetary losses in the United States (US) second only to drought and flooding. For example, chilling may lead to yield losses and lower product quality through the delayed ripening of maize. Another consequence of poor growth is the rather
15 poor ground cover of maize fields in spring, often resulting in soil erosion, increased occurrence of weeds, and reduced uptake of nutrients. A retarded uptake of mineral nitrogen could also lead to increased losses of nitrate into the ground water.

Freezing tolerance.

20 Freezing is a major environmental stress that limits where crops can be grown and that reduces yields considerably, depending on the weather in a particular growing season. In addition to exceptionally stressful years that cause measurable losses of billions of dollars, less extreme stress almost certainly causes smaller yield reductions over larger areas to produce yield reductions of similar dollar value every year. For instance, in the US, the 1995 early fall frosts are estimated to have caused losses of
25 over one billion dollars to corn and soybeans. The spring of 1998 saw an estimated \$200 M of damages to Georgia alone in the peach, blueberry and strawberry industries. The occasional freezes in Florida have shifted the citrus belt further south due to \$100 M or more losses. California sustained \$650 M of damage in 1998 to the citrus crop due to a winter freeze. In addition, certain crops such as *Eucalyptus*, which has the very favorable properties of rapid growth and good wood quality for pulping, are not able to grow in
30 the southeastern states due to occasional freezes.

 Inherent winter hardiness of the crop determines in which agricultural areas it can survive the winter. For example, for wheat, the northern central portion of the US has winters that are too cold for good winter wheat crops. Approximately 20% of the US wheat crop is spring wheat, with a market value of \$2 billion. Areas growing spring wheat could benefit by growing winter wheat that had increased
35 winter hardiness. Assuming a 25% yield increase when growing winter wheat, this would create \$500 M of increased value. Additionally, the existing winter wheat is severely stressed by freezing conditions and

should have improved yields with increased tolerance to these stresses. An estimate of the yield benefit of these traits is 10% of the \$4.4 billion winter wheat crop in the US or \$444 M of yield increase, as well as better survival in extreme freezing conditions that occur periodically.

Thus, plants more resistant to freezing, both midwinter freezing and sudden freezes, would protect a farmers' investment, improve yield and quality, and allow growers in some geographies to grow more profitable and productive crops. Additionally, winter crops such as canola, wheat and barley have 25% to 50% yield increases relative to spring planted varieties of the same crops. This yield increase is due to the "head start" the fall planted crops have over the spring planted crops and their reaching maturity earlier while the temperatures, soil moisture and lack of pathogens provide more favorable conditions.

Salt tolerance.

One in five hectares of irrigated land is damaged by salt, an important historical factor in the decline of ancient agrarian societies. This condition is only expected to worsen, further reducing the availability of arable land and crop production, since none of the top five food crops - wheat, corn, rice, potatoes, and soybean - can tolerate excessive salt.

Detrimental effects of salt on plants are a consequence of both water deficit resulting in osmotic stress (similar to drought stress) and the effects of excess sodium ions on critical biochemical processes. As with freezing and drought, high saline causes water deficit; the presence of high salt makes it difficult for plant roots to extract water from their environment (Buchanan et al. (2000) in Biochemistry and Molecular Biology of Plants, American Society of Plant Physiologists, Rockville, MD). Soil salinity is thus one of the more important variables that determines where a plant may thrive. In many parts of the world, sizable land areas are uncultivable due to naturally high soil salinity. To compound the problem, salination of soils that are used for agricultural production is a significant and increasing problem in regions that rely heavily on agriculture. The latter is compounded by over-utilization, over-fertilization and water shortage, typically caused by climatic change and the demands of increasing population. Salt tolerance is of particular importance early in a plant's lifecycle, since evaporation from the soil surface causes upward water movement, and salt accumulates in the upper soil layer where the seeds are placed. Thus, germination normally takes place at a salt concentration much higher than the mean salt level in the whole soil profile.

Drought tolerance.

While much of the weather that we experience is brief and short-lived, drought is a more gradual phenomenon, slowly taking hold of an area and tightening its grip with time. In severe cases, drought can last for many years and can have devastating effects on agriculture and water supplies. With burgeoning population and chronic shortage of available fresh water, drought is not only the number one weather related problem in agriculture, it also ranks as one of the major natural disasters of all time, causing not

only economic damage, but also loss of human lives. For example, losses from the US drought of 1988 exceeded \$40 billion, exceeding the losses caused by Hurricane Andrew in 1992, the Mississippi River floods of 1993, and the San Francisco earthquake in 1989. In some areas of the world, the effects of drought can be far more severe. In the Horn of Africa the 1984–1985 drought led to a famine that killed
5 750,000 people.

Problems for plants caused by low water availability include mechanical stresses caused by the withdrawal of cellular water. Drought also causes plants to become more susceptible to various diseases (Simpson (1981) "The Value of Physiological Knowledge of Water Stress in Plants", In Water Stress on Plants, (Simpson, G. M., Ed), Praeger, NY, pp. 235-265).

10 In addition to the many land regions of the world that are too arid for most if not all crop plants, overuse and over-utilization of available water is resulting in an increasing loss of agriculturally-usable land, a process which, in the extreme, results in desertification. The problem is further compounded by increasing salt accumulation in soils, as described above, which adds to the loss of available water in soils.

15 Water deficit is a common component of many plant stresses. Water deficit occurs in plant cells when the whole plant transpiration rate exceeds the water uptake. In addition to drought, other stresses, such as salinity and low temperature, produce cellular dehydration (McCue and Hanson (1990) *Trends Biotechnol.* 8: 358-362).

Salt and drought stress signal transduction consist of ionic and osmotic homeostasis signaling
20 pathways. The ionic aspect of salt stress is signaled via the SOS pathway where a calcium-responsive SOS3-SOS2 protein kinase complex controls the expression and activity of ion transporters such as SOS1. The pathway regulating ion homeostasis in response to salt stress has been reviewed recently by Xiong and Zhu (2002) *Plant Cell Environ.* 25: 131-139.

The osmotic component of salt stress involves complex plant reactions that overlap with drought
25 and/or cold stress responses.

Common aspects of drought, cold and salt stress response have been reviewed recently by Xiong and Zhu (2002) *supra*). Those include:

- (a) transient changes in the cytoplasmic calcium levels very early in the signaling event (Knight, (2000) *Int. Rev. Cytol.* 195: 269-324; Sanders et al. (1999) *Plant Cell* 11: 691-706);
- 30 • (b) signal transduction via mitogen-activated and/or calcium dependent protein kinases (CDPKs; see Xiong and Zhu (2002) *supra*) and protein phosphatases (Merlot et al. (2001) *Plant J.* 25: 295-303; Tähtiharju and Palva (2001) *Plant J.* 26: 461-470);
- (c) increases in abscisic acid levels in response to stress triggering a subset of responses (Xiong and Zhu (2002) *supra*, and references therein);
- 35 • (d) inositol phosphates as signal molecules (at least for a subset of the stress responsive transcriptional changes (Xiong et al. (2001) *Genes Dev.* 15: 1971-1984);

- (e) activation of phospholipases which in turn generate a diverse array of second messenger molecules, some of which might regulate the activity of stress responsive kinases (phospholipase D functions in an ABA independent pathway, Frank et al. (2000) *Plant Cell* 12: 111-124);
- (f) induction of late embryogenesis abundant (LEA) type genes including the CRT/DRE-containing COR/RD genes (Xiong and Zhu (2002) *supra*);
- (g) increased levels of antioxidants and compatible osmolytes such as proline and soluble sugars (Hasegawa et al. (2000) *Annu. Rev. Plant Mol. Plant Physiol.* 51: 463-499);
- (h) accumulation of reactive oxygen species such as superoxide, hydrogen peroxide, and hydroxyl radicals (Hasegawa et al. (2000) *supra*).

Abscisic acid biosynthesis is regulated by osmotic stress at multiple steps. Both ABA-dependent and ABA-independent osmotic stress signaling first modify constitutively expressed transcription factors, leading to the expression of early response transcriptional activators, which then activate downstream stress tolerance effector genes.

Based on the commonality of many aspects of cold, drought and salt stress responses, it can be concluded that genes that increase tolerance to cold or salt stress can also improve drought stress protection. In fact this has already been demonstrated for transcription factors (in the case of AtCBF/DREB1) and for other genes such as OsCDPK7 (Saijo et al. (2000) *Plant J.* 23: 319-327), or AVP1 (a vacuolar pyrophosphatase-proton-pump; Gaxiola et al. (2001) *Proc. Natl. Acad. Sci. USA* 98: 11444-11449).

Heat tolerance.

Germination of many crops is very sensitive to temperature. A transcription factor that would enhance germination in hot conditions would be useful for crops that are planted late in the season or in hot climates. Seedlings and mature plants that are exposed to excess heat may experience heat shock, which may arise in various organs, including leaves and particularly fruit, when transpiration is insufficient to overcome heat stress. Heat also damages cellular structures, including organelles and cytoskeleton, and impairs membrane function (Buchanan, *supra*).

Heat shock may result a decrease in overall protein synthesis, accompanied by expression of heat shock proteins. Heat shock proteins function as chaperones and are involved in refolding proteins denatured by heat.

Tolerance to low nitrogen and phosphorus.

The ability of all plants to remove nutrients from their environment is essential to survival. Thus, identification of genes that encode polypeptides with transcription factor activity may allow for the generation of transgenic plants that are better able to make use of available nutrients in nutrient-poor environments.

Among the most important macronutrients for plant growth that have the largest impact on crop yield are nitrogenous- and phosphorus-containing compounds. Nitrogen- and phosphorus- containing fertilizers are used intensively in agriculture practices today. An increase in grain crop yields from 0.5 to 1.0 metric tons per hectare to 7 metric tons per hectare accompanied the use of commercial fixed nitrogen fertilizer in production farming (Vance (2001) *Plant Physiol* 127: 390-397). Given current practices, in order to meet food production demands in years to come, considerable increases in the amount of nitrogen - and phosphorus-containing fertilizers will be required (Vance, *supra*).

Nitrogen (N) is the most abundant element on earth yet it is one of the most limiting elements to plant growth due to its lack of availability in the soil. Plants obtain N from the soil from several sources including commercial fertilizers, manure and the mineralization of organic matter. The intensive use of N fertilizers in present agricultural practices is problematic, the energy intensive Haber-Bosch process makes N fertilizer and it is estimated that the US uses annually between 3-5% of the nation's natural gas for this process. In addition to the expense of N fertilizer production and the depletion of non-renewable resources, the use of N fertilizers has led to the eutrophication of freshwater ecosystems and the contamination of drinking water due to the runoff of excess fertilizer into ground water supplies.

Phosphorus (P) is second only to N in its importance as a macronutrient for plant growth and to its impact on crop yield. Phosphorus is extremely immobile and not readily available to roots in the soil and is therefore often growth limiting to plants. Inorganic phosphate (Pi) is a constituent of several important molecules required for energy transfer, metabolic regulation and protein activation (Marschner (1995) *Mineral Nutrition of Higher Plants*, 2nd ed., Academic Press, San Diego, CA). Plants have evolved several strategies to help cope with P and N deprivation that include metabolic as well as developmental adaptations. Most, if not all, of these strategies have components that are regulated at the level of transcription and therefore are amenable to manipulation by transcription factors. Metabolic adaptations include increasing the availability of P and N by increasing uptake from the soil through the induction of high affinity and low affinity transporters, and/or increasing P and N mobilization in the plant. Developmental adaptations include increases in primary and secondary roots, increases in root hair number and length, and associations with mycorrhizal fungi (Bates and Lynch (1996) *Plant Cell Environ.* 19: 529-538; Harrison (1999) *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 50: 361-389).

Disease resistance.

Disease management is a significant expense in crop production worldwide. According to EPA reports for 1996 and 1997, US farmers spend approximately \$6 billion on fungicides annually. Despite this expenditure, according to a survey conducted by the food and agriculture organization, plant diseases still reduce worldwide crop productivity by 12% and in the United States alone, economic losses due to plant pathogens amounts to 9.1 billion dollars (FAO, 1993). Data from these reports and others demonstrate that despite the availability of chemical control only a small proportion of the losses due to disease can be prevented. Not only are fungicides and anti-bacterial treatments expensive to growers, but

their widespread application poses both environmental and health risks. The use of plant biotechnology to engineer disease resistant crops has the potential to make a significant economic impact on agriculture and forestry industries in two ways: reducing the monetary and environmental expense of fungicide application and reducing both pre-harvest and post-harvest crop losses that occur now despite the use of costly disease management practices.

Fungal, bacterial, oomycete, viral, and nematode diseases of plants are ubiquitous and important problems, and often severely impact yield and quality of crop and other plants. A very few examples of diseases of plants include:

Powdery mildew, caused by the fungi *Erysiphe*, *Sphaerotheca*, *Phyllactinia*, *Microsphaera*, *Podosphaera* or *Uncinula*, in, for example, wheat, bean, cucurbit, lettuce, pea, grape, tree fruit crops, as well as roses, phlox, lilacs, grasses, and *Euonymus*;

Fusarium-caused diseases such as *Fusarium* wilt in cucurbits, *Fusarium* head blight in barley and wheat, wilt and crown and root rot in tomatoes;

Sudden oak death, caused by the oomycete *Phytophthora ramorum*; this disease was first detected in 1995 in California tan oaks. The disease has since killed more than 100,000 tan oaks, coast live oaks, black oaks, and Shreve's oaks in coastal regions of northern California, and more recently in southwestern Oregon (Roach (2001) National Geographic News, December 6, 2001);

Black Sigatoka, a fungal disease caused by *Mycosphaerella* species that attacks banana foliage, is spreading throughout the regions of the world that are responsible for producing most of the world's banana crop;

Eutypa dieback, caused by *Eutypa lata*, affects a number of crop plants, including vine grape. *Eutypa* dieback delays shoot emergence, and causes chlorosis, stunting, and tattering of leaves;

Pierce's disease, caused by the bacterium *Xylella fastidiosa*, precludes growth of grapes in the southeastern United States, and threatens the profitable wine grape industry in northern California. The bacterium clogs the vasculature of the grapevines, resulting in foliar scorching followed by slow death of the vines. There is no known treatment for Pierce's disease;

Bacterial Spot caused by the bacterium *Xanthomonas campestris* causes serious disease problems on tomatoes and peppers. It is a significant problem in the Florida tomato industry because it spreads rapidly, especially in warm periods where there is wind-driven rain. Under these conditions, there are no adequate control measures;

Diseases caused by viruses of the family Geminiviridae are a growing agricultural problem worldwide. Geminiviruses have caused severe crop losses in tomato, cassava, and cotton. For instance, in the 1991-1992 growing season in Florida, geminiviruses caused \$140 million in damages to the tomato crop (Moffat (1991) *Science* 286: 1835). Geminiviruses have the ability to recombine between strains to produce new virulent varieties rapidly. Therefore, there is a pressing need for broad-spectrum geminivirus control;

The soybean cyst nematode, *Heterodera glycines*, causes stunting and chlorosis of soybean plants, which results in yield losses or plant death from severe infestation. Annual losses in the United States have been estimated at \$1.5 billion (University of Minnesota Extension Service).

The aforementioned pathogens represent a very small fraction of diverse species that seriously affect plant health and yield. For a more complete description of numerous plant diseases, see, for example, Vidhyasekaran (1997, Fungal Pathogenesis in Plants and Crops: Molecular Biology and Host Defense Mechanisms, Marcel Dekker, Monticello, NY), or Agrios (1997, Plant Pathology, Academic Press, New York, NY). Plants that are able to resist disease may produce significantly higher yields and improved food quality. It is thus of considerable importance to find genes that reduce or prevent disease.

Reduced shade avoidance.

Shade avoidance describes the process in which plants grown in close proximity attempt to out-compete each other by increasing stem length at the expense of leaf, fruit and storage organ development. This is caused by the plant's response to far-red radiation reflected from leaves of neighboring plants, which is mediated by phytochrome photoreceptors. Close proximity to other plants, as is produced in high-density crop plantings, increases the relative proportion of far-red irradiation, and therefore induces the shade avoidance response. Shade avoidance adversely affects biomass and yield, particularly when leaves, fruits or other storage organs constitute the desired crop (see, for example, Smith (1982) *Annu. Rev. Plant Physiol.* 33: 481-518; Ballare et al. (1990) *Science* 247: 329-332; Smith (1995) *Annu. Dev. Plant Physiol. Mol. Biol.*, 46: 289-315; and Schmitt et al. (1995), *American Naturalist*, 146: 937-953). Alteration of the shade avoidance response in tobacco through alteration of phytochrome levels has been shown to produce an increase in harvest index (leaf biomass/total biomass) at high planting density, which would result in higher yield (Robson et al. (1996) *Nature Biotechnol.* 14: 995-998).

Altered flowering time and flowering control.

Timing of flowering has a significant impact on production of agricultural products. For example, varieties with different flowering responses to environmental cues are necessary to adapt crops to different production regions or systems. Such a range of varieties have been developed for many crops, including wheat, corn, soybean, and strawberry. Improved methods for alteration of flowering time will facilitate the development of new, geographically adapted varieties.

Breeding programs for the development of new varieties can be limited by the seed-to-seed cycle. Thus, breeding new varieties of plants with multi-year cycles (such as biennials, e.g. carrot, or fruit trees, such as citrus) can be very slow. With respect to breeding programs, there would be a significant advantage in having commercially valuable plants that exhibit controllable and modified periods to flowering ("flowering times"). For example, accelerated flowering would shorten crop and tree breeding programs.

Improved flowering control allows more than one planting and harvest of a crop to be made within a single season. Early flowering would also improve the time to harvest plants in which the flower portion of the plant constitutes the product (e.g., broccoli, cauliflower, and other edible flowers). In addition, chemical control of flowering through induction or inhibition of flowering in plants could offer a significant advantage to growers who could provide for more uniform fruit production (e.g., in strawberry)

A sizable number of plants for which the vegetative portion of the plant forms the valuable crop tend to "bolt" dramatically (e.g., spinach, onions, lettuce), after which biomass production declines and product quality diminishes (e.g., through flowering-triggered senescence of vegetative parts). Delay or prevention of flowering may also reduce or preclude dissemination of pollen from transgenic plants.

Increased size and biomass.

The ability to increase the biomass or size of a plant would have several important commercial applications. Crop species may be generated that produce higher yields on larger cultivars, particularly those in which the vegetative portion of the plant is edible. For example, increasing plant leaf biomass may increase the yield of leafy vegetables for human or animal consumption. Additionally, increasing leaf biomass can be used to increase production of plant-derived pharmaceutical or industrial products. By increasing plant biomass, increased production levels of the products may be obtained from the plants. Tobacco leaves, in particular, have been employed as plant factories to generate such products. Furthermore, it may be desirable to increase crop yields of plants by increasing total plant photosynthesis. An increase in total plant photosynthesis is typically achieved by increasing leaf area of the plant. Additional photosynthetic capacity may be used to increase the yield derived from particular plant tissue, including the leaves, roots, fruits or seed. In addition, the ability to modify the biomass of the leaves may be useful for permitting the growth of a plant under decreased light intensity or under high light intensity. Modification of the biomass of another tissue, such as roots, may be useful to improve a plant's ability to grow under harsh environmental conditions, including drought or nutrient deprivation, because the roots may grow deeper into the ground. Increased biomass can also be a consequence of some strategies for increased tolerance to stresses, such as drought stress. Early in a stress response plant growth (e.g., expansion of lateral organs, increase in stem girth, etc.) can be slowed to enable the plant to activate adaptive responses. Growth rate that is less sensitive to stress-induced control can result in enhanced plant size, particularly later in development.

For some ornamental plants, the ability to provide larger varieties would be highly desirable. For many plants, including fruit-bearing trees, trees that are used for lumber production, or trees and shrubs that serve as view or wind screens, increased stature provides improved benefits in the forms of greater yield or improved screening.

Because increased yield may be quite valuable to growers, we believe that there is significant commercial opportunity for engineering pathogen tolerance or resistance using a transgenic plants with

altered expression of the instant plant transcription factors. Crops so engineered will provide higher yields, and may be used to improve the appearance of ornamentals. The present invention satisfies a need in the art by providing new compositions that are useful for engineering plants with increased biomass or size, and having the potential to increase yield.

5

Modified growth rate.

For almost all commercial crops, it is desirable to use plants that establish more quickly, since seedlings and young plants are particularly susceptible to stress conditions such as salinity or disease. Since many weeds may outgrow young crops or out-compete them for nutrients, it would also be desirable to determine means for allowing young crop plants to out compete weed species. Increasing seedling growth rate (emergence) contributes to seedling vigor and allows for crops to be planted earlier in the season with less concern for losses due to environmental factors. Early planting helps add days to the critical grain-filling period and increases yield.

Providing means to speed up or slow down plant growth would also be desirable to ornamental horticulture. If such means be provided, slow growing plants may exhibit prolonged pollen-producing or fruiting period, thus improving fertilization or extending harvesting season.

Modified senescence and cell death.

Premature senescence, triggered by various plant stresses, can limit production of both leaf biomass and seed yield. Transcription factor genes that suppress premature senescence or cell death in response to stresses can provide means for increasing yield, particularly for those plants for which the vegetative part of the plant represents the commercial product (e.g., spinach, lettuce).

Although leaf senescence is thought to be an evolutionary adaptation to recycle nutrients, the ability to control senescence in an agricultural setting has significant value. For example, a delay in leaf senescence in some maize hybrids is associated with a significant increase in yields and a delay of a few days in the senescence of soybean plants can have a large impact on yield. In an experimental setting, tobacco plants engineered to inhibit leaf senescence had a longer photosynthetic lifespan, and produced a 50% increase in dry weight and seed yield (Gan and Amasino (1995) *Science* 270: 1986-1988). Delayed flower senescence may generate plants that retain their blossoms longer and this may be of potential interest to the ornamental horticulture industry, and delayed foliar and fruit senescence could improve post-harvest shelf-life of produce.

Further, programmed cell death plays a role in other plant responses, including the resistance response to disease, and some symptoms of diseases, for example, as caused by necrotrophic pathogens such as *Botrytis cinerea* and *Sclerotinia sclerotiorum* (Dickman et al. *Proc. Natl. Acad. Sci.*, 98: 6957-6962). Localized senescence and/or cell death can be used by plants to contain the spread of harmful microorganisms. A specific localized cell death response, the "hypersensitive response", is a component of race-specific disease resistance mediated by plant resistance genes. The hypersensitive response is

thought to help limit pathogen growth and to initiate a signal transduction pathway that leads to the induction of systemic plant defenses. Accelerated senescence may be a defense against obligate pathogens such as powdery mildew that rely on healthy plant tissue for nutrients. With regard to powdery mildew, *Botrytis cinerea*, *Sclerotinia sclerotiorum* and other pathogens, transcription factors that
5 ameliorate cell death and/or damage may reduce the significant economic losses encountered, such as, for example, *Botrytis cinerea* in strawberry and grape.

Altered sugar sensing

Sugars are key regulatory molecules that affect diverse processes in higher plants including germination,
10 growth, flowering, senescence, sugar metabolism and photosynthesis. Sucrose, for example, is the major transport form of photosynthate and its flux through cells has been shown to affect gene expression and alter storage compound accumulation in seeds (source-sink relationships). Glucose-specific hexose-sensing has also been described in plants and is implicated in cell division and repression of "famine" genes (photosynthetic or glyoxylate cycles).

Altered morphology

Trichomes are branched or unbranched epidermal outgrowths or hair structures on a plant. Trichomes produce a variety of secondary biochemicals such as diterpenes and waxes, the former being important as, for example, insect pheromones, and the latter as protectants against desiccation and
20 herbivorous pests. Since diterpenes also have commercial value as flavors, aromas, pesticides and cosmetics, and potential value as anti-tumor agents and inflammation-mediating substances, they have been both products and the target of considerable research. In most cases where the metabolic pathways are impossible to engineer, increasing trichome density or size on leaves may be the only way to increase plant productivity. Thus, it would be advantageous to discover trichome-affecting transcription factor
25 genes for the purpose of increasing trichome density, size, or type to produce plants that are better protected from insects or that yield higher amounts of secondary metabolites.

The ability to manipulate wax composition, amount, or distribution could modify plant tolerance to drought and low humidity or resistance to insects, as well as plant appearance. In particular, a possible application for a transcription factor gene that reduces wax production in sunflower seed coats would be
30 to reduce fouling during seed oil processing. Antisense or co-suppression of transcription factors involved in wax biosynthesis in a tissue specific manner can be used to specifically alter wax composition, amount, or distribution in those plants and crops from which wax is either a valuable attribute or product or an undesirable constituent of plants.

In many instances, the seeds of a plant constitute a valuable crop. These include, for example, the
35 seeds of many legumes, nuts and grains. The discovery of means for producing larger seed would provide significant value by bringing about an increase in crop yield.

Modifications to flower structure may have advantageous or deleterious effects on fertility, and could be used, for example, to decrease fertility by the absence, reduction or screening of reproductive components. This could be a desirable trait, as it could be exploited to prevent or minimize the escape of the pollen of genetically modified organisms into the environment.

5 Manipulation of inflorescence branching patterns may also be used to influence yield and offer the potential for more effective harvesting techniques. For example, a "self pruning" mutation of tomato results in a determinate growth pattern and facilitates mechanical harvesting (Pnueli et al. (2001) *Plant Cell* 13(12): 2687-2702).

10 Other morphological characteristics that may be desirable in plants include those of an ornamental nature. These include changes in seed color, overall color, leaf and flower shape, leaf color, leaf size, or glossiness of leaves. Changes in plant or plant part coloration, brought about by modifying, for example, anthocyanin levels, would provide novel morphological features.

Plants that produce dark leaves may have benefits for human health; flavonoids, for example, have been used to inhibit tumor growth, prevent of bone loss, and prevention lipid oxidation in animals and humans. Plants in which leaf size is increased would likely provide greater biomass, which would be particularly valuable for crops in which the vegetative portion of the plant constitutes the product. Plants with glossy leaves generally produce greater epidermal wax, which, if it could be augmented, resulted in a pleasing appearance for many ornamentals, help prevent desiccation, and resist herbivorous insects and disease-causing agents. Plants with altered inflorescence, including, for example, larger flowers or
20 distinctive floral configurations, may have high value in the ornamental horticulture industry.

Alterations of apical dominance or plant architecture could create new plant varieties. Dwarf plants may be of potential interest to the ornamental horticulture industry, and shorter, more bushy plants may also have increased resistance to lodging.

25 Altered seed oil

The composition of seeds, particularly with respect to seed oil quantity and/or composition, is very important for the nutritional value and production of various food and feed products. Desirable improvements to oils include enhanced heat stability, improved nutritional quality through, for example, reducing the number of calories in seed, increasing the number of calories in animal feeds, or altering the
30 ratio of saturated to unsaturated lipids comprising the oils.

Altered seed protein

As with seed oils, seed protein content and composition is very important for the nutritional value and production of various food and feed products. Altered protein content or concentration in seeds
35 may be used to provide nutritional benefits and may also prolong storage capacity, increase seed pest or disease resistance, or modify germination rates. Altered amino acid composition of seeds, through altered protein composition, is also a desired objective for nutritional improvement.

Altered prenyl lipids.

Prenyl lipids, including the tocopherols, play a role in anchoring proteins in membranes or membranous organelles. Tocopherols have both anti-oxidant and vitamin E activity. Modified tocopherol composition of plants may thus be useful in improving membrane integrity and function, which may mitigate abiotic stresses such as heat stress. Increasing the anti-oxidant and vitamin content of plants through increased tocopherol content can provide useful human health benefits.

Altered glucosinolate levels

Increases or decreases in specific glucosinolates or total glucosinolate content can be desirable depending upon the particular application. For example: (i) glucosinolates are undesirable components of the oilseeds used in animal feed, since they produce toxic effects; low-glucosinolate varieties of canola have been developed to combat this problem; (ii) some glucosinolates have anti-cancer activity; thus, increasing the levels or composition of these compounds can be of use in production of nutraceuticals; and (iii) glucosinolates form part of a plant's natural defense against insects; modification of glucosinolate composition or quantity could therefore afford increased protection from herbivores. Furthermore, tissue specific promoters can be used in edible crops to ensure that these compounds accumulate specifically in particular tissues, such as the epidermis, which are not taken for human consumption.

We have identified polynucleotides encoding transcription factors, developed numerous transgenic plants using these polynucleotides, and have analyzed the plants for a variety of important traits. In so doing, we have identified important polynucleotide and polypeptide sequences for producing commercially valuable plants and crops as well as the methods for making them and using them. Other aspects and embodiments of the invention are described below and can be derived from the teachings of this disclosure as a whole.

SUMMARY OF THE INVENTION

The present invention is directed to novel recombinant polynucleotides, transgenic plants comprising the polynucleotides, and methods for producing the transgenic plants.

The recombinant polynucleotides may include any of the following sequences:

- (a) the nucleotide sequences found in the sequence listing;
- (b) nucleotide sequences encoding polypeptides found in the sequence listing;
- (c) sequence variants that are at least 70% sequence identical to any of the nucleotide sequences of (a) or (b);

- (d) orthologous and paralogous nucleotide sequences that are at least 70% identical to any of the nucleotide sequences of (a) or (b);
- (e) nucleotide sequence that hybridize to any of the nucleotide sequences of (a) or (b) under stringent conditions, which may include, for example, hybridization with wash steps of 6x SSC and 65 C for ten to thirty minutes per step; and
- (f) nucleotide sequences encoding a polypeptide having a conserved domain required for the function of regulating transcription and altering a trait in a transgenic plant, the conserved domain being at least 70% identical with a conserved domain of a polypeptide of the invention (i.e., a polypeptide listed in the sequence listing, or encoded by any of the above nucleotide sequences).

The invention also pertains to transgenic plants that may be produced by transforming plants with any recombinant polynucleotide of the invention. Due to the function of these polynucleotides, the transgenic plant will become altered phenotypically when compared with a wild-type plant. The traits that may be altered by transforming a plant with one of the present polynucleotides are numerous and varied, and may include, for example:

increased tolerance to various abiotic stresses, including cold, heat, freezing, low nitrogen and phosphorus conditions, osmotic stresses such as drought, and high salt concentrations;

increased tolerance to disease, including fungal disease, and particularly *Erysiphe*, *Fusarium*, and *Botrytis*; the present polynucleotides may be used to confer increased tolerance to multiple pathogens in transformed plants;

altered sensitivity or resistance to treatments that include glyphosate, ABA, and ACC,

altered carbon/nitrogen (C/N) sensing;

advanced or delayed flowering time;

altered floral characteristics such as flower structure, loss of flower determinacy, or reduced

fertility;

altered shoot meristem development, altered stem morphology and vascular tissue structure, and altered branching patterns;

reduced apical dominance;

altered trichome density, development, or structure;

altered root development, including root mass, branching and root hairs;

altered shade avoidance;

altered seed characteristics such as size, oil content, protein content, development, ripening, germination, or prenyl lipid content;

altered leaf characteristics, including size, mass, shape, color, glossiness, prenyl lipid content and

other chemical modifications;

slower or faster growth than wild-type;

altered cell differentiation, proliferation, and expansion;

altered phase change;
altered senescence, programmed cell death and necrosis,
increased plant size and/or biomass, including larger seedlings than controls; dwarfed plants; and
altered pigment, including anthocyanin, levels, in various plant tissues.

5 Methods for producing transgenic plants having altered traits are also encompassed by the invention. These method steps include first providing an expression vector having a recombinant polynucleotide of the invention, and at least one regulatory element flanking the polynucleotide sequence. Generally, the regulatory element(s) control expression of the recombinant polynucleotide in a target plant. The expression vector is then introduced into plant cells. The plant cells are grown into plants,
10 which are allowed to overexpress a polypeptide encoded by the recombinant polynucleotide. This overexpression results in the trait alteration, in the plant. Those plants that have altered traits are identified and selected on the basis of the desirability and degree of the altered trait.

15 Brief Description of the Sequence Listing and Figures

The file of this patent contains at least one drawing executed in color. Copies of this patent with color drawing(s) will be provided by the Patent and Trademark Office upon request and payment of the necessary fee.

The Sequence Listing provides exemplary polynucleotide and polypeptide sequences of the invention. The traits associated with the use of the sequences are included in the Examples.

20 CD-ROM1 (Copy 1) is a read-only memory computer-readable compact disc and contains a copy of the Sequence Listing in ASCII text format. The Sequence Listing is named "MBI0054.ST25.txt" and is 4,193 kilobytes in size. The copies of the Sequence Listing on the CD-ROM disc are hereby incorporated by reference in their entirety.

25 CD-ROM2 (Copy 2) is an exact copy of CD-R1 (Copy 1).
CD-ROM3 contains a computer-readable format (CRF) copy of the Sequence Listing as a text (.txt) file.

Figure 1 shows a conservative estimate of phylogenetic relationships among the orders of flowering plants (modified from Angiosperm Phylogeny Group (1998) *Ann. Missouri Bot. Gard.* 84: 1-49). Those plants with a single cotyledon (monocots) are a monophyletic clade nested within at least two major lineages of dicots; the eudicots are further divided into rosids and asterids. *Arabidopsis* is a rosid eudicot classified within the order Brassicales; rice is a member of the monocot order Poales. Figure 1
30 was adapted from Daly et al. ((2001) *Plant Physiol.* 127: 1328-1333).

Figure 2 shows a phylogenic dendrogram depicting phylogenetic relationships of higher plant taxa, including clades containing tomato and *Arabidopsis*; adapted from Ku et al. (2000) *Proc. Natl. Acad. Sci.* 97: 9121-9126; and Chase et al. (1993) *Ann. Missouri Bot. Gard.* 80: 528-580.

35 Figure 3A illustrates an example of an osmotic stress assay. The medium used in this root growth assay contained polyethylene glycol (PEG). After germination, the seedlings of a 35S::G47

overexpressing line (the eight seedlings on left labeled "OE.G47-22") appeared larger and had more root growth than the four wild-type seedlings on the right. As would be predicted by the osmotic stress assay, G47 plants showed enhanced survival and drought tolerance in a soil-based drought assay, as did G2133, a paralog of G47 (see Figures 10A and 10B). Figure 3B also demonstrates an interesting effect of G47 overexpression; the 35S::G47 plants on the left and in the center of this photograph had short, thick, fleshy inflorescences with reduced apical dominance.

Figure 4 demonstrates an example of the effects of an altered response to light. In a germination assay conducted on MS medium in darkness, overexpression of G354 resulted in more open and greenish cotyledons and thick hypocotyls compared to wild type (G354 overexpressors are labeled "G354-29" and wild-type "WT" in this figure). G354 overexpressors also had a drought-tolerance phenotype, as indicated in Example VIII, below. Closely related paralogs of this gene, G353 and G2839, showed a osmotic stress tolerance phenotype in a germination assay on media containing high sucrose. One line of 35S::G353 seedlings and several lines of 35S::G2839 were greener and had higher germination rates than controls. This suggests that G354 and its paralogs G353 and G2839 influence osmotic stress responses.

Figure 5A is a photograph of *Arabidopsis* 35S::G1274 seedlings grown on low nitrogen media supplemented with sucrose plus glutamine. Seedlings of two overexpressing lines are present on this plate (not distinguished), and both lines contained less anthocyanin than the wild-type seedlings seen in Figure 5B. The lack of anthocyanin production indicated that these lines were less stressed than control seedlings under the same conditions, a fact later confirmed in soil-based drought assays showing enhanced drought tolerance by G1274 overexpressing lines. G1274 overexpression (Figure 5C) and wild-type (Figure 5D) germination was also compared in a cold germination assay, in which the overexpressors were found to be larger and greener than the controls.

Figures 6A - 6D compare soil-based drought assays for G1274 overexpressors and wild-type control plants, which confirms the results predicted after the performance of the plate-based osmotic stress assays. 35S::G1274 lines fared much better after a period of water deprivation (Figure 6A) than control plants (Figure 6B). This distinction was particularly evident in the overexpressor plants after being ministered with water, said plants recovering to a healthy and vigorous state, as shown in Figure 6C. Conversely, none of the wild-type plants seen in Figure 6D recovered after rewatering.

Figures 7A and 7B compare G1792 overexpressing *Arabidopsis* seedling growth on a single plate (two sectors of the same plate) with medium containing 3% sucrose medium lacking nitrogen, five days after planting. The 35S::G1792 lines seen in Figure 7A generally showed greater cotyledon expansion and root growth than the wild-type seedlings in Figure 7B. Figure 7C is a photograph of a single plate showing a G1792 overexpressing line (labeled G1792-12; on left) and wild-type plants (on right) five days after inoculation with *Botrytis cinerea*, showing the chlorosis and hyphal growth in the latter control plants but not in the former overexpressors. Similar results were obtained five days after inoculation with *Erysiphe orontii* (not shown) and with *Fusarium oxysporum*, as seen in Figure 7D, with control

plants on the right showing chlorosis, and G1792 overexpressors on the left appearing to be free of the adverse effects of infection.

Figure 8A illustrates the results of root growth assays with G2999 overexpressing seedlings and controls in a high sodium chloride medium. The eight 35S::G2999 *Arabidopsis* seedlings on the left were larger, greener, and had more root growth than the four control seedlings on the right. Another member of the G2999 clade, G2998, also showed a salt tolerance phenotype and performed similarly in the plate-based salt stress assay seen Figure 8B. In the latter assay 35S::G2998 seedlings appeared large and green, whereas wild-type seedlings in the control assay plate shown in Figure 8C were small and had not yet expanded their cotyledons. As is noted below, high sodium chloride growth assays often are used to indicate osmotic stress tolerance such as drought tolerance, which was subsequently confirmed with soil-based assays conducted with G2999-overexpressing plants.

Figure 9A shows the effects of a heat assay on *Arabidopsis* wild-type and G3086-overexpressing plants. Generally, the overexpressors on the left were larger, paler, and bolted earlier than the wild type plants seen on the right in this plate. The same G3086 overexpressing lines, as exemplified by the eight seedlings on the left of Figure 9B, were also found to be larger, greener, and had more root growth in a high salt root growth assay than control plants, including the four on the right in Figure 9B.

Figures 10A and 10B compare the recovery from a drought treatment in two lines of G2133 overexpressing *Arabidopsis* plants and wild-type controls. Figure 10A shows plants of 35S::G2133 line 5 (left) and control plants (right). Figure 10B shows plants of 35S::G2133 line 3 (left) and control plants (right). Each pot contained several plants grown under 24 hours light. All were deprived of water for eight days, and are shown after re-watering. All of the plants of the G2133 overexpressor lines recovered, and all of the control plants were either dead or severely and adversely affected by the drought treatment.

DETAILED DESCRIPTION OF EXEMPLARY EMBODIMENTS

In an important aspect, the present invention relates to polynucleotides and polypeptides, for example, for modifying phenotypes of plants. Throughout this disclosure, various information sources are referred to and/or are specifically incorporated. The information sources include scientific journal articles, patent documents, textbooks, and World Wide Web browser-inactive page addresses, for example. While the reference to these information sources clearly indicates that they can be used by one of skill in the art, each and every one of the information sources cited herein are specifically incorporated in their entirety, whether or not a specific mention of "incorporation by reference" is noted. The contents and teachings of each and every one of the information sources can be relied on and used to make and use embodiments of the invention.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a

reference to "a plant" includes a plurality of such plants, and a reference to "a stress" is a reference to one or more stresses and equivalents thereof known to those skilled in the art, and so forth.

The polynucleotide sequences of the invention encode polypeptides that are members of well-known transcription factor families, including plant transcription factor families, as disclosed in Tables 4
5 - 9. Generally, the transcription factors encoded by the present sequences are involved in cell differentiation and proliferation and the regulation of growth. Accordingly, one skilled in the art would recognize that by expressing the present sequences in a plant, one may change the expression of autologous genes or induce the expression of introduced genes. By affecting the expression of similar autologous sequences in a plant that have the biological activity of the present sequences, or by
10 introducing the present sequences into a plant, one may alter a plant's phenotype to one with improved traits. The sequences of the invention may also be used to transform a plant and introduce desirable traits not found in the wild-type cultivar or strain. Plants may then be selected for those that produce the most desirable degree of over- or under-expression of target genes of interest and coincident trait improvement.

15 The sequences of the present invention may be from any species, particularly plant species, in a naturally occurring form or from any source whether natural, synthetic, semi-synthetic or recombinant. The sequences of the invention may also include fragments of the present amino acid sequences. In this context, a "fragment" refers to a fragment of a polypeptide sequence which is at least 5 to about 15 amino acids in length, most preferably at least 14 amino acids, and which retain some biological activity of a
20 transcription factor. Where "amino acid sequence" is recited to refer to an amino acid sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

As one of ordinary skill in the art recognizes, transcription factors can be identified by the
25 presence of a region or domain of structural similarity or identity to a specific consensus sequence or the presence of a specific consensus DNA-binding site or DNA-binding site motif (see, for example, Riechmann et al. (2000) *Science* 290: 2105-2110). The plant transcription factors may belong to one of the following transcription factor families: the AP2 (APETALA2) domain transcription factor family (Riechmann and Meyerowitz (1998) *Biol. Chem.* 379: 633-646); the MYB transcription factor family
30 (ENBib; Martin and Paz-Ares (1997) *Trends Genet.* 13: 67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) *Biol. Chem.* 378: 1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244: 563-571); the ankyrin-repeat protein family (Zhang et al. (1992) *Plant Cell* 4: 1575-1588); the zinc finger protein (Z) family (Klug and Schwabe (1995) *FASEB J.* 9: 597-604); Takatsuji (1998) *Cell. Mol. Life Sci.* 54:582-596); the homeobox (HB)
35 protein family (Buerglin (1994) in Guidebook to the Homeobox Genes, Duboule (ed.) Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) *Genes Dev.* 3: 1166-1178); the squamosa promoter binding proteins (SPB) (Klein et al. (1996) *Mol. Gen. Genet.* 1996 250: 7-16); the

NAM protein family (Souer et al. (1996) *Cell* 85: 159-170); the IAA/AUX proteins (Abel et al. (1995) *J. Mol. Biol.* 251: 533-549); the HLH/MYC protein family (Littlewood et al. (1994) *Prot. Profile* 1: 639-709); the DNA-binding protein (DBP) family (Tucker et al. (1994) *EMBO J.* 13: 2994-3002); the bZIP family of transcription factors (Foster et al. (1994) *FASEB J.* 8: 192-200); the Box P-binding protein (the BPF-1) family (da Costa e Silva et al. (1993) *Plant J.* 4: 125-135); the high mobility group (HMG) family (Bustin and Reeves (1996) *Prog. Nucl. Acids Res. Mol. Biol.* 54: 35-100); the scarecrow (SCR) family (Di Laurenzio et al. (1996) *Cell* 86: 423-433); the GF14 family (Wu et al. (1997) *Plant Physiol.* 114: 1421-1431); the polycomb (PCOMB) family (Goodrich et al. (1997) *Nature* 386: 44-51); the teosinte branched (TEO) family (Luo et al. (1996) *Nature* 383: 794-799); the ABI3 family (Giraudat et al. (1992) *Plant Cell* 4: 1251-1261); the triple helix (TH) family (Dehesh et al. (1990) *Science* 250: 1397-1399); the EIL family (Chao et al. (1997) *Cell* 89: 1133-44); the AT-HOOK family (Reeves and Nissen (1990) *J. Biol. Chem.* 265: 8573-8582); the S1FA family (Zhou et al. (1995) *Nucleic Acids Res.* 23: 1165-1169); the bZIPT2 family (Lu and Ferl (1995) *Plant Physiol.* 109: 723); the YABBY family (Bowman et al. (1999) *Development* 126: 2387-96); the PAZ family (Bohmert et al. (1998) *EMBO J.* 17: 170-80); a family of miscellaneous (MISC) transcription factors including the DPBF family (Kim et al. (1997) *Plant J.* 11: 1237-1251) and the SPF1 family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244: 563-571); the GARP family (Hall et al. (1998) *Plant Cell* 10: 925-936), the TUBBY family (Boggin et al (1999) *Science* 286 : 2119-2125), the heat shock family (Wu (1995) *Annu. Rev. Cell Dev. Biol.* 11: 441-469), the ENBP family (Christiansen et al. (1996) *Plant Mol. Biol.* 32: 809-821), the RING-zinc family (Jensen et al. (1998) *FEBS Letters* 436: 283-287), the PDBP family (Janik et al. (1989) *Virology* 168: 320-329), the PCF family (Cubas et al. *Plant J.* (1999) 18: 215-22), the SRS (SHI-related) family (Fridborg et al. (1999) *Plant Cell* 11: 1019-1032), the CPP (cysteine-rich polycomb-like) family (Cvitanich et al. (2000) *Proc. Natl. Acad. Sci.* 97: 8163-8168), the ARF (auxin response factor) family (Ulmasov et al. (1999) *Proc. Natl. Acad. Sci.* 96: 5844-5849), the SWI/SNF family (Collingwood et al. (1999) *J. Mol. Endocrinol.* 23: 255-275), the ACBF family (Seguin et al. (1997) *Plant Mol. Biol.* 35: 281-291), PCGL (CG-1 like) family (da Costa e Silva et al. (1994) *Plant Mol. Biol.* 25: 921-924) the ARID family (Vazquez et al. (1999) *Development* 126: 733-742), the Jumonji family (Balciunas et al. (2000), *Trends Biochem. Sci.* 25: 274-276), the bZIP-NIN family (Schauser et al. (1999) *Nature* 402: 191-195), the E2F family (Kaelin et al. (1992) *Cell* 70: 351-364) and the GRF-like family (Knaap et al. (2000) *Plant Physiol.* 122: 695-704). As indicated by any part of the list above and as known in the art, transcription factors have been sometimes categorized by class, family, and sub-family according to their structural content and consensus DNA-binding site motif, for example. Many of the classes and many of the families and sub-families are listed here. However, the inclusion of one sub-family and not another, or the inclusion of one family and not another, does not mean that the invention does not encompass polynucleotides or polypeptides of a certain family or sub-family. The list provided here is merely an example of the types of transcription factors and the knowledge available concerning the consensus sequences and consensus DNA-binding site motifs that help define them as known to those of skill in the

art (each of the references noted above are specifically incorporated herein by reference). A transcription factor may include, but is not limited to, any polypeptide that can activate or repress transcription of a single gene or a number of genes. This polypeptide group includes, but is not limited to, DNA-binding proteins, DNA-binding protein binding proteins, protein kinases, protein phosphatases, protein methyltransferases, GTP-binding proteins, and receptors, and the like.

In addition to methods for modifying a plant phenotype by employing one or more polynucleotides and polypeptides of the invention described herein, the polynucleotides and polypeptides of the invention have a variety of additional uses. These uses include their use in the recombinant production (i.e., expression) of proteins; as regulators of plant gene expression, as diagnostic probes for the presence of complementary or partially complementary nucleic acids (including for detection of natural coding nucleic acids); as substrates for further reactions, e.g., mutation reactions, PCR reactions, or the like; as substrates for cloning e.g., including digestion or ligation reactions; and for identifying exogenous or endogenous modulators of the transcription factors.

Definitions

"Nucleic acid molecule" refers to an oligonucleotide, polynucleotide or any fragment thereof. It may be DNA or RNA of genomic or synthetic origin, double-stranded or single-stranded, and combined with carbohydrate, lipids, protein, or other materials to perform a particular activity such as transformation or form a useful composition such as a peptide nucleic acid (PNA).

"Polynucleotide" is a nucleic acid molecule comprising a plurality of polymerized nucleotides, e.g., at least about 15 consecutive polymerized nucleotides, optionally at least about 30 consecutive nucleotides, at least about 50 consecutive nucleotides. A polynucleotide may be a nucleic acid, oligonucleotide, nucleotide, or any fragment thereof. In many instances, a polynucleotide comprises a nucleotide sequence encoding a polypeptide (or protein) or a domain or fragment thereof. Additionally, the polynucleotide may comprise a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions, a reporter gene, a selectable marker, or the like. The polynucleotide can be single stranded or double stranded DNA or RNA. The polynucleotide optionally comprises modified bases or a modified backbone. The polynucleotide can be, e.g., genomic DNA or RNA, a transcript (such as an mRNA), a cDNA, a PCR product, a cloned DNA, a synthetic DNA or RNA, or the like. The polynucleotide can be combined with carbohydrate, lipids, protein, or other materials to perform a particular activity such as transformation or form a useful composition such as a peptide nucleic acid (PNA). The polynucleotide can comprise a sequence in either sense or antisense orientations. "Oligonucleotide" is substantially equivalent to the terms amplicon, primer, oligomer, element, target, and probe and is preferably single stranded.

"Gene" or "gene sequence" refers to the partial or complete coding sequence of a gene, its complement, and its 5' or 3' untranslated regions. A gene is also a functional unit of inheritance, and in physical terms is a particular segment or sequence of nucleotides along a molecule of DNA (or RNA, in

the case of RNA viruses) involved in producing a polypeptide chain. The latter may be subjected to subsequent processing such as splicing and folding to obtain a functional protein or polypeptide.. A gene may be isolated, partially isolated, or be found with an organism's genome. By way of example, a transcription factor gene encodes a transcription factor polypeptide, which may be functional or require processing to function as an initiator of transcription.

Operationally, genes may be defined by the cis-trans test, a genetic test that determines whether two mutations occur in the same gene and which may be used to determine the limits of the genetically active unit (Rieger et al. (1976) Glossary of Genetics and Cytogenetics: Classical and Molecular, 4th ed., Springer Verlag, Berlin). A gene generally includes regions preceding ("leaders"; upstream) and following ("trailers"; downstream) of the coding region. A gene may also include intervening, non-coding sequences, referred to as "introns", located between individual coding segments, referred to as "exons". Most genes have an associated promoter region, a regulatory sequence 5' of the transcription initiation codon (there are some genes that do not have an identifiable promoter). The function of a gene may also be regulated by enhancers, operators, and other regulatory elements.

A "recombinant polynucleotide" is a polynucleotide that is not in its native state, e.g., the polynucleotide comprises a nucleotide sequence not found in nature, or the polynucleotide is in a context other than that in which it is naturally found, e.g., separated from nucleotide sequences with which it typically is in proximity in nature, or adjacent (or contiguous with) nucleotide sequences with which it typically is not in proximity. For example, the sequence at issue can be cloned into a vector, or otherwise recombined with one or more additional nucleic acid.

An "isolated polynucleotide" is a polynucleotide whether naturally occurring or recombinant, that is present outside the cell in which it is typically found in nature, whether purified or not. Optionally, an isolated polynucleotide is subject to one or more enrichment or purification procedures, e.g., cell lysis, extraction, centrifugation, precipitation, or the like.

A "polypeptide" is an amino acid sequence comprising a plurality of consecutive polymerized amino acid residues e.g., at least about 15 consecutive polymerized amino acid residues, optionally at least about 30 consecutive polymerized amino acid residues, at least about 50 consecutive polymerized amino acid residues. In many instances, a polypeptide comprises a polymerized amino acid residue sequence that is a transcription factor or a domain or portion or fragment thereof. Additionally, the polypeptide may comprise 1) a localization domain, 2) an activation domain, 3) a repression domain, 4) an oligomerization domain, or 5) a DNA-binding domain, or the like. The polypeptide optionally comprises modified amino acid residues, naturally occurring amino acid residues not encoded by a codon, non-naturally occurring amino acid residues.

"Protein" refers to an amino acid sequence, oligopeptide, peptide, polypeptide or portions thereof whether naturally occurring or synthetic.

"Portion", as used herein, refers to any part of a protein used for any purpose, but especially for the screening of a library of molecules which specifically bind to that portion or for the production of antibodies.

A "recombinant polypeptide" is a polypeptide produced by translation of a recombinant polynucleotide. A "synthetic polypeptide" is a polypeptide created by consecutive polymerization of isolated amino acid residues using methods well known in the art. An "isolated polypeptide," whether a naturally occurring or a recombinant polypeptide, is more enriched in (or out of) a cell than the polypeptide in its natural state in a wild-type cell, e.g., more than about 5% enriched, more than about 10% enriched, or more than about 20%, or more than about 50%, or more, enriched, i.e., alternatively denoted: 105%, 110%, 120%, 150% or more, enriched relative to wild type standardized at 100%. Such an enrichment is not the result of a natural response of a wild-type plant. Alternatively, or additionally, the isolated polypeptide is separated from other cellular components with which it is typically associated, e.g., by any of the various protein purification methods herein.

"Homology" refers to sequence similarity between a reference sequence and at least a fragment of a newly sequenced clone insert or its encoded amino acid sequence.

"Hybridization complex" refers to a complex between two nucleic acid molecules by virtue of the formation of hydrogen bonds between purines and pyrimidines.

"Identity" or "similarity" refers to sequence similarity between two polynucleotide sequences or between two polypeptide sequences, with identity being a more strict comparison. The phrases "percent identity" and "% identity" refer to the percentage of sequence similarity found in a comparison of two or more polynucleotide sequences or two or more polypeptide sequences. "Sequence similarity" refers to the percent similarity in base pair sequence (as determined by any suitable method) between two or more polynucleotide sequences. Two or more sequences can be anywhere from 0-100% similar, or any integer value therebetween. Identity or similarity can be determined by comparing a position in each sequence that may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same nucleotide base or amino acid, then the molecules are identical at that position. A degree of similarity or identity between polynucleotide sequences is a function of the number of identical or matching nucleotides at positions shared by the polynucleotide sequences. A degree of identity of polypeptide sequences is a function of the number of identical amino acids at positions shared by the polypeptide sequences. A degree of homology or similarity of polypeptide sequences is a function of the number of amino acids at positions shared by the polypeptide sequences.

The term "amino acid consensus motif" refers to the portion or subsequence of a polypeptide sequence that is substantially conserved among the polypeptide transcription factors listed in the Sequence Listing.

"Alignment" refers to a number of DNA or amino acid sequences aligned by lengthwise comparison so that components in common (i.e., nucleotide bases or amino acid residues) may be readily and graphically identified. The number of components in common is related to the homology or identity

between the sequences. Alignments may be used to identify "conserved domains" and relatedness within these domains. An alignment may suitably be determined by means of computer programs known in the art, such as MacVector (1999) (Accelrys, Inc., San Diego, CA).

5 A "conserved domain" or "conserved region" as used herein refers to a region in heterologous polynucleotide or polypeptide sequences where there is a relatively high degree of sequence identity between the distinct sequences.

With respect to polynucleotides encoding presently disclosed transcription factors, a conserved region is preferably at least 10 base pairs (bp) in length.

10 A "conserved domain", with respect to presently disclosed polypeptides refers to a domain within a transcription factor family that exhibits a higher degree of sequence homology, such as at least 26% sequence similarity, at least 16% sequence identity, preferably at least 40% sequence identity, preferably at least 65% sequence identity including conservative substitutions, and more preferably at least 80% sequence identity, and even more preferably at least 85%, or at least about 86%, or at least about 87%, or at least about 88%, or at least about 90%, or at least about 95%, or at least about 98%
15 amino acid residue sequence identity of a polypeptide of consecutive amino acid residues. A fragment or domain can be referred to as outside a conserved domain, outside a consensus sequence, or outside a consensus DNA-binding site that is known to exist or that exists for a particular transcription factor class, family, or sub-family. In this case, the fragment or domain will not include the exact amino acids of a consensus sequence or consensus DNA-binding site of a transcription factor class, family or sub-family,
20 or the exact amino acids of a particular transcription factor consensus sequence or consensus DNA-binding site. Furthermore, a particular fragment, region, or domain of a polypeptide, or a polynucleotide encoding a polypeptide, can be "outside a conserved domain" if all the amino acids of the fragment, region, or domain fall outside of a defined conserved domain(s) for a polypeptide or protein. Sequences having lesser degrees of identity but comparable biological activity are considered to be equivalents.

25 As one of ordinary skill in the art recognizes, conserved domains may be identified as regions or domains of identity to a specific consensus sequence (see, for example, Riechmann et al. (2000) *supra*). Thus, by using alignment methods well known in the art, the conserved domains of the plant transcription factors for each of the following may be determined: the AP2 (APETALA2) domain transcription factor family (Riechmann and Meyerowitz (1998) *supra*); the MYB transcription factor family (ENBib; Martin and Paz-Ares (1997) *supra*); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) *supra*; Immink et al. (2003) *supra*); the WRKY protein family (Ishiguro and Nakamura (1994) *supra*); the ankyrin-repeat protein family (Zhang et al. (1992) *supra*); the zinc finger protein (Z) family (Klug and Schwabe (1995) *supra*; Takatsuji (1998) *supra*); the homeobox (HB) protein family (Buerklin (1994) *supra*); the CAAT-element binding proteins (Forsburg and Guarente (1989) *supra*); the squamosa
35 promoter binding proteins (SPB) (Klein et al. (1996) *supra*); the NAM protein family (Souer et al. (1996) *supra*); the IAA/AUX proteins (Abel et al. (1995) *supra*); the HLH/MYC protein family (Littlewood et al. (1994) *supra*); the DNA-binding protein (DBP) family (Tucker et al. (1994) *supra*); the bZIP family

of transcription factors (Foster et al. (1994) *supra*); the Box P-binding protein (the BPF-1) family (da Costa e Silva et al. (1993) *supra*); the high mobility group (HMG) family (Bustin and Reeves (1996) *supra*); the scarecrow (SCR) family (Di Laurenzio et al. (1996) *supra*); the GF14 family (Wu et al. (1997) *supra*); the polycomb (PCOMB) family (Goodrich et al. (1997) *supra*); the teosinte branched (TEO) family (Luo et al. (1996) *supra*); the ABI3 family (Giraudat et al. (1992) *supra*); the triple helix (TH) family (Dehesh et al. (1990) *supra*); the EIL family (Chao et al. (1997) *Cell supra*); the AT-HOOK family (Reeves and Nissen (1990) *supra*); the S1FA family (Zhou et al. (1995) *supra*); the bZIPT2 family (Lu and Ferl (1995) *supra*); the YABBY family (Bowman et al. (1999) *supra*); the PAZ family (Bohmert et al. (1998) *supra*); a family of miscellaneous (MISC) transcription factors including the DPBF family (Kim et al. (1997) *supra*) and the SPF1 family (Ishiguro and Nakamura (1994) *supra*); the GARP family (Hall et al. (1998) *supra*), the TUBBY family (Boggin et al. (1999) *supra*), the heat shock family (Wu (1995) *supra*), the ENBP family (Christiansen et al. (1996) *supra*), the RING-zinc family (Jensen et al. (1998) *supra*), the PDBP family (Janik et al. (1989) *supra*), the PCF family (Cubas et al. (1999) *supra*), the SRS (SHI-related) family (Fridborg et al. (1999) *supra*), the CPP (cysteine-rich polycomb-like) family (Cvitanich et al. (2000) *supra*), the ARF (auxin response factor) family (Ulmasov et al. (1999) *supra*), the SWI/SNF family (Collingwood et al. (1999) *supra*), the ACBF family (Seguin et al. (1997) *supra*), PCGL (CG-1 like) family (da Costa e Silva et al. (1994) *supra*) the ARID family (Vazquez et al. (1999) *supra*), the Jumonji family, (Balciunas et al. (2000) *supra*), the bZIP-NIN family (Schauser et al. (1999) *supra*), the E2F family Kaelin et al. (1992) *supra*) and the GRF-like family (Knaap et al (2000) *supra*).

The conserved domains for each of polypeptides of SEQ ID NO: 2N, wherein N = 1-335 (that is, odd SEQ ID NO: 1, 3 5, 7 ... 759) are listed in Table 5. Also, many of the polypeptides of Table 5 have conserved domains specifically indicated by start and stop sites. A comparison of the regions of the polypeptides in SEQ ID NO: 2N, wherein N = 1-335 (that is, even SEQ ID NOs: 2, 4, 6, 8 ...760), or of those in Table 5, allows one of skill in the art to identify conserved domain(s) for any of the polypeptides listed or referred to in this disclosure, including those in Tables 4 - 9.

"Complementary" refers to the natural hydrogen bonding by base pairing between purines and pyrimidines. For example, the sequence A-C-G-T (5' -> 3') forms hydrogen bonds with its complements A-C-G-T (5' -> 3') or A-C-G-U (5' -> 3'). Two single-stranded molecules may be considered partially complementary, if only some of the nucleotides bond, or "completely complementary" if all of the nucleotides bond. The degree of complementarity between nucleic acid strands affects the efficiency and strength of the hybridization and amplification reactions. "Fully complementary" refers to the case where bonding occurs between every base pair and its complement in a pair of sequences, and the two sequences have the same number of nucleotides.

The terms "highly stringent" or "highly stringent condition" refer to conditions that permit hybridization of DNA strands whose sequences are highly complementary, wherein these same conditions exclude hybridization of significantly mismatched DNAs. Polynucleotide sequences capable

of hybridizing under stringent conditions with the polynucleotides of the present invention may be, for example, variants of the disclosed polynucleotide sequences, including allelic or splice variants, or sequences that encode orthologs or paralogs of presently disclosed polypeptides. Nucleic acid hybridization methods are disclosed in detail by Kashima et al. (1985) *Nature* 313:402-404, and S
5 Sambrook et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y. ("Sambrook"); and by Haymes et al., "Nucleic Acid Hybridization: A Practical Approach", IRL Press, Washington, D.C. (1985), which references are incorporated herein by reference.

In general, stringency is determined by the temperature, ionic strength, and concentration of
10 denaturing agents (e.g., formamide) used in a hybridization and washing procedure (for a more detailed description of establishing and determining stringency, see below). The degree to which two nucleic acids hybridize under various conditions of stringency is correlated with the extent of their similarity. Thus, similar nucleic acid sequences from a variety of sources, such as within a plant's genome (as in the case of paralogs) or from another plant (as in the case of orthologs) that may perform similar functions
15 can be isolated on the basis of their ability to hybridize with known transcription factor sequences. Numerous variations are possible in the conditions and means by which nucleic acid hybridization can be performed to isolate transcription factor sequences having similarity to transcription factor sequences known in the art and are not limited to those explicitly disclosed herein. Such an approach may be used to isolate polynucleotide sequences having various degrees of similarity with disclosed transcription factor
20 sequences, such as, for example, transcription factors having 60% identity, or more preferably greater than about 70% identity, most preferably 72% or greater identity with disclosed transcription factors.

The term "equivalog" describes members of a set of homologous proteins that are conserved with respect to function since their last common ancestor. Related proteins are grouped into equivalog families, and otherwise into protein families with other hierarchically defined homology types. This
25 definition is provided at the Institute for Genomic Research (TIGR) world wide web (www) website, "tigr.org" under the heading "Terms associated with TIGRFAMs".

The term "variant", as used herein, may refer to polynucleotides or polypeptides, that differ from the presently disclosed polynucleotides or polypeptides, respectively, in sequence from each other, and as set forth below.

30 With regard to polynucleotide variants, differences between presently disclosed polynucleotides and polynucleotide variants are limited so that the nucleotide sequences of the former and the latter are closely similar overall and, in many regions, identical. Due to the degeneracy of the genetic code, differences between the former and latter nucleotide sequences may be silent (i.e., the amino acids encoded by the polynucleotide are the same, and the variant polynucleotide sequence encodes the same
35 amino acid sequence as the presently disclosed polynucleotide. Variant nucleotide sequences may encode different amino acid sequences, in which case such nucleotide differences will result in amino acid substitutions, additions, deletions, insertions, truncations or fusions with respect to the similar disclosed

polynucleotide sequences. These variations result in polynucleotide variants encoding polypeptides that share at least one functional characteristic. The degeneracy of the genetic code also dictates that many different variant polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing.

5 Also within the scope of the invention is a variant of a transcription factor nucleic acid listed in the Sequence Listing, that is, one having a sequence that differs from the one of the polynucleotide sequences in the Sequence Listing, or a complementary sequence, that encodes a functionally equivalent polypeptide (i.e., a polypeptide having some degree of equivalent or similar biological activity) but differs in sequence from the sequence in the Sequence Listing, due to degeneracy in the genetic code.

10 Included within this definition are polymorphisms that may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding polypeptide, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding polypeptide.

“Allelic variant” or “polynucleotide allelic variant” refers to any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and may result in phenotypic polymorphism within populations. Gene mutations may be “silent” or may encode polypeptides having altered amino acid sequence. “Allelic variant” and “polypeptide allelic variant” may also be used with respect to polypeptides, and in this case the term refer to a polypeptide encoded by an allelic variant of a gene.

20 “Splice variant” or “polynucleotide splice variant” as used herein refers to alternative forms of RNA transcribed from a gene. Splice variation naturally occurs as a result of alternative sites being spliced within a single transcribed RNA molecule or between separately transcribed RNA molecules, and may result in several different forms of mRNA transcribed from the same gene. This, splice variants may encode polypeptides having different amino acid sequences, which may or may not have similar functions in the organism. “Splice variant” or “polypeptide splice variant” may also refer to a polypeptide encoded by a splice variant of a transcribed mRNA.

25 As used herein, “polynucleotide variants” may also refer to polynucleotide sequences that encode paralogs and orthologs of the presently disclosed polypeptide sequences. “Polypeptide variants” may refer to polypeptide sequences that are paralogs and orthologs of the presently disclosed polypeptide sequences.

30 Differences between presently disclosed polypeptides and polypeptide variants are limited so that the sequences of the former and the latter are closely similar overall and, in many regions, identical. Presently disclosed polypeptide sequences and similar polypeptide variants may differ in amino acid sequence by one or more substitutions, additions, deletions, fusions and truncations, which may be present in any combination. These differences may produce silent changes and result in a functionally equivalent transcription factor. Thus, it will be readily appreciated by those of skill in the art, that any of a variety of polynucleotide sequences is capable of encoding the transcription factors and transcription

factor homolog polypeptides of the invention. A polypeptide sequence variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties. Deliberate amino acid substitutions may thus be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the functional or biological activity of the transcription factor is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, positively charged amino acids may include lysine and arginine, and amino acids with uncharged polar head groups having similar hydrophilicity values may include leucine, isoleucine, and valine; glycine and alanine; asparagine and glutamine; serine and threonine; and phenylalanine and tyrosine (for more detail on conservative substitutions, see Table 2).

More rarely, a variant may have "non-conservative" changes, e.g., replacement of a glycine with a tryptophan. Similar minor variations may also include amino acid deletions or insertions, or both. Related polypeptides may comprise, for example, additions and/or deletions of one or more N-linked or O-linked glycosylation sites, or an addition and/or a deletion of one or more cysteine residues. Guidance in determining which and how many amino acid residues may be substituted, inserted or deleted without abolishing functional or biological activity may be found using computer programs well known in the art, for example, DNASTAR software (see USPN 5,840,544).

"Ligand" refers to any molecule, agent, or compound that will bind specifically to a complementary site on a nucleic acid molecule or protein. Such ligands stabilize or modulate the activity of nucleic acid molecules or proteins of the invention and may be composed of at least one of the following: inorganic and organic substances including nucleic acids, proteins, carbohydrates, fats, and lipids.

"Modulates" refers to a change in activity (biological, chemical, or immunological) or lifespan resulting from specific binding between a molecule and either a nucleic acid molecule or a protein.

The term "plant" includes whole plants, shoot vegetative organs/structures (e.g., leaves, stems and tubers), roots, flowers and floral organs/structures (e.g., bracts, sepals, petals, stamens, carpels, anthers and ovules), seed (including embryo, endosperm, and seed coat) and fruit (the mature ovary), plant tissue (e.g., vascular tissue, ground tissue, and the like) and cells (e.g., guard cells, egg cells, and the like), and progeny of same. The class of plants that can be used in the method of the invention is generally as broad as the class of higher and lower plants amenable to transformation techniques, including angiosperms (monocotyledonous and dicotyledonous plants), gymnosperms, ferns, horsetails, psilophytes, lycophytes, bryophytes, and multicellular algae. (See for example, Figure 1, adapted from Daly et al. (2001) *Plant Physiol.* 127: 1328-1333; Figure 2, adapted from Ku et al. (2000) *Proc. Natl. Acad. Sci.* 97: 9121-9126; and see also Tudge in *The Variety of Life*, Oxford University Press, New York, NY (2000) pp. 547-606).

A "transgenic plant" refers to a plant that contains genetic material not found in a wild-type plant of the same species, variety or cultivar. The genetic material may include a transgene, an insertional mutagenesis event (such as by transposon or T-DNA insertional mutagenesis), an activation tagging

sequence, a mutated sequence, a homologous recombination event or a sequence modified by chimeraplasty. Typically, the foreign genetic material has been introduced into the plant by human manipulation, but any method can be used as one of skill in the art recognizes.

A transgenic plant may contain an expression vector or cassette. The expression cassette typically comprises a polypeptide-encoding sequence operably linked (i.e., under regulatory control of) to appropriate inducible or constitutive regulatory sequences that allow for the expression of polypeptide. The expression cassette can be introduced into a plant by transformation or by breeding after transformation of a parent plant. A plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cells or any other plant material, e.g., a plant explant, as well as to progeny thereof, and to *in vitro* systems that mimic biochemical or cellular components or processes in a cell.

"Control plant" refers to a plant that serves as a standard of comparison for testing the results of a treatment or genetic alteration, or the degree of altered expression of a gene or gene product. Examples of control plants include plants that are untreated, or genetically unaltered (i.e., wild-type).

"Wild type", as used herein, refers to a cell, tissue or plant that has not been genetically modified to knock out or overexpress one or more of the presently disclosed transcription factors. Wild-type cells, tissue or plants may be used as controls to compare levels of expression and the extent and nature of trait modification with cells, tissue or plants in which transcription factor expression is altered or ectopically expressed, e.g., in that it has been knocked out or overexpressed.

"Fragment", with respect to a polynucleotide, refers to a clone or any part of a polynucleotide molecule that retains a usable, functional characteristic. Useful fragments include oligonucleotides and polynucleotides that may be used in hybridization or amplification technologies or in the regulation of replication, transcription or translation. A polynucleotide fragment refers to any subsequence of a polynucleotide, typically, of at least about 9 consecutive nucleotides, preferably at least about 30 nucleotides, more preferably at least about 50 nucleotides, of any of the sequences provided herein. Exemplary polynucleotide fragments are the first sixty consecutive nucleotides of the transcription factor polynucleotides listed in the Sequence Listing. Exemplary fragments also include fragments that comprise a region that encodes a conserved domain of a transcription factor.

Fragments may also include subsequences of polypeptides and protein molecules, or a subsequence of the polypeptide. Fragments may have uses in that they may have antigenic potential. In some cases, the fragment or domain is a subsequence of the polypeptide which performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA-binding site or domain that binds to a DNA promoter region, an activation domain, or a domain for protein-protein interactions, and may initiate transcription. Fragments can vary in size from as few as 3 amino acids to the full length of the intact polypeptide, but are preferably at least about 30 amino acids in length and more preferably at least about 60 amino acids

in length. Exemplary polypeptide fragments are the first twenty consecutive amino acids of a mammalian protein encoded by are the first twenty consecutive amino acids of the transcription factor polypeptides listed in the Sequence Listing. Exemplary fragments also include fragments that comprise a conserved domain of a transcription factor, for example, amino acid residues 11-80 of G47 (SEQ ID NO: 12), as
5 noted in Table 5.

The invention also encompasses production of DNA sequences that encode transcription factors and transcription factor derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to
10 introduce mutations into a sequence encoding transcription factors or any fragment thereof.

"Derivative" refers to the chemical modification of a nucleic acid molecule or amino acid sequence. Chemical modifications can include replacement of hydrogen by an alkyl, acyl, or amino group or glycosylation, pegylation, or any similar process that retains or enhances biological activity or lifespan of the molecule or sequence.

15 A "trait" refers to a physiological, morphological, biochemical, or physical characteristic of a plant or particular plant material or cell. In some instances, this characteristic is visible to the human eye, such as seed or plant size, or can be measured by biochemical techniques, such as detecting the protein, starch, or oil content of seed or leaves, or by observation of a metabolic or physiological process, e.g. by measuring uptake of carbon dioxide, or by the observation of the expression level of a gene or genes, e.g.,
20 by employing Northern analysis, RT-PCR, microarray gene expression assays, or reporter gene expression systems, or by agricultural observations such as stress tolerance, yield, or pathogen tolerance. Any technique can be used to measure the amount of, comparative level of, or difference in any selected chemical compound or macromolecule in the transgenic plants, however.

"Trait modification" refers to a detectable difference in a characteristic in a plant ectopically
25 expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild-type plant. In some cases, the trait modification can be evaluated quantitatively. For example, the trait modification can entail at least about a 2% increase or decrease in an observed trait (difference), at least a 5% difference, at least about a 10% difference, at least about a 20% difference, at least about a 30%, at least about a 50%, at least about a 70%, or at least about a 100%, or an even greater difference
30 compared with a wild-type plant. It is known that there can be a natural variation in the modified trait. Therefore, the trait modification observed entails a change of the normal distribution of the trait in the plants compared with the distribution observed in wild-type plants.

The term "transcript profile" refers to the expression levels of a set of genes in a cell in a particular state, particularly by comparison with the expression levels of that same set of genes in a cell
35 of the same type in a reference state. For example, the transcript profile of a particular transcription factor in a suspension cell is the expression levels of a set of genes in a cell overexpressing that transcription factor compared with the expression levels of that same set of genes in a suspension cell that has normal

levels of that transcription factor. The transcript profile can be presented as a list of those genes whose expression level is significantly different between the two treatments, and the difference ratios. . Differences and similarities between expression levels may also be evaluated and calculated using statistical and clustering methods.

5 “Ectopic expression or altered expression” in reference to a polynucleotide indicates that the pattern of expression in, e.g., a transgenic plant or plant tissue, is different from the expression pattern in a wild-type plant or a reference plant of the same species. The pattern of expression may also be compared with a reference expression pattern in a wild-type plant of the same species. For example, the polynucleotide or polypeptide is expressed in a cell or tissue type other than a cell or tissue type in which
10 the sequence is expressed in the wild-type plant, or by expression at a time other than at the time the sequence is expressed in the wild-type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild-type plant. The term also refers to altered expression patterns that are produced by lowering the levels of expression to below the detection level or completely abolishing
15 expression. The resulting expression pattern can be transient or stable, constitutive or inducible. In reference to a polypeptide, the term "ectopic expression or altered expression" further may relate to altered activity levels resulting from the interactions of the polypeptides with exogenous or endogenous modulators or from interactions with factors or as a result of the chemical modification of the polypeptides.

20 The term “overexpression” as used herein refers to a greater expression level of a gene in a plant, plant cell or plant tissue, compared to expression in a wild-type plant, cell or tissue, at any developmental or temporal stage for the gene. Overexpression can occur when, for example, the genes encoding one or more transcription factors are under the control of a strong expression signal, such as one of the promoters described herein (e.g., the cauliflower mosaic virus 35S transcription initiation region).
25 Overexpression may occur throughout a plant or in specific tissues of the plant, depending on the promoter used, as described below.

 Overexpression may take place in plant cells normally lacking expression of polypeptides functionally equivalent or identical to the present transcription factors. Overexpression may also occur in plant cells where endogenous expression of the present transcription factors or functionally equivalent
30 molecules normally occurs, but such normal expression is at a lower level.. Overexpression thus results in a greater than normal production, or “overproduction” of the transcription factor in the plant, cell or tissue.

 The term “phase change” refers to a plant's progression from embryo to adult, and, by some definitions, the transition wherein flowering plants gain reproductive competency. It is believed that
35 phase change occurs either after a certain number of cell divisions in the shoot apex of a developing plant, or when the shoot apex achieves a particular distance from the roots. Thus, altering the timing of phase changes may affect a plant's size, which, in turn, may affect yield and biomass.

"Tolerance" results from specific, heritable characteristics of a host plant that allow a pathogen to develop and multiply in the host while the host, either by lacking receptor sites for, or by inactivating or compensating for the irritant secretions of the pathogen, still manages to thrive or, in the case of crop plants, produce a good crop. Tolerant plants are susceptible to the pathogen but are not killed by it and generally show little damage from the pathogen (Agrios (1988) Plant Pathology, 3rd ed. Academic Press, N.Y., p. 129).

"Resistance", also referred to as "true resistance", results when a plant contains one or more genes that make the plant and a potential pathogen more or less incompatible with each other, either because of a lack of chemical recognition between the host and the pathogen, or because the host plant can defend itself against the pathogen by defense mechanisms already present or activated in response to infection (Agrios (1988)) Plant Pathology, 3rd ed. Academic Press, N.Y., p. 125).

A "sample" with respect to a material containing nucleic acid molecules may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; genomic DNA, RNA, or cDNA in solution or bound to a substrate; a cell; a tissue; a tissue print; a forensic sample; and the like. In this context "substrate" refers to any rigid or semi-rigid support to which nucleic acid molecules or proteins are bound and includes membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, capillaries or other tubing, plates, polymers, and microparticles with a variety of surface forms including wells, trenches, pins, channels and pores. A substrate may also refer to a reactant in a chemical or biological reaction, or a substance acted upon (e.g., by an enzyme).

"Substantially purified" refers to nucleic acid molecules or proteins that are removed from their natural environment and are isolated or separated, and are at least about 60% free, preferably about 75% free, and most preferably about 90% free, from other components with which they are naturally associated.

Traits That May Be Modified in Overexpressing or Knock-out Plants

Trait modifications of particular interest include those to seed (such as embryo or endosperm), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought, water saturation, radiation and ozone; improved tolerance to microbial, fungal or viral diseases; improved tolerance to pest infestations, including insects, nematodes, mollicutes, parasitic higher plants or the like; decreased herbicide sensitivity; improved tolerance of heavy metals or enhanced ability to take up heavy metals; improved growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotype that can be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenillipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition.

Physical plant characteristics that can be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves, inflorescences, and roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that can be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, osmotic sensitivity to soluble sugar concentrations, biomass or transpiration characteristics, as well as plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

Transcription Factors Modify Expression of Endogenous Genes

Expression of genes that encode transcription factors that modify expression of endogenous genes, polynucleotides, and proteins are well known in the art. In addition, transgenic plants comprising isolated polynucleotides encoding transcription factors may also modify expression of endogenous genes, polynucleotides, and proteins. Examples include Peng et al. (1997, *Genes Development* 11: 3194-3205) and Peng et al. (1999, *Nature*, 400: 256-261). In addition, many others have demonstrated that an *Arabidopsis* transcription factor expressed in an exogenous plant species elicits the same or very similar phenotypic response. See, for example, Fu et al. (2001, *Plant Cell* 13: 1791-1802); Nandi et al. (2000, *Curr. Biol.* 10: 215-218); Coupland (1995, *Nature* 377: 482-483); and Weigel and Nilsson (1995, *Nature* 377: 482-500).

In another example, Mandel et al. (1992, *Cell* 71:133-143) and Suzuki et al. (2001, *Plant J.* 28: 409-418) teach that a transcription factor expressed in another plant species elicits the same or very similar phenotypic response of the endogenous sequence, as often predicted in earlier studies of *Arabidopsis* transcription factors in *Arabidopsis* (see Mandel et al. 1992, *supra*; Suzuki et al. 2001, *supra*).

Other examples include Müller et al. (2001, *Plant J.* 28: 169-179); Kim et al. (2001, *Plant J.* 25: 247-259); Kyoizuka and Shimamoto (2002, *Plant Cell Physiol.* 43: 130-135); Boss and Thomas (2002, *Nature*, 416: 847-850); He et al. (2000, *Transgenic Res.* 9: 223-227); and Robson et al. (2001, *Plant J.* 28: 619-631).

In yet another example, Gilmour et al. (1998, *Plant J.* 16: 433-442) teach an *Arabidopsis* AP2 transcription factor, CBF1 (SEQ ID NO: 2239), which, when overexpressed in transgenic plants, increases plant freezing tolerance. Jaglo et al. (2001, *Plant Physiol.* 127: 910-917) further identified sequences in *Brassica napus* which encode CBF-like genes and that transcripts for these genes accumulated rapidly in response to low temperature. Transcripts encoding CBF-like proteins were also found to accumulate rapidly in response to low temperature in wheat, as well as in tomato. An alignment of the CBF proteins from *Arabidopsis*, *B. napus*, wheat, rye, and tomato revealed the presence of conserved consecutive amino acid residues, PKK/RPAGR_xKF_xETRHP and DSAWR, that bracket the

AP2/EREBP DNA binding domains of the proteins and distinguish them from other members of the AP2/EREBP protein family. (See Jaglo et al. *supra*.)

Transcription factors mediate cellular responses and control traits through altered expression of genes containing cis-acting nucleotide sequences that are targets of the introduced transcription factor. It is well appreciated in the Art that the effect of a transcription factor on cellular responses or a cellular trait is determined by the particular genes whose expression is either directly or indirectly (e.g., by a cascade of transcription factor binding events and transcriptional changes) altered by transcription factor binding. In a global analysis of transcription comparing a standard condition with one in which a transcription factor is overexpressed, the resulting transcript profile associated with transcription factor overexpression is related to the trait or cellular process controlled by that transcription factor. For example, the PAP2 gene (and other genes in the MYB family) have been shown to control anthocyanin biosynthesis through regulation of the expression of genes known to be involved in the anthocyanin biosynthetic pathway (Bruce et al. (2000) *Plant Cell* 12: 65-79; and Borevitz et al. (2000) *Plant Cell* 12: 2383-2393). Further, global transcript profiles have been used successfully as diagnostic tools for specific cellular states (e.g., cancerous vs. non-cancerous; Bhattacharjee et al. (2001) *Proc. Natl. Acad. Sci. USA* 98: 13790-13795; and Xu et al. (2001) *Proc Natl Acad Sci, USA* 98: 15089-15094). Consequently, it is evident to one skilled in the art that similarity of transcript profile upon overexpression of different transcription factors would indicate similarity of transcription factor function.

Polypeptides and Polynucleotides of the Invention

The present invention provides, among other things, transcription factors (TFs), and transcription factor homolog polypeptides, and isolated or recombinant polynucleotides encoding the polypeptides, or novel sequence variant polypeptides or polynucleotides encoding novel variants of transcription factors derived from the specific sequences provided here. These polypeptides and polynucleotides may be employed to modify a plant's characteristics.

Exemplary polynucleotides encoding the polypeptides of the invention were identified in the *Arabidopsis thaliana* GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. In addition, further exemplary polynucleotides encoding the polypeptides of the invention were identified in the plant GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. Polynucleotide sequences meeting such criteria were confirmed as transcription factors.

Additional polynucleotides of the invention were identified by screening *Arabidopsis thaliana* and/or other plant cDNA libraries with probes corresponding to known transcription factors under low

stringency hybridization conditions. Additional sequences, including full length coding sequences were subsequently recovered by the rapid amplification of cDNA ends (RACE) procedure, using a commercially available kit according to the manufacturer's instructions. Where necessary, multiple rounds of RACE are performed to isolate 5' and 3' ends. The full-length cDNA was then recovered by a routine end-to-end polymerase chain reaction (PCR) using primers specific to the isolated 5' and 3' ends. Exemplary sequences are provided in the Sequence Listing.

The polynucleotides of the invention can be or were ectopically expressed in overexpressor or knockout plants and the changes in the characteristic(s) or trait(s) of the plants observed. Therefore, the polynucleotides and polypeptides can be employed to improve the characteristics of plants.

The polynucleotides of the invention can be or were ectopically expressed in overexpressor plant cells and the changes in the expression levels of a number of genes, polynucleotides, and/or proteins of the plant cells observed. Therefore, the polynucleotides and polypeptides can be employed to change expression levels of a genes, polynucleotides, and/or proteins of plants.

Producing Polypeptides

The polynucleotides of the invention include sequences that encode transcription factors and transcription factor homolog polypeptides and sequences complementary thereto, as well as unique fragments of coding sequence, or sequence complementary thereto. Such polynucleotides can be, e.g., DNA or RNA, e.g., mRNA, cRNA, synthetic RNA, genomic DNA, cDNA synthetic DNA, oligonucleotides, etc. The polynucleotides are either double-stranded or single-stranded, and include either, or both sense (i.e., coding) sequences and antisense (i.e., non-coding, complementary) sequences. The polynucleotides include the coding sequence of a transcription factor, or transcription factor homolog polypeptide, in isolation, in combination with additional coding sequences (e.g., a purification tag, a localization signal, as a fusion-protein, as a pre-protein, or the like), in combination with non-coding sequences (e.g., introns or inteins, regulatory elements such as promoters, enhancers, terminators, and the like), and/or in a vector or host environment in which the polynucleotide encoding a transcription factor or transcription factor homolog polypeptide is an endogenous or exogenous gene.

A variety of methods exist for producing the polynucleotides of the invention. Procedures for identifying and isolating DNA clones are well known to those of skill in the art, and are described in, e.g., Berger and Kimmel, Guide to Molecular Cloning Techniques, *Methods in Enzymology*, vol. 152 Academic Press, Inc., San Diego, CA ("Berger"); Sambrook et al. Molecular Cloning - A Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989 ("Sambrook") and Current Protocols in Molecular Biology, Ausubel et al. eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 2000) ("Ausubel").

Alternatively, polynucleotides of the invention, can be produced by a variety of in vitro amplification methods adapted to the present invention by appropriate selection of specific or degenerate

primers. Examples of protocols sufficient to direct persons of skill through in vitro amplification methods, including the polymerase chain reaction (PCR) the ligase chain reaction (LCR), Qbeta-replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the invention are found in Berger (supra), Sambrook (supra), and

- 5 Ausubel (supra), as well as Mullis et al. (1987) PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, CA (1990) (Innis). Improved methods for cloning in vitro amplified nucleic acids are described in Wallace et al. US Pat. No. 5,426,039. Improved methods for amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) *Nature* 369: 684-685 and the references cited therein, in which PCR amplicons of up to 40kb are generated. One of skill will
- 10 appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR expansion and sequencing using reverse transcriptase and a polymerase. See, e.g., Ausubel, Sambrook and Berger, all *supra*.

- Alternatively, polynucleotides and oligonucleotides of the invention can be assembled from fragments produced by solid-phase synthesis methods. Typically, fragments of up to approximately 100
- 15 bases are individually synthesized and then enzymatically or chemically ligated to produce a desired sequence, e.g., a polynucleotide encoding all or part of a transcription factor. For example, chemical synthesis using the phosphoramidite method is described, e.g., by Beaucage et al. (1981) *Tetrahedron Letters* 22: 1859-1869; and Matthes et al. (1984) *EMBO J.* 3: 801-805. According to such methods, oligonucleotides are synthesized, purified, annealed to their complementary strand, ligated and then
- 20 optionally cloned into suitable vectors. And if so desired, the polynucleotides and polypeptides of the invention can be custom ordered from any of a number of commercial suppliers.

Homologous Sequences

- Sequences homologous, i.e., that share significant sequence identity or similarity, to those
- 25 provided in the Sequence Listing, derived from *Arabidopsis thaliana* or from other plants of choice, are also an aspect of the invention. Homologous sequences can be derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn (maize), potato, cotton, rice, rape, oilseed rape (including canola), sunflower, alfalfa, clover, sugarcane, and turf; or fruits and vegetables, such as banana, blackberry,
- 30 blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, pumpkin, spinach, squash, sweet corn, tobacco, tomato, tomatillo, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, Brussels sprouts, and kohlrabi). Other crops, including fruits and vegetables, whose phenotype can be changed and which
- 35 comprise homologous sequences include barley; rye; millet; sorghum; currant; avocado; citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries; nuts such as the walnut and peanut; endive; leek; roots such as arrowroot, beet, cassava, turnip, radish, yam, and sweet potato; and beans. The

homologous sequences may also be derived from woody species, such as pine, poplar and eucalyptus, or mint or other labiates. In addition, homologous sequences may be derived from plants that are evolutionarily-related to crop plants, but which may not have yet been used as crop plants. Examples include deadly nightshade (*Atropa belladonna*), related to tomato; jimson weed (*Datura stramonium*),
5 related to peyote; and teosinte (*Zea* species), related to corn (maize).

Orthologs and Paralogs

Homologous sequences as described above can comprise orthologous or paralogous sequences. Several different methods are known by those of skill in the art for identifying and defining these
10 functionally homologous sequences. Three general methods for defining orthologs and paralogs are described; an ortholog, paralog or homolog may be identified by one or more of the methods described below.

Orthologs and paralogs are evolutionarily related genes that have similar sequence and similar functions. Orthologs are structurally related genes in different species that are derived by a speciation
15 event. Paralogs are structurally related genes within a single species that are derived by a duplication event.

Within a single plant species, gene duplication may cause two copies of a particular gene, giving rise to two or more genes with similar sequence and often similar function known as paralogs. A paralog is therefore a similar gene formed by duplication within the same species. Paralogs typically cluster
20 together or in the same clade (a group of similar genes) when a gene family phylogeny is analyzed using programs such as CLUSTAL (Thompson et al. (1994) *Nucleic Acids Res.* 22: 4673-4680; Higgins et al. (1996) *Methods Enzymol.* 266: 383-402). Groups of similar genes can also be identified with pair-wise BLAST analysis (Feng and Doolittle (1987) *J. Mol. Evol.* 25: 351-360). For example, a clade of very similar MADS domain transcription factors from *Arabidopsis* all share a common function in flowering
25 time (Ratcliffe et al. (2001) *Plant Physiol.* 126: 122-132), and a group of very similar AP2 domain transcription factors from *Arabidopsis* are involved in tolerance of plants to freezing (Gilmour et al. (1998) *Plant J.* 16: 433-442). Analysis of groups of similar genes with similar function that fall within one clade can yield sub-sequences that are particular to the clade. These sub-sequences, known as
30 consensus sequences, can not only be used to define the sequences within each clade, but define the functions of these genes; genes within a clade may contain paralogous sequences, or orthologous sequences that share the same function (see also, for example, Mount (2001), in Bioinformatics: Sequence and Genome Analysis Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, page 543.)

Speciation, the production of new species from a parental species, can also give rise to two or
35 more genes with similar sequence and similar function. These genes, termed orthologs, often have an identical function within their host plants and are often interchangeable between species without losing function. Because plants have common ancestors, many genes in any plant species will have a

corresponding orthologous gene in another plant species. Once a phylogenetic tree for a gene family of one species has been constructed using a program such as CLUSTAL (Thompson et al. (1994) *Nucleic Acids Res.* 22: 4673-4680; Higgins et al. (1996) *supra*) potential orthologous sequences can be placed into the phylogenetic tree and their relationship to genes from the species of interest can be determined.

- 5 Orthologous sequences can also be identified by a reciprocal BLAST strategy. Once an orthologous sequence has been identified, the function of the ortholog can be deduced from the identified function of the reference sequence.

Transcription factor gene sequences are conserved across diverse eukaryotic species lines (Goodrich et al. (1993) *Cell* 75: 519-530; Lin et al. (1991) *Nature* 353: 569-571; Sadowski et al. (1988) *Nature* 335: 563-564). Plants are no exception to this observation; diverse plant species possess

10 transcription factors that have similar sequences and functions.

Orthologous genes from different organisms have highly conserved functions, and very often essentially identical functions (Lee et al. (2002) *Genome Res.* 12: 493-502; Remm et al. (2001) *J. Mol. Biol.* 314: 1041-1052). Paralogous genes, which have diverged through gene duplication, may retain

15 similar functions of the encoded proteins. In such cases, paralogs can be used interchangeably with respect to certain embodiments of the instant invention (for example, transgenic expression of a coding sequence). An example of such highly related paralogs is the CBF family, with three well-defined members in *Arabidopsis* and at least one ortholog in *Brassica napus* (SEQ ID NOs: 2238, 2240, 2242, and 2244, respectively), all of which control pathways involved in both freezing and drought stress

20 (Gilmour et al. (1998) *Plant J.* 16: 433-442; Jaglo et al. (1998) *Plant Physiol.* 127: 910-917).

The following references represent a small sampling of the many studies that demonstrate that conserved transcription factor genes from diverse species are likely to function similarly (i.e., regulate similar target sequences and control the same traits), and that transcription factors may be transformed into diverse species to confer or improve traits.

- 25 (1) The *Arabidopsis* NPR1 gene regulates systemic acquired resistance (SAR); over-expression of NPR1 leads to enhanced resistance in *Arabidopsis*. When either *Arabidopsis* NPR1 or the rice NPR1 ortholog was overexpressed in rice (which, as a monocot, is diverse from *Arabidopsis*), challenge with the rice bacterial blight pathogen *Xanthomonas oryzae* pv. *Oryzae*, the transgenic plants displayed enhanced resistance (Chern et al. (2001) *Plant J.* 27: 101-113). NPR1 acts through activation of
- 30 expression of transcription factor genes, such as TGA2 (Fan and Dong (2002) *Plant Cell* 14: 1377-1389).

- (2) E2F genes are involved in transcription of plant genes for proliferating cell nuclear antigen (PCNA). Plant E2Fs share a high degree of similarity in amino acid sequence between monocots and dicots, and are even similar to the conserved domains of the animal E2Fs. Such conservation indicates a functional similarity between plant and animal E2Fs. E2F transcription factors that regulate meristem
- 35 development act through common cis-elements, and regulate related (PCNA) genes (Kosugi and Ohashi, (2002) *Plant J.* 29: 45-59).

(3) The ABI5 gene (ABA insensitive 5) encodes a basic leucine zipper factor required for ABA response in the seed and vegetative tissues. Co-transformation experiments with ABI5 cDNA constructs in rice protoplasts resulted in specific transactivation of the ABA-inducible wheat, *Arabidopsis*, bean, and barley promoters. These results demonstrate that sequentially similar ABI5 transcription factors are key targets of a conserved ABA signaling pathway in diverse plants. (Gampala et al. (2001) *J. Biol. Chem.* 277: 1689-1694).

(4) Sequences of three *Arabidopsis* GAMYB-like genes were obtained on the basis of sequence similarity to GAMYB genes from barley, rice, and *L. temulentum*. These three *Arabidopsis* genes were determined to encode transcription factors (AtMYB33, AtMYB65, and AtMYB101) and could substitute for a barley GAMYB and control alpha-amylase expression (Gocal et al. (2001) *Plant Physiol.* 127: 1682-1693).

(5) The floral control gene LEAFY from *Arabidopsis* can dramatically accelerate flowering in numerous dicotyledonous plants. Constitutive expression of *Arabidopsis* LEAFY also caused early flowering in transgenic rice (a monocot), with a heading date that was 26-34 days earlier than that of wild-type plants. These observations indicate that floral regulatory genes from *Arabidopsis* are useful tools for heading date improvement in cereal crops (He et al. (2000) *Transgenic Res.* 9: 223-227).

(6) Bioactive gibberellins (GAs) are essential endogenous regulators of plant growth. GA signaling tends to be conserved across the plant kingdom. GA signaling is mediated via GAI, a nuclear member of the GRAS family of plant transcription factors. *Arabidopsis* GAI has been shown to function in rice to inhibit gibberellin response pathways (Fu et al. (2001) *Plant Cell* 13: 1791-1802).

(7) The *Arabidopsis* gene SUPERMAN (SUP), encodes a putative transcription factor that maintains the boundary between stamens and carpels. By over-expressing *Arabidopsis* SUP in rice, the effect of the gene's presence on whorl boundaries was shown to be conserved. This demonstrated that SUP is a conserved regulator of floral whorl boundaries and affects cell proliferation (Nandi et al. (2000) *Curr. Biol.* 10: 215-218).

(8) Maize, petunia and *Arabidopsis* myb transcription factors that regulate flavonoid biosynthesis are very genetically similar and affect the same trait in their native species, therefore sequence and function of these myb transcription factors correlate with each other in these diverse species (Borevitz et al. (2000) *Plant Cell* 12: 2383-2394).

(9) Wheat reduced height-1 (Rht-B1/Rht-D1) and maize dwarf-8 (d8) genes are orthologs of the *Arabidopsis* gibberellin insensitive (GAI) gene. Both of these genes have been used to produce dwarf grain varieties that have improved grain yield. These genes encode proteins that resemble nuclear transcription factors and contain an SH2-like domain, indicating that phosphotyrosine may participate in gibberellin signaling. Transgenic rice plants containing a mutant GAI allele from *Arabidopsis* have been shown to produce reduced responses to gibberellin and are dwarfed, indicating that mutant GAI orthologs could be used to increase yield in a wide range of crop species (Peng et al. (1999) *Nature* 400: 256-261).

Transcription factors that are homologous to the listed sequences will typically share, in at least one conserved domain, at least about 70% amino acid sequence identity, and with regard to zinc finger transcription factors, at least about 50% amino acid sequence identity. More closely related transcription factors can share at least about 70%, or about 75% or about 80% or about 90% or about 95% or about 98% or more sequence identity with the listed sequences, or with the listed sequences but excluding or outside a known consensus sequence or consensus DNA-binding site, or with the listed sequences excluding one or all conserved domain. Factors that are most closely related to the listed sequences share, e.g., at least about 85%, about 90% or about 95% or more % sequence identity to the listed sequences, or to the listed sequences but excluding or outside a known consensus sequence or consensus DNA-binding site or outside one or all conserved domain. At the nucleotide level, the sequences will typically share at least about 40% nucleotide sequence identity, preferably at least about 50%, about 60%, about 70% or about 80% sequence identity, and more preferably about 85%, about 90%, about 95% or about 97% or more sequence identity to one or more of the listed sequences, or to a listed sequence but excluding or outside a known consensus sequence or consensus DNA-binding site, or outside one or all conserved domain. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein. Conserved domains within a transcription factor family may exhibit a higher degree of sequence homology, such as at least 65% amino acid sequence identity including conservative substitutions, and preferably at least 80% sequence identity, and more preferably at least 85%, or at least about 86%, or at least about 87%, or at least about 88%, or at least about 90%, or at least about 95%, or at least about 98% sequence identity. Transcription factors that are homologous to the listed sequences should share at least 30%, or at least about 60%, or at least about 75%, or at least about 80%, or at least about 90%, or at least about 95% amino acid sequence identity over the entire length of the polypeptide or the homolog.

Percent identity can be determined electronically, e.g., by using the MEGALIGN program (DNASTAR, Inc. Madison, Wis.). The MEGALIGN program can create alignments between two or more sequences according to different methods, for example, the clustal method. (See, for example, Higgins and Sharp (1988) *Gene* 73: 237-244.) The clustal algorithm groups sequences into clusters by examining the distances between all pairs. The clusters are aligned pairwise and then in groups. Other alignment algorithms or programs may be used, including FASTA, BLAST, or ENTREZ, FASTA and BLAST, and which may be used to calculate percent similarity. These are available as a part of the GCG sequence analysis package (University of Wisconsin, Madison, Wis.), and can be used with or without default settings. ENTREZ is available through the National Center for Biotechnology Information. In one embodiment, the percent identity of two sequences can be determined by the GCG program with a gap weight of 1, e.g., each amino acid gap is weighted as if it were a single amino acid or nucleotide mismatch between the two sequences (see USPN 6,262,333).

Other techniques for alignment are described in *Methods in Enzymology*, vol. 266, Computer Methods for Macromolecular Sequence Analysis (1996), ed. Doolittle, Academic Press, Inc., San Diego, Calif., USA. Preferably, an alignment program that permits gaps in the sequence is utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments (see 5 Shpaer (1997) *Methods Mol. Biol.* 70: 173-187). Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer. This approach improves ability to pick up distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Nucleic acid- 10 encoded amino acid sequences can be used to search both protein and DNA databases.

The percentage similarity between two polypeptide sequences, e.g., sequence A and sequence B, is calculated by dividing the length of sequence A, minus the number of gap residues in sequence A, minus the number of gap residues in sequence B, into the sum of the residue matches between sequence A and sequence B, times one hundred. Gaps of low or of no similarity between the two amino acid 15 sequences are not included in determining percentage similarity. Percent identity between polynucleotide sequences can also be counted or calculated by other methods known in the art, e.g., the Jotun Hein method. (See, e.g., Hein (1990) *Methods Enzymol.* 183: 626-645.) Identity between sequences can also be determined by other methods known in the art, e.g., by varying hybridization conditions (see US Patent Application No. 20010010913).

The percent identity between two conserved domains of a transcription factor DNA-binding domain consensus polypeptide sequence can be as low as 16%, as exemplified in the case of GATA1 family of eukaryotic Cys₂/Cys₂-type zinc finger transcription factors. The DNA-binding domain consensus polypeptide sequence of the GATA1 family is CX₂CX₁₇CX₂C, where X is any amino acid residue. (See, for example, Takatsuji, supra.) Other examples of such conserved consensus polypeptide 25 sequences with low overall percent sequence identity are well known to those of skill in the art.

Thus, the invention provides methods for identifying a sequence similar or paralogous or orthologous or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant phenotype or gene function with a sequence. In the methods, a sequence 30 database is provided (locally or across an internet or intranet) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

In addition, one or more polynucleotide sequences or one or more polypeptides encoded by the polynucleotide sequences may be used to search against a BLOCKS (Bairoch et al. (1997) *Nucleic Acids Res.* 25: 217-221), PFAM, and other databases which contain previously identified and annotated motifs, 35 sequences and gene functions. Methods that search for primary sequence patterns with secondary structure gap penalties (Smith et al. (1992) *Protein Engineering* 5: 35-51) as well as algorithms such as Basic Local Alignment Search Tool (BLAST; Altschul (1993) *J. Mol. Evol.* 36: 290-300; Altschul et al.

(1990) *supra*), BLOCKS (Henikoff and Henikoff (1991) *Nucleic Acids Res.* 19: 6565-6572), Hidden Markov Models (HMM; Eddy (1996) *Curr. Opin. Str. Biol.* 6: 361-365; Sonnhammer et al. (1997) *Proteins* 28: 405-420), and the like, can be used to manipulate and analyze polynucleotide and polypeptide sequences encoded by polynucleotides. These databases, algorithms and other methods are well known in the art and are described in Ausubel et al. (1997; Short Protocols in Molecular Biology, John Wiley & Sons, New York, NY, unit 7.7) and in Meyers (1995; Molecular Biology and Biotechnology, Wiley VCH, New York, NY, p 856-853).

A further method for identifying or confirming that specific homologous sequences control the same function is by comparison of the transcript profile(s) obtained upon overexpression or knockout of two or more related transcription factors. Since transcript profiles are diagnostic for specific cellular states, one skilled in the art will appreciate that genes that have a highly similar transcript profile (e.g., with greater than 50% regulated transcripts in common, more preferably with greater than 70% regulated transcripts in common, most preferably with greater than 90% regulated transcripts in common) will have highly similar functions. Fowler et al. (2002) *Plant Cell* 14: 1675-79) have shown that three paralogous AP2 family genes (CBF1, CBF2 and CBF3), each of which is induced upon cold treatment, and each of which can condition improved freezing tolerance, have highly similar transcript profiles. Once a transcription factor has been shown to provide a specific function, its transcript profile becomes a diagnostic tool to determine whether putative paralogs or orthologs have the same function.

Furthermore, methods using manual alignment of sequences similar or homologous to one or more polynucleotide sequences or one or more polypeptides encoded by the polynucleotide sequences may be used to identify regions of similarity and conserved domains. Such manual methods are well-known of those of skill in the art and can include, for example, comparisons of tertiary structure between a polypeptide sequence encoded by a polynucleotide which comprises a known function with a polypeptide sequence encoded by a polynucleotide sequence which has a function not yet determined. Such examples of tertiary structure may comprise predicted alpha helices, beta-sheets, amphipathic helices, leucine zipper motifs, zinc finger motifs, proline-rich regions, cysteine repeat motifs, and the like.

Orthologs and paralogs of presently disclosed transcription factors may be cloned using compositions provided by the present invention according to methods well known in the art. cDNAs can be cloned using mRNA from a plant cell or tissue that expresses one of the present transcription factors. Appropriate mRNA sources may be identified by interrogating Northern blots with probes designed from the present transcription factor sequences, after which a library is prepared from the mRNA obtained from a positive cell or tissue. Transcription factor-encoding cDNA is then isolated using, for example, PCR, using primers designed from a presently disclosed transcription factor gene sequence, or by probing with a partial or complete cDNA or with one or more sets of degenerate probes based on the disclosed sequences. The cDNA library may be used to transform plant cells. Expression of the cDNAs of interest is detected using, for example, methods disclosed herein such as microarrays, Northern blots, quantitative

PCR, or any other technique for monitoring changes in expression. Genomic clones may be isolated using similar techniques to those.

Identifying Polynucleotides or Nucleic Acids by Hybridization

Polynucleotides homologous to the sequences illustrated in the Sequence Listing and tables can be identified, e.g., by hybridization to each other under stringent or under highly stringent conditions. Single stranded polynucleotides hybridize when they associate based on a variety of well characterized physical-chemical forces, such as hydrogen bonding, solvent exclusion, base stacking and the like. The stringency of a hybridization reflects the degree of sequence identity of the nucleic acids involved, such that the higher the stringency, the more similar are the two polynucleotide strands. Stringency is influenced by a variety of factors, including temperature, salt concentration and composition, organic and non-organic additives, solvents, etc. present in both the hybridization and wash solutions and incubations (and number thereof), as described in more detail in the references cited above.

Encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, including any of the transcription factor polynucleotides within the Sequence Listing, and fragments thereof under various conditions of stringency (See, for example, Wahl and Berger (1987) *Methods Enzymol.* 152: 399-407; and Kimmel (1987) *Methods Enzymol.* 152: 507-511). In addition to the nucleotide sequences listed in Tables 4 - 9, full length cDNA, orthologs, and paralogs of the present nucleotide sequences may be identified and isolated using well-known methods. The cDNA libraries, orthologs, and paralogs of the present nucleotide sequences may be screened using hybridization methods to determine their utility as hybridization target or amplification probes.

With regard to hybridization, conditions that are highly stringent, and means for achieving them, are well known in the art. See, for example, Sambrook et al. (1989) "*Molecular Cloning: A Laboratory Manual*" (2nd ed., Cold Spring Harbor Laboratory); Berger and Kimmel, eds., (1987) "Guide to Molecular Cloning Techniques", In *Methods in Enzymology*: 152: 467-469; and Anderson and Young (1985) "Quantitative Filter Hybridisation." In: Hames and Higgins, ed., Nucleic Acid Hybridisation, A Practical Approach. Oxford, IRL Press, 73-111.

Stability of DNA duplexes is affected by such factors as base composition, length, and degree of base pair mismatch. Hybridization conditions may be adjusted to allow DNAs of different sequence relatedness to hybridize. The melting temperature (T_m) is defined as the temperature when 50% of the duplex molecules have dissociated into their constituent single strands. The melting temperature of a perfectly matched duplex, where the hybridization buffer contains formamide as a denaturing agent, may be estimated by the following equations:

(I) DNA-DNA:

$$T_m(^{\circ}\text{C}) = 81.5 + 16.6(\log [\text{Na}^+]) + 0.41(\% \text{ G+C}) - 0.62(\% \text{ formamide}) - 500/L$$

(II) DNA-RNA:

$$T_m(^{\circ}\text{C}) = 79.8 + 18.5(\log [\text{Na}^+]) + 0.58(\% \text{ G+C}) + 0.12(\% \text{ G+C})^2 - 0.5(\% \text{ formamide}) - 820/L$$

(III) RNA-RNA:

$$5 \quad T_m(^{\circ}\text{C}) = 79.8 + 18.5(\log [\text{Na}^+]) + 0.58(\% \text{ G+C}) + 0.12(\% \text{ G+C})^2 - 0.35(\% \text{ formamide}) - 820/L$$

where L is the length of the duplex formed, $[\text{Na}^+]$ is the molar concentration of the sodium ion in the hybridization or washing solution, and $\% \text{ G+C}$ is the percentage of (guanine+cytosine) bases in the hybrid. For imperfectly matched hybrids, approximately 1°C is required to reduce the melting
 10 temperature for each 1% mismatch.

Hybridization experiments are generally conducted in a buffer of pH between 6.8 to 7.4, although the rate of hybridization is nearly independent of pH at ionic strengths likely to be used in the hybridization buffer (Anderson et al. (1985) *supra*). In addition, one or more of the following may be used to reduce non-specific hybridization: sonicated salmon sperm DNA or another non-complementary
 15 DNA, bovine serum albumin, sodium pyrophosphate, sodium dodecylsulfate (SDS), polyvinylpyrrolidone, ficoll and Denhardt's solution. Dextran sulfate and polyethylene glycol 6000 act to exclude DNA from solution, thus raising the effective probe DNA concentration and the hybridization signal within a given unit of time. In some instances, conditions of even greater stringency may be desirable or required to reduce non-specific and/or background hybridization. These conditions may be created with
 20 the use of higher temperature, lower ionic strength and higher concentration of a denaturing agent such as formamide.

Stringency conditions can be adjusted to screen for moderately similar fragments such as homologous sequences from distantly related organisms, or to highly similar fragments such as genes that duplicate functional enzymes from closely related organisms. The stringency can be adjusted either
 25 during the hybridization step or in the post-hybridization washes. Salt concentration, formamide concentration, hybridization temperature and probe lengths are variables that can be used to alter stringency (as described by the formula above). As a general guidelines high stringency is typically performed at $T_m - 5^{\circ}\text{C}$ to $T_m - 20^{\circ}\text{C}$, moderate stringency at $T_m - 20^{\circ}\text{C}$ to $T_m - 35^{\circ}\text{C}$ and low stringency at $T_m - 35^{\circ}\text{C}$ to $T_m - 50^{\circ}\text{C}$ for duplex >150 base pairs. Hybridization may be performed at low to moderate
 30 stringency ($25-50^{\circ}\text{C}$ below T_m), followed by post-hybridization washes at increasing stringencies. Maximum rates of hybridization in solution are determined empirically to occur at $T_m - 25^{\circ}\text{C}$ for DNA-DNA duplex and $T_m - 15^{\circ}\text{C}$ for RNA-DNA duplex. Optionally, the degree of dissociation may be assessed after each wash step to determine the need for subsequent, higher stringency wash steps.

High stringency conditions may be used to select for nucleic acid sequences with high degrees of
 35 identity to the disclosed sequences. An example of stringent hybridization conditions obtained in a filter-based method such as a Southern or northern blot for hybridization of complementary nucleic acids that have more than 100 complementary residues is about 5°C to 20°C lower than the thermal melting point

(T_m) for the specific sequence at a defined ionic strength and pH. Conditions used for hybridization may include about 0.02 M to about 0.15 M sodium chloride, about 0.5% to about 5% casein, about 0.02% SDS or about 0.1% N-laurylsarcosine, about 0.001 M to about 0.03 M sodium citrate, at hybridization temperatures between about 50° C and about 70° C. More preferably, high stringency conditions are about 0.02 M sodium chloride, about 0.5% casein, about 0.02% SDS, about 0.001 M sodium citrate, at a temperature of about 50° C. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire DNA molecule or selected portions, e.g., to a unique subsequence, of the DNA.

Stringent salt concentration will ordinarily be less than about 750 mM NaCl and 75 mM trisodium citrate. Increasingly stringent conditions may be obtained with less than about 500 mM NaCl and 50 mM trisodium citrate, to even greater stringency with less than about 250 mM NaCl and 25 mM trisodium citrate. Low stringency hybridization can be obtained in the absence of organic solvent, e.g., formamide, whereas high stringency hybridization may be obtained in the presence of at least about 35% formamide, and more preferably at least about 50% formamide. Stringent temperature conditions will ordinarily include temperatures of at least about 30° C, more preferably of at least about 37° C, and most preferably of at least about 42° C with formamide present. Varying additional parameters, such as hybridization time, the concentration of detergent, e.g., sodium dodecyl sulfate (SDS) and ionic strength, are well known to those skilled in the art. Various levels of stringency are accomplished by combining these various conditions as needed.

The washing steps that follow hybridization may also vary in stringency; the post-hybridization wash steps primarily determine hybridization specificity, with the most critical factors being temperature and the ionic strength of the final wash solution. Wash stringency can be increased by decreasing salt concentration or by increasing temperature. Stringent salt concentration for the wash steps will preferably be less than about 30 mM NaCl and 3 mM trisodium citrate, and most preferably less than about 15 mM NaCl and 1.5 mM trisodium citrate.

Thus, hybridization and wash conditions that may be used to bind and remove polynucleotides with less than the desired homology to the nucleic acid sequences or their complements that encode the present transcription factors include, for example:

6X SSC at 65° C;

50% formamide, 4X SSC at 42° C; or

0.5X SSC, 0.1% SDS at 65° C;

with, for example, two wash steps of 10 - 30 minutes each. Useful variations on these conditions will be readily apparent to those skilled in the art.

A person of skill in the art would not expect substantial variation among polynucleotide species encompassed within the scope of the present invention because the highly stringent conditions set forth in the above formulae yield structurally similar polynucleotides.

If desired, one may employ wash steps of even greater stringency, including about 0.2x SSC, 0.1% SDS at 65° C and washing twice, each wash step being about 30 min, or about 0.1 x SSC, 0.1% SDS at 65° C and washing twice for 30 min. The temperature for the wash solutions will ordinarily be at least about 25° C, and for greater stringency at least about 42° C. Hybridization stringency may be increased further by using the same conditions as in the hybridization steps, with the wash temperature raised about 3° C to about 5° C, and stringency may be increased even further by using the same conditions except the wash temperature is raised about 6° C to about 9° C. For identification of less closely related homologs, wash steps may be performed at a lower temperature, e.g., 50° C.

An example of a low stringency wash step employs a solution and conditions of at least 25° C in 30 mM NaCl, 3 mM trisodium citrate, and 0.1% SDS over 30 min. Greater stringency may be obtained at 42° C in 15 mM NaCl, with 1.5 mM trisodium citrate, and 0.1% SDS over 30 min. Even higher stringency wash conditions are obtained at 65° C -68° C in a solution of 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. Wash procedures will generally employ at least two final wash steps. Additional variations on these conditions will be readily apparent to those skilled in the art (see, for example, US Patent Application No. 20010010913).

Stringency conditions can be selected such that an oligonucleotide that is perfectly complementary to the coding oligonucleotide hybridizes to the coding oligonucleotide with at least about a 5-10x higher signal to noise ratio than the ratio for hybridization of the perfectly complementary oligonucleotide to a nucleic acid encoding a transcription factor known as of the filing date of the application. It may be desirable to select conditions for a particular assay such that a higher signal to noise ratio, that is, about 15x or more, is obtained. Accordingly, a subject nucleic acid will hybridize to a unique coding oligonucleotide with at least a 2x or greater signal to noise ratio as compared to hybridization of the coding oligonucleotide to a nucleic acid encoding known polypeptide. The particular signal will depend on the label used in the relevant assay, e.g., a fluorescent label, a colorimetric label, a radioactive label, or the like. Labeled hybridization or PCR probes for detecting related polynucleotide sequences may be produced by oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide.

Encompassed by the invention are polynucleotide sequences encoding polypeptides capable of regulating transcription, said polynucleotide sequences being capable of hybridizing to the claimed polynucleotide sequences, including those listed in the Sequence Listing, or polynucleotides that encode the polypeptides listed in the Sequence Listing, and specifically SEQ ID NOs: 1-2237, and fragments thereof under various conditions of stringency. (See, e.g., Wahl and Berger (1987) *Methods Enzymol.* 152: 399-407; Kimmel (1987) *Methods Enzymol.* 152: 507-511.) Estimates of homology are provided by either DNA-DNA or DNA-RNA hybridization under conditions of stringency as is well understood by those skilled in the art (Hames and Higgins, Eds. (1985) Nucleic Acid Hybridisation, IRL Press, Oxford, U.K.). Stringency conditions can be adjusted to screen for moderately similar fragments, such as homologous sequences from distantly related organisms, to highly similar fragments, such as genes that

duplicate functional enzymes from closely related organisms. Post-hybridization washes determine stringency conditions.

Identifying Polynucleotides or Nucleic Acids with Expression Libraries

5 In addition to hybridization methods, transcription factor homolog polypeptides can be obtained by screening an expression library using antibodies specific for one or more transcription factors. With the provision herein of the disclosed transcription factor, and transcription factor homolog nucleic acid sequences, the encoded polypeptide(s) can be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or polyclonal) specific for the polypeptide(s) in
10 question. Antibodies can also be raised against synthetic peptides derived from transcription factor, or transcription factor homolog, amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988), Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression library produced from the plant from which it is desired to clone additional transcription factor homologs, using the methods
15 described above. The selected cDNAs can be confirmed by sequencing and enzymatic activity.

Sequence Variations

It will readily be appreciated by those of skill in the art, that any of a variety of polynucleotide sequences are capable of encoding the transcription factors and transcription factor homolog polypeptides
20 of the invention. Due to the degeneracy of the genetic code, many different polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing. Nucleic acids having a sequence that differs from the sequences shown in the Sequence Listing, or complementary sequences, that encode functionally equivalent peptides (i.e., peptides having some degree of equivalent or similar biological activity) but differ in sequence from the
'25 sequence shown in the Sequence Listing due to degeneracy in the genetic code, are also within the scope of the invention.

Altered polynucleotide sequences encoding polypeptides include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polynucleotide encoding a polypeptide with at least one functional characteristic of the instant polypeptides. Included within this definition are
30 polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding the instant polypeptides, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding the instant polypeptides.

Allelic variant refers to any of two or more alternative forms of a gene occupying the same
35 chromosomal locus. Allelic variation arises naturally through mutation, and may result in phenotypic polymorphism within populations. Gene mutations can be silent (i.e., no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequence. The term allelic variant is

also used herein to denote a protein encoded by an allelic variant of a gene. Splice variant refers to alternative forms of RNA transcribed from a gene. Splice variation arises naturally through use of alternative splicing sites within a transcribed RNA molecule, or less commonly between separately transcribed RNA molecules, and may result in several mRNAs transcribed from the same gene. Splice variants may encode polypeptides having altered amino acid sequence. The term splice variant is also used herein to denote a protein encoded by a splice variant of an mRNA transcribed from a gene.

Those skilled in the art would recognize that, for example, G47, SEQ ID NO: 12, represents a single transcription factor; allelic variation and alternative splicing may be expected to occur. Allelic variants of SEQ ID NO: 11 can be cloned by probing cDNA or genomic libraries from different individual organisms according to standard procedures. Allelic variants of the DNA sequence shown in SEQ ID NO: 11, including those containing silent mutations and those in which mutations result in amino acid sequence changes, are within the scope of the present invention, as are proteins which are allelic variants of SEQ ID NO: 12. cDNAs generated from alternatively spliced mRNAs, which retain the properties of the transcription factor are included within the scope of the present invention, as are polypeptides encoded by such cDNAs and mRNAs. Allelic variants and splice variants of these sequences can be cloned by probing cDNA or genomic libraries from different individual organisms or tissues according to standard procedures known in the art (see USPN 6,388,064).

Thus, in addition to the sequences set forth in the Sequence Listing, the invention also encompasses related nucleic acid molecules that include allelic or splice variants of SEQ ID NO: 2N - 1, where N = 1- 335, sequences that are orthologous to SEQ ID NOs: 761-1348, 1557-2101, and 2124-2237), sequences that are orthologous to paralogous to SEQ ID NOs: 1349-1556, variant sequences that have been shown to confer an altered trait listed in Table 4 (SEQ ID NOs: 2102-2123) listed in the Sequence Listing, and sequences that are complementary to any of the above nucleotide sequences. Related nucleic acid molecules also include nucleotide sequences encoding a polypeptide comprising or consisting essentially of a substitution, modification, addition and/or deletion of one or more amino acid residues compared to the polypeptides as set forth in the Sequence Listing. Such related polypeptides may comprise, for example, additions and/or deletions of one or more N-linked or O-linked glycosylation sites, or an addition and/or a deletion of one or more cysteine residues.

For example, Table 1 illustrates, e.g., that the codons AGC, AGT, TCA, TCC, TCG, and TCT all encode the same amino acid: serine. Accordingly, at each position in the sequence where there is a codon encoding serine, any of the above trinucleotide sequences can be used without altering the encoded polypeptide.

Table 1

Amino acid			Possible Codons						
Alanine	Ala	A	GCA	GCC	GCG	GCU			
Cysteine	Cys	C	TGC	TGT					
Aspartic acid	Asp	D	GAC	GAT					
Glutamic acid	Glu	E	GAA	GAG					
Phenylalanine	Phe	F	TTC	TTT					
Glycine	Gly	G	GGA	GGC	GGG	GGT			
Histidine	His	H	CAC	CAT					
Isoleucine	Ile	I	ATA	ATC	ATT				
Lysine	Lys	K	AAA	AAG					
Leucine	Leu	L	TTA	TTG	CTA	CTC	CTG	CTT	
Methionine	Met	M	ATG						
Asparagine	Asn	N	AAC	AAT					
Proline	Pro	P	CCA	CCC	CCG	CCT			
Glutamine	Gln	Q	CAA	CAG					
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGT	
Serine	Ser	S	AGC	AGT	TCA	TCC	TCG	TCT	
Threonine	Thr	T	ACA	ACC	ACG	ACT			
Valine	Val	V	GTA	GTC	GTG	GTT			
Tryptophan	Trp	W	TGG						
Tyrosine	Tyr	Y	TAC	TAT					

Sequence alterations that do not change the amino acid sequence encoded by the polynucleotide are termed "silent" variations. With the exception of the codons ATG and TGG, encoding methionine and tryptophan, respectively, any of the possible codons for the same amino acid can be substituted by a variety of techniques, e.g., site-directed mutagenesis, available in the art. Accordingly, any and all such variations of a sequence selected from the above table are a feature of the invention.

In addition to silent variations, other conservative variations that alter one, or a few amino acids in the encoded polypeptide, can be made without altering the function of the polypeptide, these conservative variants are, likewise, a feature of the invention.

For example, substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing, are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) *Methods Enzymol.* (1993) vol. 217, Academic Press) or the other methods noted below. Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof can be combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure. Preferably, the polypeptide encoded by the DNA performs the desired function.

Conservative substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 2 when it is desired to maintain the activity of the protein. Table 2 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as conservative substitutions.

Table 2

Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Gln	Asn
Cys	Ser
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr; Gly
Thr	Ser; Val
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Similar substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 3 when it is desired to maintain the activity of the protein. Table 3 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as structural and functional substitutions. For example, a residue in column 1 of Table 3 may be substituted with a residue in column 2; in addition, a residue in column 2 of Table 3 may be substituted with the residue of column

Table 3

Residue	Similar Substitutions
Ala	Ser; Thr; Gly; Val; Leu; Ile
Arg	Lys; His; Gly
Asn	Gln; His; Gly; Ser; Thr
Asp	Glu; Ser; Thr
Gln	Asn; Ala
Cys	Ser; Gly
Glu	Asp
Gly	Pro; Arg
His	Asn; Gln; Tyr; Phe; Lys; Arg
Ile	Ala; Leu; Val; Gly; Met
Leu	Ala; Ile; Val; Gly; Met
Lys	Arg; His; Gln; Gly; Pro
Met	Leu; Ile; Phe
Phe	Met; Leu; Tyr; Trp; His; Val; Ala
Ser	Thr; Gly; Asp; Ala; Val; Ile; His
Thr	Ser; Val; Ala; Gly
Trp	Tyr; Phe; His
Tyr	Trp; Phe; His
Val	Ala; Ile; Leu; Gly; Thr; Ser; Glu

5 Substitutions that are less conservative than those in Table 2 can be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other
10 residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

15

Further Modifying Sequences of the Invention – Mutation/Forced Evolution

In addition to generating silent or conservative substitutions as noted, above, the present invention optionally includes methods of modifying the sequences of the Sequence Listing. In the methods, nucleic acid or protein modification methods are used to alter the given sequences to produce new sequences and/or to chemically or enzymatically modify given sequences to change the properties of the nucleic acids or proteins.

Thus, in one embodiment, given nucleic acid sequences are modified, e.g., according to standard mutagenesis or artificial evolution methods to produce modified sequences. The modified sequences may be created using purified natural polynucleotides isolated from any organism or may be synthesized from purified compositions and chemicals using chemical means well known to those of skill in the art. For example, Ausubel, *supra*, provides additional details on mutagenesis methods. Artificial forced evolution methods are described, for example, by Stemmer (1994) *Nature* 370: 389-391, Stemmer (1994) *Proc. Natl. Acad. Sci.* 91: 10747-10751, and US Patents 5,811,238, 5,837,500, and 6,242,568. Methods for engineering synthetic transcription factors and other polypeptides are described, for example, by Zhang et al. (2000) *J. Biol. Chem.* 275: 33850-33860, Liu et al. (2001) *J. Biol. Chem.* 276: 11323-11334, and Isalan et al. (2001) *Nature Biotechnol.* 19: 656-660. Many other mutation and evolution methods are also available and expected to be within the skill of the practitioner.

Similarly, chemical or enzymatic alteration of expressed nucleic acids and polypeptides can be performed by standard methods. For example, sequence can be modified by addition of lipids, sugars, peptides, organic or inorganic compounds, by the inclusion of modified nucleotides or amino acids, or the like. For example, protein modification techniques are illustrated in Ausubel, *supra*. Further details on chemical and enzymatic modifications can be found herein. These modification methods can be used to modify any given sequence, or to modify any sequence produced by the various mutation and artificial evolution modification methods noted herein.

Accordingly, the invention provides for modification of any given nucleic acid by mutation, evolution, chemical or enzymatic modification, or other available methods, as well as for the products produced by practicing such methods, e.g., using the sequences herein as a starting substrate for the various modification approaches.

For example, optimized coding sequence containing codons preferred by a particular prokaryotic or eukaryotic host can be used e.g., to increase the rate of translation or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced using a non-optimized sequence. Translation stop codons can also be modified to reflect host preference. For example, preferred stop codons for *Saccharomyces cerevisiae* and mammals are TAA and TGA, respectively. The preferred stop codon for monocotyledonous plants is TGA, whereas insects and *E. coli* prefer to use TAA as the stop codon.

The polynucleotide sequences of the present invention can also be engineered in order to alter a coding sequence for a variety of reasons, including but not limited to, alterations which modify the

sequence to facilitate cloning, processing and/or expression of the gene product. For example, alterations are optionally introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, to introduce splice sites, etc.

5 Furthermore, a fragment or domain derived from any of the polypeptides of the invention can be combined with domains derived from other transcription factors or synthetic domains to modify the biological activity of a transcription factor. For instance, a DNA-binding domain derived from a transcription factor of the invention can be combined with the activation domain of another transcription factor or with a synthetic activation domain. A transcription activation domain assists in initiating
10 transcription from a DNA-binding site. Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) *Proc. Natl. Acad. Sci.* 95: 376-381; Aoyama et al. (1995) *Plant Cell* 7: 1773-1785), peptides derived from bacterial sequences (Ma and Ptashne (1987) *Cell* 51: 113-119) and synthetic peptides (Giniger and Ptashne (1987) *Nature* 330: 670-672).

15 Expression and Modification of Polypeptides

Typically, polynucleotide sequences of the invention are incorporated into recombinant DNA (or RNA) molecules that direct expression of polypeptides of the invention in appropriate host cells, transgenic plants, in vitro translation systems, or the like. Due to the inherent degeneracy of the genetic code, nucleic acid sequences which encode substantially the same or a functionally equivalent amino acid
20 sequence can be substituted for any listed sequence to provide for cloning and expressing the relevant homolog.

The transgenic plants of the present invention comprising recombinant polynucleotide sequences are generally derived from parental plants, which may themselves be non-transformed (or non-transgenic) plants. These transgenic plants may either have a transcription factor gene "knocked out" (for
25 example, with a genomic insertion by homologous recombination, an antisense or ribozyme construct) or expressed to a normal or wild-type extent. However, overexpressing transgenic "progeny" plants will exhibit greater mRNA levels, wherein the mRNA encodes a transcription factor, that is, a DNA-binding protein that is capable of binding to a DNA regulatory sequence and inducing transcription, and preferably, expression of a plant trait gene. Preferably, the mRNA expression level will be at least three-
30 fold greater than that of the parental plant, or more preferably at least ten-fold greater mRNA levels compared to said parental plant, and most preferably at least fifty-fold greater compared to said parental plant.

Vectors, Promoters, and Expression Systems

35 The present invention includes recombinant constructs comprising one or more of the nucleic acid sequences herein. The constructs typically comprise a vector, such as a plasmid, a cosmid, a phage, a virus (e.g., a plant virus), a bacterial artificial chromosome (BAC), a yeast artificial chromosome (YAC),

or the like, into which a nucleic acid sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available.

5 General texts that describe molecular biological techniques useful herein, including the use and production of vectors, promoters and many other relevant topics, include Berger, Sambrook, *supra* and Ausubel, *supra*. Any of the identified sequences can be incorporated into a cassette or vector, e.g., for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in Weissbach
10 and Weissbach (1989) Methods for Plant Molecular Biology, Academic Press, and Gelvin et al. (1990) Plant Molecular Biology Manual, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella et al. (1983) *Nature* 303: 209, Bevan (1984) *Nucleic Acids Res.* 12: 8711-8721, Klee (1985) *Bio/Technology* 3: 637-642, for dicotyledonous plants.

15 Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods can involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou (1991) *Bio/Technology* 9: 957-962) and corn (Gordon-Kamm (1990) *Plant Cell* 2: 603-618) can be produced. An immature embryo can also be a
20 good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks et al. (1993) *Plant Physiol.* 102: 1077-1084; Vasil (1993) *Bio/Technology* 10: 667-674; Wan and Lemeaux (1994) *Plant Physiol.* 104: 37-48, and for *Agrobacterium*-mediated DNA transfer (Ishida et al. (1996) *Nature Biotechnol.* 14: 745-750).

 Typically, plant transformation vectors include one or more cloned plant coding sequence
25 (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

30 A potential utility for the transcription factor polynucleotides disclosed herein is the isolation of promoter elements from these genes that can be used to program expression in plants of any genes. Each transcription factor gene disclosed herein is expressed in a unique fashion, as determined by promoter elements located upstream of the start of translation, and additionally within an intron of the transcription factor gene or downstream of the termination codon of the gene. As is well known in the art, for a
35 significant portion of genes, the promoter sequences are located entirely in the region directly upstream of the start of translation. In such cases, typically the promoter sequences are located within 2.0 kb of the

start of translation, or within 1.5 kb of the start of translation, frequently within 1.0 kb of the start of translation, and sometimes within 0.5 kb of the start of translation.

The promoter sequences can be isolated according to methods known to one skilled in the art.

Examples of constitutive plant promoters which can be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (*see, e.g.,* Odell et al. (1985) *Nature* 313: 810-812); the nopaline synthase promoter (An et al. (1988) *Plant Physiol.* 88: 547-552); and the octopine synthase promoter (Fromm et al. (1989) *Plant Cell* 1: 977-984).

A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of a TF sequence in plants. Choice of a promoter is based largely on the phenotype of interest and is determined by such factors as tissue (e.g., seed, fruit, root, pollen, vascular tissue, flower, carpel, etc.), inducibility (e.g., in response to wounding, heat, cold, drought, light, pathogens, etc.), timing, developmental stage, and the like. Numerous known promoters have been characterized and can favorably be employed to promote expression of a polynucleotide of the invention in a transgenic plant or cell of interest. For example, tissue specific promoters include: seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No. 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) *Plant Mol. Biol.* 11: 651-662), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) *Plant Mol. Biol.* 37: 977-988), flower-specific (Kaiser et al. (1995) *Plant Mol. Biol.* 28: 231-243), pollen (Baerson et al. (1994) *Plant Mol. Biol.* 26: 1947-1959), carpels (Ohl et al. (1990) *Plant Cell* 2: 837-848), pollen and ovules (Baerson et al. (1993) *Plant Mol. Biol.* 22: 255-267), auxin-inducible promoters (such as that described in van der Kop et al. (1999) *Plant Mol. Biol.* 39: 979-990 or Baumann et al., (1999) *Plant Cell* 11: 323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) *Plant Mol. Biol.* 38: 743-753), promoters responsive to gibberellin (Shi et al. (1998) *Plant Mol. Biol.* 38: 1053-1060, Willmott et al. (1998) *Plant Molec. Biol.* 38: 817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley et al. (1993) *Plant Mol. Biol.* 22: 13-23), light (e.g., the pea rbcS-3A promoter, Kuhlemeier et al. (1989) *Plant Cell* 1: 471-478, and the maize rbcS promoter, Schaffner and Sheen (1991) *Plant Cell* 3: 997-1012); wounding (e.g., *wun1*, Siebertz et al. (1989) *Plant Cell* 1: 961-968); pathogens (such as the PR-1 promoter described in Buchel et al. (1999) *Plant Mol. Biol.* 40: 387-396, and the PDF1.2 promoter described in Manners et al. (1998) *Plant Mol. Biol.* 38: 1071-1080), and chemicals such as methyl jasmonate or salicylic acid (Gatz (1997) *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at

senescence (Gan and Amasino (1995) *Science* 270: 1986-1988); or late seed development (Odell et al. (1994) *Plant Physiol.* 106: 447-458).

Plant expression vectors can also include RNA processing signals that can be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors can include additional regulatory sequences from the 3'-untranslated region of plant genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Additional Expression Elements

Specific initiation signals can aid in efficient translation of coding sequences. These signals can include, e.g., the ATG initiation codon and adjacent sequences. In cases where a coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only coding sequence (e.g., a mature protein coding sequence), or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon can be separately provided. The initiation codon is provided in the correct reading frame to facilitate transcription. Exogenous transcriptional elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers appropriate to the cell system in use.

Expression Hosts

The present invention also relates to host cells which are transduced with vectors of the invention, and the production of polypeptides of the invention (including fragments thereof) by recombinant techniques. Host cells are genetically engineered (i.e., nucleic acids are introduced, e.g., transduced, transformed or transfected) with the vectors of this invention, which may be, for example, a cloning vector or an expression vector comprising the relevant nucleic acids herein. The vector is optionally a plasmid, a viral particle, a phage, a naked nucleic acid, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the relevant gene. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, Sambrook, *supra* and Ausubel, *supra*.

The host cell can be a eukaryotic cell, such as a yeast cell, or a plant cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Plant protoplasts are also suitable for some applications. For example, the DNA fragments are introduced into plant tissues, cultured plant cells or plant protoplasts by standard methods including electroporation (Fromm et al. (1985) *Proc. Natl. Acad. Sci.* 82: 5824-5828, infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al. (1982) Molecular Biology of Plant Tumors Academic Press, New York, NY, pp. 549-560; US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or

particles, or on the surface (Klein et al. (1987) *Nature* 327: 70-73), use of pollen as vector (WO 85/01856), or use of *Agrobacterium tumefaciens* or *A. rhizogenes* carrying a T-DNA plasmid in which DNA fragments are cloned. The T-DNA plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and a portion is stably integrated into the plant genome (Horsch et al. (1984) *Science* 233: 496-498; Fraley et al. (1983) *Proc. Natl. Acad. Sci.* 80: 4803-4807).

The cell can include a nucleic acid of the invention that encodes a polypeptide, wherein the cell expresses a polypeptide of the invention. The cell can also include vector sequences, or the like. Furthermore, cells and transgenic plants that include any polypeptide or nucleic acid above or throughout this specification, e.g., produced by transduction of a vector of the invention, are an additional feature of the invention.

For long-term, high-yield production of recombinant proteins, stable expression can be used. Host cells transformed with a nucleotide sequence encoding a polypeptide of the invention are optionally cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The protein or fragment thereof produced by a recombinant cell may be secreted, membrane-bound, or contained intracellularly, depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides encoding mature proteins of the invention can be designed with signal sequences which direct secretion of the mature polypeptides through a prokaryotic or eukaryotic cell membrane.

20 Modified Amino Acid Residues

Polypeptides of the invention may contain one or more modified amino acid residues. The presence of modified amino acids may be advantageous in, for example, increasing polypeptide half-life, reducing polypeptide antigenicity or toxicity, increasing polypeptide storage stability, or the like. Amino acid residue(s) are modified, for example, co-translationally or post-translationally during recombinant production or modified by synthetic or chemical means.

Non-limiting examples of a modified amino acid residue include incorporation or other use of acetylated amino acids, glycosylated amino acids, sulfated amino acids, prenylated (e.g., farnesylated, geranylgeranylated) amino acids, PEG modified (e.g., "PEGylated") amino acids, biotinylated amino acids, carboxylated amino acids, phosphorylated amino acids, etc. References adequate to guide one of skill in the modification of amino acid residues are replete throughout the literature.

The modified amino acid residues may prevent or increase affinity of the polypeptide for another molecule, including, but not limited to, polynucleotide, proteins, carbohydrates, lipids and lipid derivatives, and other organic or synthetic compounds.

35 Identification of Additional Factors

A transcription factor provided by the present invention can also be used to identify additional endogenous or exogenous molecules that can affect a phenotype or trait of interest. On the one hand, such

molecules include organic (small or large molecules) and/or inorganic compounds that affect expression of (i.e., regulate) a particular transcription factor. Alternatively, such molecules include endogenous molecules that are acted upon either at a transcriptional level by a transcription factor of the invention to modify a phenotype as desired. For example, the transcription factors can be employed to identify one or more downstream genes that are subject to a regulatory effect of the transcription factor. In one approach, a transcription factor or transcription factor homolog of the invention is expressed in a host cell, e.g., a transgenic plant cell, tissue or explant, and expression products, either RNA or protein, of likely or random targets are monitored, e.g., by hybridization to a microarray of nucleic acid probes corresponding to genes expressed in a tissue or cell type of interest, by two-dimensional gel electrophoresis of protein products, or by any other method known in the art for assessing expression of gene products at the level of RNA or protein. Alternatively, a transcription factor of the invention can be used to identify promoter sequences (such as binding sites on DNA sequences) involved in the regulation of a downstream target. After identifying a promoter sequence, interactions between the transcription factor and the promoter sequence can be modified by changing specific nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA-binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences can be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the transcription factors with their promoters (Bulyk et al. (1999) *Nature Biotechnol.* 17: 573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification can occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any method suitable for detecting protein-protein interactions can be employed. Among the methods that can be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in Chien et al. ((1991) *Proc. Natl. Acad. Sci.* 88: 9578-9582) and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify

the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions can be preformed.

Identification of Modulators

5 In addition to the intracellular molecules described above, extracellular molecules that alter activity or expression of a transcription factor, either directly or indirectly, can be identified. For example, the methods can entail first placing a candidate molecule in contact with a plant or plant cell. The molecule can be introduced by topical administration, such as spraying or soaking of a plant, or incubating a plant in a solution containing the molecule, and then the molecule's effect on the expression
10 or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide can be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence can be detected by use of microarrays, Northernblots, quantitative PCR, or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds.) Current
15 Protocols in Molecular Biology, John Wiley & Sons (1998, and supplements through 2001). Changes in the activity of the transcription factor can be monitored, directly or indirectly, by assaying the function of the transcription factor, for example, by measuring the expression of promoters known to be controlled by the transcription factor (using promoter-reporter constructs), measuring the levels of transcripts using microarrays, Northern blots, quantitative PCR, etc. Such changes in the expression levels can be
20 correlated with modified plant traits and thus identified molecules can be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

Essentially any available composition can be tested for modulatory activity of expression or activity of any nucleic acid or polypeptide herein. Thus, available libraries of compounds such as chemicals, polypeptides, nucleic acids and the like can be tested for modulatory activity. Often, potential
25 modulator compounds can be dissolved in aqueous or organic (e.g., DMSO-based) solutions for easy delivery to the cell or plant of interest in which the activity of the modulator is to be tested. Optionally, the assays are designed to screen large modulator composition libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on micrometer plates in robotic assays).

30 In one embodiment, high throughput screening methods involve providing a combinatorial library containing a large number of potential compounds (potential modulator compounds). Such "combinatorial chemical libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as target compounds.

35 A combinatorial chemical library can be, e.g., a collection of diverse chemical compounds generated by chemical synthesis or biological synthesis. For example, a combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (e.g., in one

example, amino acids) in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound of a set length). Exemplary libraries include peptide libraries, nucleic acid libraries, antibody libraries (see, e.g., Vaughn et al. (1996) *Nature Biotechnol.* 14: 309-314 and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al. *Science* (1996) 274: 1520-1522 and US Patent 5,593,853), peptide nucleic acid libraries (see, e.g., US Patent 5,539,083), and small organic molecule libraries (see, e.g., benzodiazepines, in Baum *Chem. & Engineering News* Jan 18, 1993, page 33; isoprenoids, US Patent 5,569,588; thiazolidinones and metathiazanones, US Patent 5,549,974; pyrrolidines, US Patents 5,525,735 and 5,519,134; morpholino compounds, US Patent 5,506,337) and the like.

Preparation and screening of combinatorial or other libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., US Patent 5,010,175; Furka, (1991) *Int. J. Pept. Prot. Res.* 37: 487-493; and Houghton et al. (1991) *Nature* 354: 84-88). Other chemistries for generating chemical diversity libraries can also be used.

In addition, as noted, compound screening equipment for high-throughput screening is generally available, e.g., using any of a number of well known robotic systems that have also been developed for solution phase chemistries useful in assay systems. These systems include automated workstations including an automated synthesis apparatus and robotic systems utilizing robotic arms. Any of the above devices are suitable for use with the present invention, e.g., for high-throughput screening of potential modulators. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art.

Indeed, entire high-throughput screening systems are commercially available. These systems typically automate entire procedures including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. Similarly, microfluidic implementations of screening are also commercially available.

The manufacturers of such systems provide detailed protocols the various high throughput. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like. The integrated systems herein, in addition to providing for sequence alignment and, optionally, synthesis of relevant nucleic acids, can include such screening apparatus to identify modulators that have an effect on one or more polynucleotides or polypeptides according to the present invention.

In some assays it is desirable to have positive controls to ensure that the components of the assays are working properly. At least two types of positive controls are appropriate. That is, known transcriptional activators or inhibitors can be incubated with cells or plants, for example, in one sample of the assay, and the resulting increase/decrease in transcription can be detected by measuring the resulting increase in RNA levels and/or protein expression, for example, according to the methods herein. It will be appreciated that modulators can also be combined with transcriptional activators or inhibitors to find

modulators that inhibit transcriptional activation or transcriptional repression. Either expression of the nucleic acids and proteins herein or any additional nucleic acids or proteins activated by the nucleic acids or proteins herein, or both, can be monitored.

In an embodiment, the invention provides a method for identifying compositions that modulate the activity or expression of a polynucleotide or polypeptide of the invention. For example, a test compound, whether a small or large molecule, is placed in contact with a cell, plant (or plant tissue or explant), or composition comprising the polynucleotide or polypeptide of interest and a resulting effect on the cell, plant, (or tissue or explant) or composition is evaluated by monitoring, either directly or indirectly, one or more of: expression level of the polynucleotide or polypeptide, activity (or modulation of the activity) of the polynucleotide or polypeptide. In some cases, an alteration in a plant phenotype can be detected following contact of a plant (or plant cell, or tissue or explant) with the putative modulator, e.g., by modulation of expression or activity of a polynucleotide or polypeptide of the invention. Modulation of expression or activity of a polynucleotide or polypeptide of the invention may also be caused by molecular elements in a signal transduction second messenger pathway and such modulation can affect similar elements in the same or another signal transduction second messenger pathway.

Subsequences

Also contemplated are uses of polynucleotides, also referred to herein as oligonucleotides, typically having at least 12 bases, preferably at least 15, more preferably at least 20, 30, or 50 bases, which hybridize under at least highly stringent (or ultra-high stringent or ultra-ultra-high stringent conditions) conditions to a polynucleotide sequence described above. The polynucleotides may be used as probes, primers, sense and antisense agents, and the like, according to methods as noted *supra*.

Subsequences of the polynucleotides of the invention, including polynucleotide fragments and oligonucleotides are useful as nucleic acid probes and primers. An oligonucleotide suitable for use as a probe or primer is at least about 15 nucleotides in length, more often at least about 18 nucleotides, often at least about 21 nucleotides, frequently at least about 30 nucleotides, or about 40 nucleotides, or more in length. A nucleic acid probe is useful in hybridization protocols, e.g., to identify additional polypeptide homologs of the invention, including protocols for microarray experiments. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook, *supra*, and Ausubel, *supra*.

In addition, the invention includes an isolated or recombinant polypeptide including a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotides of the invention. For example, such polypeptides, or domains or fragments thereof, can be used as immunogens, e.g., to produce antibodies specific for the polypeptide sequence, or as probes

for detecting a sequence of interest. A subsequence can range in size from about 15 amino acids in length up to and including the full length of the polypeptide.

To be encompassed by the present invention, an expressed polypeptide which comprises such a polypeptide subsequence performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA binding domain that activates transcription, e.g., by binding to a specific DNA promoter region an activation domain, or a domain for protein-protein interactions.

10 Production of Transgenic Plants

Modification of Traits

The polynucleotides of the invention are favorably employed to produce transgenic plants with various traits, or characteristics, that have been modified in a desirable manner, e.g., to improve the seed characteristics of a plant. For example, alteration of expression levels or patterns (e.g., spatial or temporal expression patterns) of one or more of the transcription factors (or transcription factor homologs) of the invention, as compared with the levels of the same protein found in a wild-type plant, can be used to modify a plant's traits. An illustrative example of trait modification, improved characteristics, by altering expression levels of a particular transcription factor is described further in the Examples and the Sequence Listing.

20

Arabidopsis as a model system

Arabidopsis thaliana is the object of rapidly growing attention as a model for genetics and metabolism in plants. *Arabidopsis* has a small genome, and well-documented studies are available. It is easy to grow in large numbers and mutants defining important genetically controlled mechanisms are either available, or can readily be obtained. Various methods to introduce and express isolated homologous genes are available (see Koncz et al., eds., Methods in Arabidopsis Research (1992) World Scientific, New Jersey, NJ, in "Preface"). Because of its small size, short life cycle, obligate autogamy and high fertility, *Arabidopsis* is also a choice organism for the isolation of mutants and studies in morphogenetic and development pathways, and control of these pathways by transcription factors (Koncz *supra*, p. 72). A number of studies introducing transcription factors into *A. thaliana* have demonstrated the utility of this plant for understanding the mechanisms of gene regulation and trait alteration in plants. (See, for example, Koncz *supra*, and US Patent Number 6,417,428).

Homologous genes introduced into transgenic plants.

Homologous genes that may be derived from any plant, or from any source whether natural, synthetic, semi-synthetic or recombinant, and that share significant sequence identity or similarity to those provided by the present invention, may be introduced into plants, for example, crop plants, to

confer desirable or improved traits. Consequently, transgenic plants may be produced that comprise a recombinant expression vector or cassette with a promoter operably linked to one or more sequences homologous to presently disclosed sequences. The promoter may be, for example, a plant or viral promoter.

5 The invention thus provides for methods for preparing transgenic plants, and for modifying plant traits. These methods include introducing into a plant a recombinant expression vector or cassette comprising a functional promoter operably linked to one or more sequences homologous to presently disclosed sequences. Plants and kits for producing these plants that result from the application of these methods are also encompassed by the present invention.

10 Transcription factors of interest for the modification of plant traits

Currently, the existence of a series of maturity groups for different latitudes represents a major barrier to the introduction of new valuable traits. Any trait (e.g. disease resistance) has to be bred into each of the different maturity groups separately, a laborious and costly exercise. The availability of single
15 strain, which could be grown at any latitude, would therefore greatly increase the potential for introducing new traits to crop species such as soybean and cotton.

For many of the specific effects, traits and utilities listed in Table 4 and Table 6 that may be conferred to plants, one or more transcription factor genes may be used to increase or decrease, advance or delay, or improve or prove deleterious to a given trait. For example, overexpression of a transcription
20 factor gene that naturally occurs in a plant may cause early flowering relative to non-transformed or wild-type plants. By knocking out the gene, or suppressing the gene (with, for example, antisense suppression) the plant may experience delayed flowering. Similarly, overexpressing or suppressing one or more genes can impart significant differences in production of plant products, such as different fatty acid ratios. Thus, suppressing a gene that causes a plant to be more sensitive to cold may improve a plant's tolerance
25 of cold. More than one transcription factor gene may be introduced into a plant, either by transforming the plant with one or more vectors comprising two or more transcription factors, or by selective breeding of plants to yield hybrid crosses that comprise more than one introduced transcription factor.

A listing of specific effects and utilities that the presently disclosed transcription factor genes
30 have on plants, as determined by direct observation and assay analysis, is provided in Table 4. Table 4 shows the polynucleotides identified by SEQ ID NO; Gene ID No. (GID); and if the polynucleotide was tested in a transgenic assay. The first column shows the polynucleotide SEQ ID NO; the second column shows the GID; the third column shows whether the gene was overexpressed (OE) or knocked out (KO) in plant studies; the fourth column shows the category of modified trait resulting from the knock out or
35 overexpression of the polynucleotide in the transgenic plant; and the fifth column ("Experimental Observations"), includes specific observations made with respect to the polynucleotide of the respective first column.

Table 4. Traits, trait categories, and effects and utilities that transcription factor genes have on plants.

SEQ ID NO:	GID	OE/KO	Category	Experimental Observations
1	G2	OE	Flowering time	Late flowering
3	G12	OE/KO	Morphology; altered programmed cell death Growth regulator; altered ethylene sensitivity Dev and morph; Morphology: other	Leaf and hypocotyl cell death; knockout seedlings germinated in the dark on 1-aminocyclopropane-1-carboxylic acid-containing media were more stunted than controls Formation of necrotic lesions
5	G15	OE OE	Dev and morph; flower Flowering time	Altered flower morphology Late flowering
7	G30	OE	Leaf; altered shape Leaf; dark green leaves Leaf; glossy leaves Light response; Long petioles Light response; Long hypocotyls Light response; Long cotyledons	Long cotyledons, petioles and hypocotyls, dark green, glossy leaves; shade avoidance
9	G46	OE OE	Dev and morph; Size Abiotic stress; Drought	Increased biomass Increased tolerance to drought in a soil-based assay
11	G47	OE OE OE OE OE	Flowering time Abiotic stress; osmotic stress Dev and morph; Architecture Dev and morph; stem Abiotic stress; drought	Late flowering Better root growth under osmotic stress Altered architecture and inflorescence development Altered structure of vascular tissues Increased tolerance to drought in a soil-based assay
13	G129	OE	Flowering time Leaf: altered shape Flower: homeotic transformation	Early flowering Leaf shape Homeotic transformation
15 and 2102	G131	OE OE OE OE	Dev and morph; size Flowering time Dev and morph; Leaf Dev and morph; Flower Dev and morph; Inflorescence	Small plants Early flowering Curled leaves Loss of flower determinacy, terminal flowers Altered inflorescence determinacy
17	G133	OE	Flower: homeotic transformation	Homeotic transformation
19	G134	OE	Flower: homeotic transformation Abiotic stress; cold sensitivity	Homeotic transformation Increased sensitivity to cold
21	G135	OE OE OE OE	Dev and morph; Leaf Dev and morph; Inflorescence Dev and morph; Flower Flowering time	Curled leaves Altered inflorescence determinacy; terminal flowers Loss of flower determinacy, Early flowering
23	G136	OE	Morphology; altered flower development Flowering time Leaf; altered shape Morphology: size	Altered flower development (tiny petals) Early flowering Small, upward curling leaves Small plant
25	G137	OE	Flowering time Inflorescence; Terminal flowers	Early flowering Terminal flower formation Leaf curling

			Leaf; altered shape	
27	G138	OE	Flowering time	Early flowering
29	G139	OE	Expression; drought	This gene was induced in rosette leaves in response to drought treatments
31	G140	OE	Flower: homeotic transformation Flowering time	Homeotic transformation Early flowering
33	G142	OE	Flowering time	Early flowering
35	G145	OE	Flowering time Inflorescence; terminal flowers	Early flowering Terminal flower
37	G146	OE	Flowering time	Early flowering
39	G148	OE	Flowering time Inflorescence; terminal flowers	Early flowering Terminal flower
41	G151	OE	Seed; Large seed	Larger seed size than controls
43	G153	OE OE	Flowering time Abiotic stress; Nutrient uptake	Early flowering Altered C/N sensing
45	G155	OE	Altered sugar sensing Flowering time Abiotic stress; osmotic stress Inflorescence; terminal flower	Increased sensitivity to glucose Early flowering Increased sensitivity to mannitol Terminal flower
47	G171	OE OE OE	Expression; heat Expression; chilling Expression; <i>Fusarium</i>	Expression was induced in leaves by heat Expression was induced in leaves by cold Expression was induced in leaves by <i>Fusarium</i>
49	G172	OE	Flowering time	Early flowering
51	G173	OE	Flowering time	Late flowering
53	G200	OE	Nutrient; tolerance to low N C/N sensing Leaf; altered shape Leaf; light green leaves Flowering time	Seedlings contained less anthocyanin and were greener on high sucrose medium lacking nitrogen, and on similar media supplemented with glutamine; mature plants had small, light green pointed leaves; early flowering
55	G224	OE	Leaf: altered shape Abiotic stress; cold tolerance Altered sugar sensing	Altered leaf shape Increased tolerance to cold Seedling vigor on high glucose
57	G244	OE OE OE	Expression; auxin Expression; drought Expression; ABA	Expression was induced by auxin Expression was induced by drought Expression was induced by abscisic acid
59	G246	OE	Light response; shade avoidance Flowering time	Shade avoidance Early flowering
61	G253	OE OE OE	Size; small plants Dev and morph; Leaf Dev and morph; Inflorescence	Reduced plant size Heart shaped and dark green leaves Short inflorescence internodes
63	G268	OE	Plant size; large plants	Increased biomass
65	G287	OE	Dev and morph; Size	Increased biomass
67	G309	OE OE OE	Flowering time Plant size; small plants Leaf; altered coloration	Late flowering Reduced plant size Dark green leaves
69	G314	OE	Dev and morph; Size	Increased biomass
71	G319	OE	Plant size; Increased size Flowering time Leaf; altered shape	Increased size; late flowering; wrinkled, short broad leaves

73 and 2103	G324	OE	Flowering time	Late flowering
		OE	Size; large plants	Increased biomass
75	G344	OE	Abiotic stress; chilling	More sensitive to chilling in germination assay
		OE	Growth regulator; altered sugar sensing	Altered sugar sensing phenotype: more sensitive to glucose in a germination assay
77	G351	OE	Altered light response	Leaf orientation and light green coloration
1379	G353	OE	Abiotic stress; osmotic stress	Seedlings were larger and greener on PEG-containing media
1381	G354	OE	Abiotic stress; drought	Increased tolerance to drought in a soil-based assay
79	G355	OE	Nutrient; Tolerance to low PO ₄	Enhanced growth under limiting phosphate in root growth assay, and better growth in high NaCl
			Abiotic stress; sodium chloride tolerance	
81	G366	OE	Dev and morph; Lethal when overexpressed	Lethal when overexpressed
83	G370	KO	Abiotic stress; osmotic stress	Short, round leaves; flowers showed a striking increase in trichome density on sepals, and carried ectopic trichomes on petals, anthers, and carpels; aerial rosettes occur when a secondary inflorescence meristem develops; knockout was more sensitive to osmotic stress in a germination assay and produced bushy rosettes, small, shiny plants
		OE	Leaf; altered shape Morphology; increased trichome density Morphology; altered timing of phase change	
85	G372	OE	Leaf; altered shape Flowering time	Altered leaf shape Late flowering
87	G374	KO	Dev and morph; Embryo lethal	Lethality at early stages of embryo development
89	G380	OE	Flowering time	Late flowering
91 and 2104	G386	OE	Biochem: misc;	Increased pigment production
		OE	Biochemistry: other Dev and morph; Size	Reduced plant size
93	G416	OE	Flowering time	Early flowering
95	G434	OE	Flowering time	Late flowering
97	G438	OE	Leaf; altered shape	Larger, flatter leaves than those of controls at late stages of development
			Leaf Plant size; increased size	
99	G446	OE	Altered architecture	Altered branching
			Leaf; altered shape	Altered leaf shape
101	G468	OE	Leaf; altered shape	Wrinkled leaves
103	G478	OE	Altered light response	Long petioles
			Altered sugar sensing	More sensitive to glucose
105	G485	KO	Flowering time	Late flowering
		OE	Flowering time	Early flowering
107	G521	OE	Leaf; cell expansion	Cell expansion
109	G549	OE	Dev and morph; Inflorescence	Altered inflorescence determinacy
		OE	Dev and morph; Size	Reduced plant size
		OE	Flowering time	Early flowering
111	G550	OE	Morphology; altered flowers Abiotic stress; heat tolerance Expression; sodium chloride Expression; auxin Pigment; high anthocyanin	Early flowers were small with poor organ formation, late flowers were normal; less tolerant to heat stress in a growth assay; high anthocyanin level; G550 expression is induced in response to heat, auxin and salt stress
113	G571	OE	Hormone sensitivity; altered ABA response Abiotic stress; drought Abiotic stress; osmotic stress	This gene is also strongly induced in rosette leaves by ABA, drought, osmotic stress and Erysiphe

			Expression; Erysiphe	
115	G581	OE	Nutrient; tolerance to low N Seed; altered coloration Seed; Large seed Flowering time Pigment; Increased anthocyanin	Overexpressing lines germinated better on plates containing low N or plates with low N supplemented with glutamine, seedlings also had less anthocyanin accumulation when compared to wild-type controls; increased seed size, altered seed color; late flowering
117	G600	OE	Leaf; light green leaves Flowering time Plant size; small plants	Small, flat, short and grayish or light green rosette leaves; early flowering; smaller plants
119 and 2105	G624	OE	Nutrient uptake; tolerance to low PO ₄	Better root growth on media lacking phosphate
		OE	Abiotic stress; sodium chloride tolerance	Increased tolerance to sodium chloride
		OE	Increased size	Increased biomass
		OE	Flowering time	Late flowering
121	G627	OE	Flowering time	Early flowering
123	G646	OE	Leaf; altered shape	Very narrow downward curled dark green leaves
125 and 2106	G651	OE	Dev and morph; Leaf	Altered leaf shape and gray leaves
		OE	Abiotic stress; Cold	Increased sensitivity to cold in a germination assay
		OE	Dev and morph; Root	Altered root branching
		OE	Dev and morph; Size	Reduced plant size
		OE	Dev and morph Flower	Altered flower morphology
127	G652	OE/KO	Leaf biochemistry; ; increased glucosinolates Seed biochemistry; increased seed prenyl lipids Seed biochemistry; decreased seed oil Delayed senescence	Knockout had increase in the leaf glucosinolate M39480 and seed a-tocopherol, decrease in seed oil; overexpressor showed delayed senescence
129	G707	OE	Abiotic stress; Nutrient uptake	Altered C/N sensing
		OE	Dev and morph; Leaf	Dark green leaves
		OE	Biochem: misc; Biochemistry: other	Increased pigment production
		OE	Flowering time	Late flowering
131	G728	OE	Abiotic stress; cold tolerance	Increased tolerance to cold
133	G730	OE	Dev and morph; Root	Reduced secondary root growth
		OE	Dev and morph; Morphology: other	Abaxialization of adaxial surfaces
135	G738	OE	Flowering time Plant size; small plants Pigment; High anthocyanin	Late flowering; small seedlings; high anthocyanin levels in leaf petioles; smaller plants
137 and 2107	G744	OE	Flowering time	Late flowering
131	G752	OE	Flowering time	Late flowering
141	G807	OE OE OE OE OE OE	Abiotic stress; chilling tolerance Expression; heat Expression: auxin Fast growth Light response; long petioles Light response; long hypocotyls	Seedling vigor was improved in T1 transformants and T2 progeny, seedlings were reproducibly larger, grew faster and showed longer hypocotyl and petioles than controls; expression of this gene moderately upon heat shock and auxin treatment
143	G811	OE	Leaf; dark green leaves Size; small plants	Dark green leaves Reduced size
145	G839	OE	Nutrient; tolerance to low N	Increased tolerance to nitrogen-limited medium

			Flowering time	Late flowering
147	G846	OE	Dev and morph Flower	Gamete lethal
149	G852	OE	Flowering time Size; large plants	Late flowering Large plant
151	G905	OE	Flowering time Altered sugar sensing Leaf; altered shape	Late flowering Seedling vigor on high glucose Altered leaf shape
153	G916	OE	Growth regulator; altered sugar sensing Nutrient; tolerance to low N Light response; Long hypocotyls Morphology; Narrow cotyledons Abiotic stress: drought tolerance	Larger seedlings than wild type in high sucrose, seedlings were larger and had less anthocyanin on high sucrose plates that were nitrogen deficient, with or without glutamine supplementation; disproportionately long hypocotyls and narrow cotyledons Increased tolerance to drought in a soil-based assay
155	G926	KO KO KO	Hormone sensitivity Abiotic stress; Osmotic stress Abiotic stress; Drought	Reduced sensitivity to ABA Increased tolerance to osmotic stress (salt and sucrose) Increased tolerance to drought in a soil-based assay
157	G957	OE	Leaf; altered shape	Wrinkled, curled leaves
159	G961	OE KO	Dev and morph; Seed Seed biochemistry; Seed oil	Altered seed development and germination Increased seed oil
161	G975	OE	Leaf biochemistry; Leaf fatty acids Abiotic stress; Drought	Increased wax in leaves Increased tolerance to drought in a soil-based assay
163	G1011	OE	Morphology; altered flowers Leaf; altered shape Flowering time Morphology; increased trichome density	Floral organ abscission was delayed, with stamens, petals, and sepals persisting following pollination; increased trichome density on sepals and ectopic trichomes on carpels; rounded leaves; early flowering
165	G1013	OE	Slow growth Flower alterations Altered light response Leaf; altered shape Altered C/N sensing	Slow growth rate Multiple flower alterations Light response: leaf orientation Altered leaf shape C/N sensing: better germination
167	G1017	OE	Abiotic stress; Sodium chloride tolerance	Increased tolerance to sodium chloride
169	G1033	OE	Premature senescence Altered sugar sensing Abiotic stress; osmotic stress tolerance	Premature leaf senescence Increased seedling vigor on sucrose Increased tolerance to sucrose
171 and 2108	G1037	OE	Abiotic stress; Sodium chloride tolerance	Increased tolerance to sodium chloride
173	G1082	OE	Light response; long hypocotyls	Longer hypocotyls than controls
175	G1100	OE	Leaf; altered shape Leaf; dark green leaves Morphology; altered flowers Abiotic stress Expression; SA Expression; drought	Dark green, pointed leaves, large dark green rosettes; stunted inflorescence growth and abnormal flowers; slower growth rate; this gene is strongly and specifically induced by drought and salicylic acid
177	G1108	OE	Altered sugar sensing	Less sensitive to glucose
179	G1113	OE OE	Increased plant size Flowering time	Increased biomass Late flowering
181	G1128	OE	Leaf; altered shape Leaf; dark green leaves Morphology; Changes to	Dark green, narrow contorted leaves; premature leaf and flower senescence; little or no seed development

			flower Growth rate; altered rate of senescence Seed; altered development	
183	G1136	OE	Flowering time Nutrient; sensitivity to low N	Late flowering Increased sensitivity to nitrogen
185	G1142	OE	Flowering time Leaf; altered shape	Late flowering Altered leaf shape
187 and 2109	G1150	OE OE OE	Abiotic stress; Nutrient uptake Flowering time Dev and morph; Size	Altered C/N sensing Late flowering Increased biomass
189	G1206	OE	Abiotic stress; drought tolerance	Increased seedling vigor under drought conditions, seedlings larger and greener than controls
191	G1247	OE	Size; small plant Leaf; altered shape	Altered leaf shape Reduced plant size
193	G1274	OE OE OE OE OE OE OE	Abiotic stress; Cold Abiotic stress; Chilling Abiotic stress; Drought Dev and morph; Inflorescence Abiotic stress; Nutrient uptake Abiotic stress; Nutrient uptake Dev and morph; Leaf	More tolerant to cold in a germination assay More tolerant to chilling in a seedling growth assay Increased tolerance to drought in a soil-based assay Altered inflorescence architecture Increased tolerance to low nitrogen Altered C/N sensing Large leaves
195	G1276	OE	Flowering time	Late flowering
197	G1289	OE	Plant size; small	All overexpressing lines showed reduced size
199	G1313	OE	Size; large plant	Increased seedling size
201	G1327	OE	Leaf; dark green leaves	Dark green leaves
203	G1340	OE	Plant size; small	All overexpressing lines showed reduced size
205	G1341	OE	Dev and morph; Leaf	Dark green leaves, leaf curling
207	G1357	OE OE OE OE OE	Flowering time Hormone sensitivity Abiotic stress; Chilling Dev and morph; Leaf Abiotic stress; Drought	Late flowering Insensitive to ABA More tolerant to chilling stress in a growth assay Altered leaf shape and dark green leaves Increased tolerance to drought in a soil-based assay
209	G1361	OE	Flowering time Leaf; altered shape	Late flowering Altered leaf shape
211	G1384	OE	Dev and morph; lethal when overexpressed	Lethal when overexpressed
213	G1389	OE	Leaf; altered shape Leaf; dark green leaves	Inner rosette leaves were dark green, narrow, and curled in T1 plants
215	G1412	OE OE	Abiotic stress; Osmotic stress Hormone sensitivity	Increased tolerance to osmotic stress ABA insensitive
217	G1420	OE	Morphology; long cotyledons Leaf; altered shape Leaf; dark green leaves Growth regulator; altered sugar sensing Morphology; altered flower	Long flower organs (sepal and petal), mildly serrated, narrow, darker green leaves (including pedicel); poor growth on glucose; long narrow cotyledons
219	G1423	OE	Leaf; dark green leaves Plant size; small plants	Dark green leaf coloration compared to wild-type, indicating a change in the levels of chlorophyll, carotenoids, or flavonoids; transformants were distinctly small

221	G1446	OE	Flowering time	Late flowering
223	G1451	OE	Leaf; large leaves Flowering time Size; large plant	Large leaf size Late flowering Increased plant size
225	G1452	OE OE OE OE OE	Flowering time Dev and morph; Leaf Abiotic stress; Osmotic stress Abiotic stress; drought Hormone sensitivity Dev and morph; Trichome	Late flowering Altered leaf shape, dark green leaves Better germination on sucrose and salt Increased tolerance to drought in a soil-based assay Reduced sensitivity to ABA Reduced trichome density
227	G1468	OE OE OE OE	Flowering time Dev and morph; size Dev and morph; leaf Dev and morph; Morphology: other	Late flowering Increased biomass Grayish and narrow leaves Slow growth rate
229	G1474	OE	Flowering time Inflorescence; altered architecture Size; small plants	Late flowering Altered inflorescence architecture Reduced plant size
231	G1476	OE	Fast growth Leaf; altered shape	Faster seedling growth rate; rounded, contorted leaves
233	G1482	OE	Increased pigment	Increased anthocyanins in leaf
235	G1483	OE	Abiotic stress; Nutrient uptake	Altered C/N sensing
237	G1493	OE	Altered sugar sensing Leaf; altered shape Flowering time	Seedling vigor on high glucose Altered leaf shape Late flowering
239	G1507	OE	Expression: altered ABA response Expression; heat Expression; <i>Fusarium</i> Expression: altered response to SA	This gene is induced by ABA, heat, <i>Fusarium</i> , and salicylic acid
241	G1510	OE	Leaf; dark green leaves Altered light response	Dark green leaves Long hypocotyls
243	G1535	OE	Slow growth Leaf; altered shape Altered sugar sensing Altered C/N sensing	Slow growth rate Altered leaf shape and coloration Dark green seedling on high glucose C/N sensing: more anthocyanin on nitrogen-limited media
245	G1538	OE	Flowering time Abiotic stress; sodium chloride tolerance Leaf; altered shape Expression; heat Expression; SA	Early flowering; improved tolerance to salt stress in a root growth assay; larger seedlings with more secondary root growth than wild-type; longer leaf petioles; expression induced in leaves by heat and salicylic acid treatments
247	G1539	OE	Altered trichome structure Altered cell differentiation Flower; altered carpel development	Altered trichome structure Altered cell differentiation Ectopic carpel development
249	G1549	OE	Size; small plant Slow growth Leaf; altered shape	Reduced plant size Slow growth rate Altered leaf shape and coloration
251	G1554	OE OE	Flowering time Dev and morph; Leaf	Late flowering Dark green leaves
253	G1556	OE	Dev and morph; Lethal when overexpressed	Lethal when overexpressed

255	G1557	OE	Abiotic stress; sodium chloride tolerance	Increased tolerance to sodium chloride
257	G1585	OE	Dev and morph Leaf; altered shape	Altered cell differentiation Altered leaf shape
259	G1591	OE	Flower; altered carpel development Morphology; altered cell differentiation	Ectopic carpel development Altered cell differentiation
261	G1593	OE	Inflorescence; altered architecture Leaf; altered shape and coloration	Altered inflorescence architecture Altered leaf shape and coloration
263	G1660	OE	Abiotic stress; sodium chloride tolerance	More root growth and seedling vigor in high salt
265	G1718	OE	Leaf; altered coloration	Pale gray leaves
267	G1730	OE	Abiotic stress; osmotic stress tolerance	Large and green seedlings on mannitol and glucose
269	G1743	OE	Inflorescence; altered architecture Leaf; altered shape and coloration	Altered inflorescence architecture Altered leaf shape, dark green leaves
271	G1753	OE	Altered sugar sensing Abiotic stress; osmotic stress tolerance Inflorescence; altered architecture	Altered inflorescence architecture Better germination on high sucrose media
273	G1772	OE	Size; small plant	Reduced plant size
275	G1779	OE	Abiotic stress; chilling	Mature plants have enhanced tolerance to chilling stress for a long time period
277	G1792	OE OE OE OE OE OE	Disease; <i>Erysiphe</i> Disease; <i>Fusarium</i> Disease; <i>Botrytis</i> Dev and morph; Leaf Nutrient uptake; tolerance to low N Abiotic stress; Drought	Increased resistance to <i>Erysiphe</i> Increased resistance to <i>Fusarium</i> Increased resistance to <i>Botrytis</i> Dark green, shiny leaves Increased tolerance to low nitrogen Increased tolerance to drought in a soil-based assay
279	G1796	OE	Inflorescence; Short internodes Leaf; altered shape Leaf; dark green leaves	Flower carpel alterations (thickened club-like carpels); short internodes; dark curled leaves
281	G1797	OE OE	Flowering time Dev and morph Flower	Early flowering Flower organs persisted following fertilization
283	G1798	OE OE	Flowering time Dev and morph; Inflorescence	Early flowering Multiple inflorescence defects
285	G1808	OE	Abiotic stress; chilling	Mature overexpressing plants were less tolerant to cold
287	G1816	OE	Trichome; glabrous leaves Abiotic stress; osmotic stress tolerance Root; increased hairs Altered sugar sensing Altered C/N sensing	Glabrous leaves Increased tolerance to high glucose Increased root hairs Increased tolerance to high glucose C/N sensing: improved tolerance to low nitrogen
289	G1823	OE	Flowering time	Early flowering
291	G1825	OE	Flowering time Leaf; altered shape	Early flowering Altered leaf shape
293	G1832	OE	Dev and morph; Lethal when	Lethal when overexpressed

			overexpressed	
295	G1837	OE	Abiotic stress; sodium chloride tolerance	More root growth and seedling vigor in high salt
		OE	Abiotic stress; chilling tolerance	Enhanced tolerance, better growth of seedlings under chilling conditions
297	G1840	OE	Dev and morph; Morphology: other	Formation of necrotic lesions
299	G1846	OE	Leaf; altered shape Leaf; dark green leaves	Dark green leaves, poorly developed inflorescences
301	G1850	OE	Dev and morph; Lethal when overexpressed	Lethal when overexpressed
303	G1863	KO	Abiotic stress; sodium chloride	Decreased germination under salt stress
		OE	Leaf; altered shape and coloration Flowering time	Altered leaf shape and coloration Late flowering
305	G1893	OE	Hormone sensitivity; altered ABA response; altered cotyledons Morphology Leaf; altered shape	Insensitivity to ABA; rectangular cotyledons; seedlings contain more anthocyanin; leaves were small with serrated margins
307	G1917	OE	Leaf; altered shape	Leaves are elongated and curled; with frilly, serrated margins
309	G1923	OE	Abiotic stress; heat	This gene is up-regulated by <i>Fusarium</i> and <i>Erysiphe</i> infection, as well as auxin, heat and osmotic stress treatments
		OE	Abiotic stress; osmotic stress	
		OE	Expression; Fusarium	
		OE	Expression; Erysiphe	
		OE	Hormone sensitivity; auxin	
311	G1928	OE	Abiotic stress; cold tolerance	Increased tolerance to cold
313	G1932	OE	Leaf; altered shape Leaf; dark green leaves	Leaves were dark green with jagged leaf margins
315	G1938	OE	Leaf; altered shape Leaf; dark green leaves Abiotic stress; osmotic stress Plant size; small plants	Curled, contorted leaves, dark green leaves; slow growth rate; more sensitive to osmotic stress
317	G1945	OE	Leaf; altered shape Flowering time	Altered leaf shape Late flowering
319	G1957	OE	Dev and morph; Lethal when overexpressed	Lethal due to meristem defects
321	G1968	OE	Nutrient; tolerance to low N	Overexpression resulted in more tolerance to chilling stress in a growth assay compared to control plants; overexpressing lines contained more anthocyanins when grown under low nitrogen, or low nitrogen plus glutamate, in a germination assay
323	G1983	OE	Leaf; altered shape Leaf; dark green leaves Flowering time Size; small plants	Dark green leaves; late flowering; small plants
325	G1985	OE	Dev and morph; phase change and floral reversion Dev and morph; aerial rosettes	Phase change and floral reversion Aerial rosettes
327	G1988	OE	Nutrient; Tolerance to low N Nutrient; Tolerance to low PO ₄ Flowering time Light response; Long petiole Light response; Long hypocotyl	Better growth on low nitrogen plus glutamine, better growth on low phosphate; long hypocotyl, long petiole, early flowering

329	G1990	OE	Dev and morph; Morphology: other	Lethal when overexpressed
331	G1993	OE	Leaf; altered shape Size; small plant size	Short petioles and round leaf shape Reduced plant size
333	G1995	OE	Morphology; increased trichome number Nutrient; Tolerance to low N Nutrient; Tolerance to low PO ₄ Inflorescence; altered aerial rosettes Morphology; altered timing of phase change	Increased trichome number on sepals, ectopic trichomes on carpels yield enhanced production of leaf, flower, and outer ovule epidermis products; slightly less tolerant to low nitrogen and low phosphorus; aerial rosettes occurred when a secondary inflorescence meristem developed in a manner comparable to a primary shoot meristem during the vegetative phase of growth, with aerial rosette-like structures and floral organs being bract-like
335	G1998	OE	Flowering time	Late flowering
337	G1999	OE	Flowering time	Late flowering
339	G2035	OE	Abiotic stress; sodium chloride tolerance	Increased seedling vigor in high sodium chloride
341 and 2110	G2041	OE	Abiotic stress; Sodium chloride tolerance	Increased tolerance to sodium chloride
343	G2051	OE	Abiotic stress; Cold	Increased tolerance to cold in a germination assay
345	G2060	OE	Abiotic stress; sodium chloride tolerance	More root growth and seedling vigor in high salt
347	G2063	OE	Abiotic stress; cold tolerance	Increased seedling vigor in cold
349	G2070	OE OE OE	Abiotic stress; chilling Abiotic stress; heat Expression; altered ABA response	Mature overexpressing plants were less tolerant to cold; gene was induced by ABA, cold and heat
351	G2071	OE	Flowering time	Early flowering
353	G2084	OE	Leaf; altered shape	Short petioles, and rounded, slightly dark green leaves
355	G2085	OE	Leaf; altered shape and coloration Seed; increased size, altered color Trichome; increased density	Altered leaf shape, dark green leaves Increased seed size, altered seed color Increased trichome density
357 and 2111	G2106	OE	Flowering time	Late flowering
359	G2109	OE	Hormone sensitivity; altered ABA response	Much less sensitive to ABA in a germination assay than wild-type
361	G2111	OE	Sugar sensing; Sugar sensing	Altered sugar sensing response; decreased growth and small, pale seedlings on glucose medium
363	G2129	OE	Flowering time	Early flowering
1495	G2133	OE	Abiotic stress; drought	Increased tolerance to drought in a soil-based assay
365	G2142	OE OE	Abiotic stress; tolerance to low PO ₄ Flowering time	More tolerant to phosphate deprivation in a root growth assay Accelerated flowering time
367	G2146	OE	Hormone sensitivity; altered ABA response Flowering time Inflorescence; Short internodes Leaf; dark green leaves	Insensitive to ABA in a germination assay; late flowering; more branching, short internodes, inflorescences were shorter and bushier than wild type; dark green appearance
369	G2184	OE	Flowering time	Early flowering
371	G2207	OE	Hormone sensitivity; altered ABA response Abiotic stress; sodium chloride tolerance	Increased tolerance to osmotic stress under high salt or sucrose and less sensitive to ABA in germination assays; late flowering; narrow dark green leaves

			Abiotic stress; osmotic tolerance Flowering time Leaf; altered shape Leaf; dark green leaves	
373	G2213	OE	Dev and morph; Morphology: other	Lethal when overexpressed
375	G2226	OE	Inflorescence; altered architecture Size; small plants Leaf; altered shape and coloration	Altered inflorescence architecture Reduced plant size Altered leaf shape, dark green leaves
377	G2227	OE	Size; small plant size Leaf; altered shape	Reduced plant size Altered leaf shape
379	G2239	OE	Altered C/N sensing	C/N sensing: Better germination on low nitrogen with sucrose or sucrose plus glutamine
381	G2251	OE OE OE OE	Dev and morph; Size Dev and morph; Leaf Dev and morph; Inflorescence Flowering time	Reduced plant size Round and dark green leaves Short inflorescence internodes Late flowering
383	G2269	OE	Flowering time	Late flowering
385	G2298	OE	Dev and morph; Lethal when overexpressed	Lethal when overexpressed
387	G2311	OE	Flowering time	Early flowering
389	G2317	OE	Abiotic stress; cold tolerance Abiotic stress; sodium chloride	Increased tolerance to cold Increased seedling vigor on high sodium chloride
391 and 2112	G2319	OE OE	Abiotic stress; Sodium chloride tolerance Flowering time	Increased tolerance to sodium chloride Late flowering
393	G2334	OE OE OE	Dev and morph; Size Flowering time Dev and morph; Leaf	Increased biomass Late flowering Dark green leaves and altered leaf shape
395	G2371	OE	Leaf; altered coloration Seed; altered coloration	Dark green leaves Altered seed coloration
397	G2372	OE OE OE OE	Dev and morph; Size Dev and morph; Leaf Flowering time Dev and morph; Inflorescence	Reduced plant size Dark green leaves Early flowering Altered inflorescence determinacy and reduced fertility
399	G2375	OE	Leaf; altered shape Plant size; small plants	Small, narrow leaves; plants were distinctly smaller than wild type
401	G2382	OE	Hormone sensitivity; altered ABA response	Insensitive to ABA in germination assays
403	G2394	OE	Abiotic stress; sodium chloride tolerance	Enhanced germination on high sodium chloride
405	G2404	OE	Abiotic stress; sodium chloride tolerance	Enhanced root growth on high sodium chloride
407	G2432	OE	Light response; altered shade avoidance Leaf; altered shape Flowering time Morphology; Narrow cotyledons	Shade avoidance; narrow, upward pointing leaves; delayed flowering, infertile flowers; narrow cotyledons; poorly developed roots
409	G2443	OE	Flowering time	Early flowering
411, 2113 and	G2453	OE	Biochem: misc; Biochemistry: other	Increased pigment production

2114		OE	Abiotic stress; Sodium chloride tolerance	Increased tolerance to sodium chloride
		OE	Dev and morph; Leaf	Altered leaf shape and dark green leaves
		OE	Dev and morph; Size	Reduced plant size
413	G2455	OE	Leaf; altered shape	Leaves are narrow and curled downward
415	G2456	OE	Dev and morph; Leaf	Curled and dark green leaves
		OE	Biochem: misc;	Increased pigment production
		OE	Biochemistry: other	
		OE	Dev and morph; Size	Reduced plant size
417	G2457	OE	Flower alterations	Multiple flower alterations
			Leaf; altered shape	Altered leaf shape
			Abiotic stress; sodium chloride tolerance	Increased root growth and less bleaching on high sodium chloride
419	G2459	OE	Dev and morph; Size	Reduced plant size
		OE	Dev and morph; Leaf	Curled leaves
		OE	Biochem: misc;	Increased pigment production
			Biochemistry: other	
421	G2467	OE	Premature senescence	Early senescence
423	G2492	OE	Size; small plants	Reduced plant size
425	G2505	OE	Abiotic stress; drought tolerance	Increased tolerance to drought in a soil-based assay
427	G2515	OE	Flowering time	Early flowering
		OE	Dev and morph; Inflorescence	Altered inflorescence determinacy
		OE	Dev and morph Flower	Altered flower morphology
		OE	Dev and morph; Size	Reduced size
429	G2525	OE	Abiotic stress; cold sensitivity	Increased sensitivity to cold
431	G2536	OE	Leaf; large leaf size	Large leaf size
			Size; large plant size	Increased plant size
			Delayed senescence	Delayed senescence
433	G2543	OE	Abiotic stress; cold sensitivity	Increased sensitivity to cold
435	G2550	OE	Leaf; altered shape and coloration	Altered leaf shape, dark green leaves
			Inflorescence; altered architecture	Altered inflorescence architecture
437 and 2115	G2559	OE	Flowering time	Late flowering
439	G2565	OE	Dev and morph; Size	Reduced plant size
		OE	Dev and morph; Leaf	Grayish leaf coloration and altered leaf shape
441	G2567	OE	Abiotic stress; chilling tolerance	Enhanced tolerance, better growth under chilling conditions
443	G2570	OE	Dev and morph; Morphology: other	Lethal when overexpressed
445	G2571	OE	Inflorescence; Branching changes	Changes in coloration, branching patterns, and leaf and flower development, branching, sympodial in the inflorescence, similar to that shown by tomato plants
			Leaf; altered shape	
447	G2574	OE	Premature senescence	Premature leaf senescence
			Size; small plants	Reduced plant size
449	G2575	OE	Dev and morph; Leaf	Altered leaf shape
		OE	Dev and morph; Inflorescence	Altered inflorescence architecture
451	G2579	OE	Dev and morph; Silique	Altered silique size and shape
		OE	Dev and morph Flower	Increased carpel size and infertile

		OE	Dev and morph; Size	Reduced plant size
		OE	Dev and morph; Leaf	Altered leaf shape
		OE	Abiotic stress; Chilling	Increased tolerance to chilling in a plate-based growth assay
453	G2585	OE	Seed; Large seed	Larger seed size than controls
455	G2587	OE	Dev and morph; lethal when overexpressed	Lethal when overexpressed
457	G2592	OE	Abiotic stress; cold sensitivity	Increased sensitivity to cold
459	G2597	OE	Abiotic stress; chilling	This gene was induced in leaf tissue following cold treatments at 4° C
461	G2603	OE	Abiotic stress; cold sensitivity	Increased sensitivity to cold
463	G2604	OE	Abiotic stress; Nutrient uptake	Altered C/N sensing
		OE	Flowering time	Late flowering
		OE	Dev and morph; Leaf	Altered leaf surface, gray leaves
465	G2616	OE	Dev and morph; Size	Reduced plant size
		OE	Dev and morph; Inflorescence	Altered inflorescence architecture and flower development
467	G2617	OE	Hormone sensitivity; altered ABA response Fast growth Leaf; altered shape	More ABA insensitive than wild-type in a germination assay; faster growth rate for seedlings and early stage plants; short petioles, short pedicels and wrinkled, curled, rounded leaves
469	G2628	OE	Flowering time	Early flowering
		OE	Leaf; altered shape	Rounded leaves;
		OE	Plant size; small plants	Small plants
471	G2632	OE	Abiotic stress; Chilling	Increased sensitivity to chilling in a growth-based assay
473	G2633	OE	Flowering time	Early flowering
475	G2636	OE	Leaf; altered shape Morphology; altered meristem development Morphology; lobed cotyledons	Alterations in the pattern of rosette leaf initiation by the shoot meristem; lobed leaves; adventitious shoots on the adaxial surface of lobed cotyledons
477 and 2116	G2639	OE	Dev and morph; Inflorescence	Short inflorescence internodes
		OE	Flowering time	Early flowering
		OE	Dev and morph Flower	Altered flower morphology and poorly fertile
479	G2640	OE	Dev and morph Flower	Altered flower morphology and poor fertility
		OE	Dev and morph; Size	Reduced plant size
		OE	Dev and morph; Leaf	Dark green leaves with glossy surfaces
		OE	Dev and morph; Inflorescence	Short inflorescence internodes
481	G2649	OE	Dev and morph; Inflorescence	Short inflorescence internodes
		OE	Dev and morph; Leaf	Dark green, glossy leaf surface and elongated leaf shape
		OE	Dev and morph Flower	Altered flower morphology and poorly fertile
		OE	Dev and morph; Size	Reduced plant size
483	G2650	OE	Flowering time Light response; Long petioles Light response; Long hypocotyls Light response; Upright leaves Abiotic stress; chilling	Early flowering; T2 plants developed excessive numbers of small axillary rosette leaves, long narrow leaves; elongated petioles; long hypocotyls; leaves were held in a more upright orientation than controls (potential shade avoidance); larger seedlings and mature plants than controls; larger seedlings than controls under chilling conditions; increased number of axillary meristems in the rosettes

			tolerance Size; Increased plant size Morphology; More meristems	
485	G2655	OE	Dev and morph; Root	Poorly developed and greenish roots
487	G2661	OE	Growth regulator; altered sugar sensing Leaf; dark green leaves	Better germination on glucose with greener cotyledons than wild-type; darker plants
489 and 2117	G2679	OE	Dev and morph; Morphology: other	Enhanced seedling vigor
491	G2682	OE	Dev and morph; Size	Reduced plant size
		OE	Dev and morph; Leaf	Curled leaves
493	G2686	OE	Leaf; altered shape	Rounded leaves with slightly lobed margins
495	G2690	OE	Leaf; altered shape Leaf; dark green leaves	Narrow, dark green leaves that roll down at the margins
497	G2691	OE	Abiotic stress; sodium chloride tolerance	Higher germination in high salt
499	G2694	OE	Flowering time Size; increased size Leaf; altered shape and coloration Dev and morph; flower alterations Inflorescence; altered inflorescence architecture Altered light response	Late flowering Increased seedling size Altered inflorescence architecture Altered leaf shape, dark green leaves Multiple flower alterations Long petioles and leaf orientation
501	G2699	OE	Leaf; altered shape and size	Long petioles and large leaves
503	G2702	OE	Dev and morph; Size	Reduced plant size
		OE	Dev and morph; Leaf	Altered leaf shape
505	G2717	OE	Abiotic stress; Osmotic stress	Increased tolerance to osmotic stress (salt and sucrose)
		OE	Abiotic stress; sodium chloride tolerance	
		OE	Abiotic stress; drought tolerance	Increased tolerance to drought in a soil-based assay
		OE	Hormone sensitivity; altered ABA response	Insensitive to ABA in germination assays
		OE	Size; increased plant size	Larger seedlings
507	G2718	OE	Dev and morph; Root	Increased root hair density
		OE	Dev and morph; Trichome	Reduced trichome density
		OE	Abiotic stress; Nutrient uptake	Increased tolerance to low nitrogen
		OE	Biochem: misc; Biochemistry: other	Reduced pigment production
509	G2723	OE	Flowering time	Late flowering
511	G2741	OE	Flowering time	Late flowering
		OE	Dev and morph; Size	Increased biomass
513	G2743	OE	Morphology; altered flower development Flowering time	Delayed flowering; altered flower development (sepals, petals and stamens were reduced in size, pollen production was poor)
515	G2747	OE	Root; reduced root formation Leaf; altered shape	Long petioles and slightly narrow elongated leaf blades, little or no secondary root formation
517	G2754	OE	Dev and morph Flowering time	Shade avoidance Early flowering
519	G2757	OE	Size; small plant size	Reduced plant size
521	G2763	OE	Flowering time	Late flowering
		OE	Abiotic stress; chilling	More sensitive to chilling temperatures during growth

		OE	Growth regulator; altered sugar sensing	More sensitive to glucose
		OE	Pigment; high anthocyanin	More anthocyanin accumulation in seedlings
		OE	Leaf; dark green leaves	Dark green leaves
523	G2765	OE	Slow growth	Retarded growth at early stages
525 and 2118	G2768	OE	Dev and morph; Leaf	Increased leaf size
		OE	Dev and morph Flower	Increased petal number, loss of floral determinacy
527 and 2119	G2771	OE	Dev and morph; Leaf	Altered leaf shape and dark green leaves
		OE	Abiotic stress; Chilling	Reduced anthocyanins in a chilling growth assay
		OE	Flowering time	Late flowering
		OE	Dev and morph; Light response	Elongated hypocotyl and pale in coloration
529	G2776	OE	Abiotic stress; osmotic tolerance Growth regulator; altered sugar sensing	Seedlings grown on high sucrose were larger with green cotyledons compared with wild-type seedlings
531	G2777	OE	Flowering time	Early flowering
533	G2779	OE	Dev and morph Flowering time	Pale leaf coloration Early flowering
535	G2783	OE	Premature senescence Size; small plant	Early senescence Reduced plant size
537 and 2120	G2784	OE	Dev and morph; Inflorescence	Altered inflorescence architecture
		OE	Dev and morph; Morphology: other	Slow growth rate
		OE	Dev and morph; Leaf	Dark green and curled leaves
		OE	Abiotic stress; Cold	Increase tolerance to cold in a germination assay
539	G2790	OE	Abiotic stress; chilling	Mature overexpressing plants were less tolerant to cold
541 and 2121	G2802	OE	Flowering time	Early and late flowering
543	G2805	OE	Flowering time	Early flowering
545	G2826	OE	Morphology; increased trichome density Inflorescence; ectopic aerial rosettes Morphology; altered timing of phase change	Flowers had increased trichome density on sepals and possessed ectopic trichomes on the carpels; overexpressors developed aerial rosettes at axillary nodes, indicating a disruption in phase change in the inflorescence
547	G2830	OE	Altered C/N sensing	C/N sensing
549	G2832	OE	Flowering time Leaf; altered coloration	Early flowering Pale gray leaf color
551	G2834	OE	Slow growth rate	Slow growth rate
553	G2837	OE	Leaf; altered shape and coloration	Altered leaf shape, dark green leaves
555	G2838	OE	Flowering time Size; large plant Leaf; altered coloration Trichome; increased density Flower; multiple alterations	Late flowering Increased seedling size Aerial rosettes Dark green leaves Increased trichome density Multiple flower alterations
557	G2839	OE	Abiotic stress; osmotic stress tolerance	Better germination on high sucrose; increased resistance to osmotic stress; small, contorted leaves
		OE	Leaf; altered shape	that are upcurled at margins, short petioles; poorly
		OE	Growth regulator: altered sugar sensing	developed flowers with downward-pointing short
		OE	Inflorescence; Architectural	pedicels

			change	
559	G2846	OE	Leaf; altered shape and coloration Flowering time Size; small plant	Altered leaf shape, dark green leaves Late flowering Reduced plant size
561	G2847	OE	Leaf; altered coloration Size; small plant	Dark green leaves Reduced plant size
563	G2850	OE	Leaf; altered shape and coloration	Curled, dark green leaves
565	G2851	OE	Leaf; small leaves Leaf; altered shape Leaf; dark green leaves Slow growing	Small, dark green, curled and wrinkled leaves; small plants, slow growing
567	G2854	OE	Hormone sensitivity; altered ABA response Growth regulator; altered sugar sensing	Better germination on high ABA and sucrose-containing media
569	G2859	OE	Leaf; altered shape and coloration Inflorescence; altered architecture Altered light response	Altered leaf shape and light green leaves Inflorescence architecture Long hypocotyls, cotyledons; light green plants
571	G2865	OE	Hormone sensitivity; altered ABA response	Insensitive to ABA in germination assays
573	G2866	OE	Dev and morph; Leaf	Curled leaves
575	G2869	OE	Dev and morph; Morphology: other	Lethal when overexpressed
577	G2884	OE OE OE OE	Dev and morph; Morphology: other Dev and morph; Size Dev and morph Flower Dev and morph; Light response	Abnormal embryo development Reduced plant size Multiple flower defects and low fertility Long and green hypocotyls
579	G2885	OE	Dev and morph; cell differentiation Abiotic stress; cold tolerance	Altered cell differentiation Decreased tolerance to cold
581	G2887	OE	Dev and morph; Lethal when overexpressed	Lethal when overexpressed
583	G2888	OE	Leaf; altered shape	Altered leaf shape
585	G2898	OE	Sugar sensing	Better germination on high glucose media
587 and 2122	G2907	OE	Dev and morph; Senescence	Accelerated senescence
589	G2913	OE	Nutrient; tolerance to low N	Less anthocyanin on nitrogen-limited media
591	G2930	OE	Abiotic stress; chilling tolerance	Mature plants have enhanced tolerance to chilling stress
593	G2933	OE	Seed; Large seed Abiotic stress; chilling tolerance	Big seeds; larger plants; more tolerant to chilling stress in growth assays
595	G2934	OE	Size; small plant	Reduced plant size
597	G2958	OE	Inflorescence; altered architecture Leaf; altered shape and coloration Size; small plants	Altered inflorescence architecture Altered leaf shape, dark green leaves Reduced plant size
599	G2964	OE	Flowering time Dev and morph; aerial rosettes	Late flowering Aerial rosettes
601	G2967	OE	Flowering time	Early flowering

603	G2969	OE	Hormone sensitivity; altered ABA response	Increased tolerance to sucrose and ABA in germination assays
605	G2972	OE	Nutrient; Tolerance to low PO ₄	Overexpressing lines had more tolerance to low phosphate conditions
607	G2979	OE OE OE	Flowering time Dev and morph; Size Dev and morph Flower	Late flowering Increased biomass Increased flower organ size and number
609	G2981	OE	Nutrient; Tolerance to low N	Greener, larger seedlings on low nitrogen medium supplemented with glutamine
611	G2982	OE	Abiotic stress; drought tolerance	Plants transformed with this gene displayed increased tolerance to dehydration stress in a soil-based assay
613	G2983	OE	Flower; ectopic carpel formation Dev and morph; altered cell proliferation Altered root Dev and morph; altered cell differentiation, trichome cell fate	Ectopic carpel formation Altered cell proliferation Altered growth pattern, proliferation and root hair density Altered cell differentiation, trichome cell fate
615	G2990	OE	Nutrient; tolerance to low N	Altered response to nitrogen deprivation, including more root growth and more anthocyanin production in some lines, more bleaching in others when grown on low nitrogen, indicating this gene is involved in the response to nutrient limitation
617	G2992	OE	Hormone sensitivity; altered ABA response Flowering time Abiotic stress; sodium chloride tolerance Nutrient; Tolerance to low N Root; Fewer lateral roots Leaf; altered shape Plant size; small plants	Enhanced ability to germinate on high NaCl and high ABA; less tolerant to low nitrogen; early flowering; fewer lateral roots; altered leaf shape; smaller plants
619	G2993	OE OE OE OE OE	Dev and morph; Light response Dev and morph; Root Flowering time Abiotic stress; Osmotic stress Abiotic stress; Chilling	Elongated hypocotyl and altered leaf orientation Altered root branching Late flowering Increased sensitivity to osmotic stress Increased sensitivity to chilling in a growth assay
621	G2996	OE	Abiotic stress; osmotic stress	Increased sensitivity to mannitol in root growth inhibition assays, (no secondary root growth) indicating this gene influences osmotic stress response
623	G2998	OE	Abiotic stress; sodium chloride tolerance	Better germination in high NaCl; late flowering
625	G2999	OE OE OE	Abiotic stress; sodium chloride tolerance Abiotic stress: drought tolerance Flowering time	Increased tolerance to high sodium chloride Increased tolerance to drought in a soil-based assay
627	G3002	OE	Flowering time	Early flowering
629 and 2123	G3003	OE	Flowering time	Late flowering
631	G3008	OE	Leaf size	Large leaf size
633	G3017	OE	Size; small plant size	Reduced plant size

635	G3021	OE	Flowering time Leaf; altered shape and coloration Inflorescence; altered architecture	Late flowering Altered inflorescence architecture Altered leaf shape, dark green leaves
637	G3032	OE	Dev and morph; Light response	Altered leaf orientation
		OE	Flowering time	Early flowering
639	G3044	OE	Flowering time	Early flowering
		OE	Leaf; altered shape	Narrow, serrated leaves
		OE	Leaf; light green leaves	Pale leaves
641	G3054	OE	Hormone sensitivity; altered ABA response	Reduced sensitivity to ABA
643	G3055	OE	Hormone sensitivity; altered ABA response	Insensitive to ABA in germination assays
645	G3059	OE	Dev and morph; Senescence	Accelerated senescence
		OE	Dev and morph; Leaf	Dark green leaves and altered leaf shape
		OE	Dev and morph; Inflorescence	Altered inflorescence architecture
		OE	Dev and morph; Morphology: other	Altered cotyledon shape
		OE	Dev and morph; Size	Reduced plant size
647	G3060	OE	Flowering time	Some lines flowered early, and others flowered late
649	G3061	OE	Flowering time	Early flowering
651	G3067	OE	Hormone sensitivity; altered ABA response	Insensitive to ABA in germination assays
653	G3070	OE	Dev and morph; Leaf	Gray leaf coloration
655	G3076	OE	Abiotic stress; Drought	Increased tolerance to drought
657	G3083	OE	Abiotic stress; sodium chloride tolerance	Higher germination in high salt
659	G3084	OE	Leaf; altered shape	Altered leaf shape
661	G3086	OE	Flowering time Abiotic stress; heat tolerance Abiotic stress; sodium chloride tolerance Abiotic stress: drought tolerance	Early flowering Increased tolerance to heat Increased tolerance to high sodium chloride Increased tolerance to drought in a soil-based assay
663	G3091	OE	Dev and morph; Morphology: other	Retarded growth rate
		OE	Dev and morph; Leaf	Altered leaf shape and dark green leaves
665	G3094	OE	Dev and morph; Leaf	Serrated leaves and long petioles
		OE	Dev and morph; Flower	Altered flower morphology
667	G3095	OE	Dev and morph; Leaf	Altered leaf shape and dark green leaves
		OE	Dev and morph; Morphology: other	Slow growth rate
669	G3111	OE	Dev and morph; Leaf	Altered leaf shape and dark green leaves
		OE	Flowering time	Late flowering
		OE	Dev and morph; Senescence	Accelerated senescence

Table 5 shows the polypeptides identified by SEQ ID NO; Gene ID (GID) No; the transcription factor family to which the polypeptide belongs, and conserved domains of the polypeptide. The first column shows the polypeptide SEQ ID NO; the third column shows the transcription factor family to which the polynucleotide belongs; and the fourth column shows the amino acid residue positions of the conserved domain in amino acid (AA) coordinates.

Table 5. Gene families and conserved domains

Polypeptide SEQ ID NO:	GID No.	Family	Conserved Domains in Amino Acid Coordinates
2	G2	129-195, 221-288	AP2
4	G12	27-94	AP2
6	G15	281-357, 383-451	AP2
8	G30	17-35	AP2
10	G46	107-175	AP2
12	G47	11-80	AP2
14	G129	18-73	MADS
16	G131	1-57	MADS
18	G133	1-57	MADS
20	G134	1-57	MADS
22	G135	1-57	MADS
24	G136	18-74	MADS
26	G137	1-57	MADS
28	G138	1-57	MADS
30	G139	1-57	MADS
32	G140	16-72	MADS
34	G142	2-57	MADS
36	G145	1-57	MADS
38	G146	1-57	MADS
40	G148	1-57	MADS
42	G151	2-57	MADS
44	G153	1-57	MADS
46	G155	1-57	MADS
48	G171	1-57	MADS
50	G172	12-68	MADS
52	G173	1-57	MADS
54	G200	12-116	MYB-(R1)R2R3
56	G224	7-114	PMR
58	G244	14-114	MYB-(R1)R2R3
60	G246	57-159	MYB-(R1)R2R3
62	G253	16-116	MYB-(R1)R2R3
64	G268	186-689	AKR
66	G287	293-354	MISC
68	G309	226-506	SCR
70	G314	54-300	SCR
72	G319	12-42	Z-CO-like
74	G324	245-291	RING/C3H2C3
76	G344	166-192	GATA/Zn
78	G351	77-97, 118-140	Z-C2H2
1380	G353	41-61, 84-104	Z-C2H2
1382	G354	42-62, 88-109	Z-C2H2
80	G355	49-69, 94-116	Z-C2H2
82	G366	40-60	Z-C2H2
84	G370	97-117	Z-C2H2
86	G372	141-180	RING/C3HC4
88	G374	35-67, 286-318	Z-ZPF
90	G380	637-677	RING/C3H2C3
92	G386	133-193	HB

94	G416	451-511	HB
96	G434	39-99	HB
98	G438	22-85	HB
100	G446	53-389	ARF
102	G468	86-102, 141-171	IAA
104	G478	186-281	SBP
106	G485	21-116	CAAT
108	G521	7-156	NAC
110	G549	1-395	MISC
112	G550	134-180	Z-Dof
114	G571	160-220, 441-452	bZIP
116	G581	339-396	HLH/MYC
118	G600	115-290	DBP
120	G624	327-406	ABI3/VP-1
122	G627	1-57	MADS
124	G646	55-97	Z-Dof
126	G651	5-31, 162-182, 208-231	Z-C2H2
128	G652	28-49, 137-151, 182-196	Z-CLDSH
130	G707	109-169	HB
132	G728	206-255	GARP
134	G730	169-217	GARP
136	G738	351-393	Z-Dof
138	G744	176-217	RING/C3H2C3
140	G752	439-479	RING/C3H2C3
142	G807	12-76	HS
144	G811	18-108	HS
146	G839	60-185, 290-353	AKR
148	G846	222-531, 679-719, 840-923	SWI/SNF
150	G852	225-593	SCR
152	G905	118-159	RING/C3H2C3
154	G916	293-349	WRKY
156	G926	174-226	CAAT
158	G957	12-182	NAC
160	G961	12-180	NAC
162	G975	4-71	AP2
164	G1011	2-57	MADS
166	G1013	114-170	WRKY
168	G1017	9-382	ARF
170	G1033	52-123	HMG
172	G1037	11-134, 200-248	GARP
174	G1082	1-53, 503-613	BZIPT2
176	G1100	96-137	RING/C3H2C3
178	G1108	363-403	RING/C3H2C3
180	G1113	85-128	RING/C3H2C3
182	G1128	181-247	AT-hook
184	G1136	397-474	HLH/MYC
186	G1142	63-123	HLH/MYC
188	G1150	887-907	PAZ
190	G1206	494-668	ENBP
192	G1247	18-141	MYB-(R1)R2R3
194	G1274	111-164	WRKY

196	G1276	158-224, 250-316	AP2
198	G1289	207-286, 464-493	AKR
200	G1313	32-135	MYB-(R1)R2R3
202	G1327	14-116	MYB-(R1)R2R3
204	G1340	54-142	TH
206	G1341	1-34, 288-398	BZIPT2
208	G1357	16-153	NAC
210	G1361	59-200	NAC
212	G1384	127-194	AP2
214	G1389	30-87	TEO
216	G1412	13-162	NAC
218	G1420	221-280	WRKY
220	G1423	6-62	MADS
222	G1446	1-405	MISC
224	G1451	22-357	ARF
226	G1452	30-177	NAC
228	G1468	95-115, 170-190	Z-C2H2
230	G1474	41-68	Z-C2H2
232	G1476	37-57	Z-C2H2
234	G1482	5-63	Z-CO-like
236	G1483	17-66	Z-CO-like
238	G1493	242-289	GARP
240	G1507	219-247	RING/C3HC4
242	G1510	230-263	GATA/Zn
244	G1535	109-169	HB
246	G1538	66-126	HB
248	G1539	76-136	HB
250	G1549	75-135	HB
252	G1554	238-287	GARP
254	G1556	19-67	GARP
256	G1557	19-67	GARP
258	G1585	55-115	HB
260	G1591	8-68	HB
262	G1593	227-290	HB
264	G1660	362-476	DBP
266	G1718	113-153	RING/C3H2C3
268	G1730	103-144	RING/C3H2C3
270	G1743	94-136	RING/C3H2C3
272	G1753	12-80	AP2
274	G1772	123-176	RING/C3HC4
276	G1779	190-239	GATA/Zn
278	G1792	17-85	AP2
280	G1796	54-121	AP2
282	G1797	1-57	MADS
284	G1798	1-57	MADS
286	G1808	140-200	bZIP
288	G1816	31-81	MYB-related
290	G1823	205-252	GARP
292	G1825	55-103	GARP
294	G1832	67-87, 150-166, 213-233	Z-C2H2
296	G1837	1-53, 398-507	BZIPT2
298	G1840	87-154	AP2

300	G1846	16-83	AP2
302	G1850	56-149	HS
304	G1863	77-186	GRF-like
306	G1893	73-185	Z-C2H2
308	G1917	153-179	GATA/Zn
310	G1923	23-153	NAC
312	G1928	101-121, 178-198	Z-C2H2
314	G1932	9-76	AP2
316	G1938	74-143	PCF
318	G1945	49-71	AT-hook
320	G1957	52-143	ABI3/VP-1
322	G1968	64-84, 368-390	Z-C2H2
324	G1983	71-147	Z-C3H
326	G1985	37-57	Z-C2H2
328	G1988	5-50	Z-CO-like
330	G1990	184-204, 261-283	Z-C2H2
332	G1993	23-43	Z-C2H2
334	G1995	93-113	Z-C2H2
336	G1998	5-71	Z-CO-like
338	G1999	15-55	Z-CO-like
340	G2035	93-259	AKR
342	G2041	670-906, 1090-1175	SWI/SNF
344	G2051	7-158	NAC
346	G2060	204-263	WRKY
348	G2063	7-63	MADS
350	G2070	45-137	bZIP
352	G2071	307-358	bZIP
354	G2084	41-172	RING/C3HC4
356	G2085	214-241	GATA/Zn
358	G2106	56-139, 165-233	AP2
360	G2109	1-57	MADS
362	G2111	1-57	MADS
364	G2129	71-140	bZIP
1496	G2133	11-83	AP2
366	G2142	43-120	HLH/MYC
368	G2146	136-200	HLH/MYC
370	G2184	17-147	NAC
372	G2207	180-227, 546-627	bZIP-NIN
374	G2213	156-205	bZIP-NIN
376	G2226	103-144	RING/C3H2C3
378	G2227	199-239	RING/C3H2C3
380	G2239	128-169	RING/C3H2C3
382	G2251	89-132	RING/C3H2C3
384	G2269	136-177	RING/C3H2C3
386	G2298	4-71	AP2
388	G2311	5-58	MYB-related
390	G2317	48-110	MYB-related
392	G2319	32-120	MYB-related
394	G2334	82-118, 150-194	GRF-like
396	G2371	25-127	ABI3/VP-1
398	G2372	18-378	ARF
400	G2375	51-148	TH

402	G2382	90-177, 246-333	TH
404	G2394	355-395	RING/C3H2C3
406	G2404	319-359	RING/C3H2C3
408	G2432	64-106	Z-Dof
410	G2443	20-86	Z-CO-like
412	G2453	130-176	YABBY
414	G2455	136-153	YABBY
416	G2456	148-195	YABBY
418	G2457	110-127	YABBY
420	G2459	50-97	YABBY
422	G2467	25-118	HS
424	G2492	616-860	ENBP
426	G2505	9-137	NAC
428	G2515	1-57	MADS
430	G2525	196-308	DBP
432	G2536	5-135	NAC
434	G2543	31-91	HB
436	G2550	345-408	HB
438	G2559	60-170	DBP
440	G2565	243-292	GARP
442	G2567	18-384	ARF
444	G2570	235-283	GARP
446	G2571	133-200	AP2
448	G2574	225-284	WRKY
450	G2575	137-192	WRKY
452	G2579	52-119	AP2
454	G2585	103-162	WRKY
456	G2587	108-165	WRKY
458	G2592	119-429	TUBBY
460	G2597	62-200	TUBBY
462	G2603	104-389	TUBBY
464	G2604	34-64, 73-103	Z-LSDlike
466	G2616	79-139	HB
468	G2617	57-77	Z-C2H2
470	G2628	36-105	bZIP
472	G2632	170-221	CAAT
474	G2633	123-490	SCR
476	G2636	14-146	NAC
478	G2639	114-167	SRS
480	G2640	146-189	SRS
482	G2649	112-155	SRS
484	G2650	34-91	TEO
486	G2655	106-180	HLH/MYC
488	G2661	40-100	HLH/MYC
490	G2679	107-177	CPP
492	G2682	67-181	CPP
494	G2686	122-173	WRKY
496	G2690	46-113	AP2
498	G2691	78-145	AP2
500	G2694	1-446	OTHER
502	G2699	54-407	SCR
504	G2702	31-131	MYB-(R1)R2R3

506	G2717	5-58	MYB-related
508	G2718	21-76	MYB-related
510	G2723	12-174	MYB-related
512	G2741	140-205	GARP
514	G2743	201-249	GARP
516	G2747	19-113	ABI3/VP-1
518	G2754	198-393, 554-638	SWI/SNF
520	G2757	35-123, 348-434	TH
522	G2763	140-210	HLH/MYC
524	G2765	124-190	HLH/MYC
526	G2768	288-346	DBP
528	G2771	333-433	HLH/MYC
530	G2776	144-210	HLH/MYC
532	G2777	278-350	HLH/MYC
534	G2779	144-213	HLH/MYC
536	G2783	63-124, 151-235, 262-318	ACBF-like
538	G2784	139-260	DBP
540	G2790	137-200	HLH/MYC
542	G2802	48-196	NAC
544	G2805	2-169	NAC
546	G2826	75-95	Z-C2H2
548	G2830	245-266	Z-C2H2
550	G2832	11-31, 66-86, 317-337	Z-C2H2
552	G2834	246-266, 335-356	Z-C2H2
554	G2837	140-160	Z-C2H2
556	G2838	57-77	Z-C2H2
558	G2839	34-60, 85-113	Z-C2H2
560	G2846	266-329	HLH/MYC
562	G2847	205-268	HLH/MYC
564	G2850	318-381	HLH/MYC
566	G2851	248-309	HLH/MYC
568	G2854	110-250	ACBF-like
570	G2859	145-226	HLH/MYC
572	G2865	86-162	HLH/MYC
574	G2866	84-100, 139-168	IAA
576	G2869	26-409	ARF
578	G2884	228-276	GARP
580	G2885	196-243	GARP
582	G2887	4-180	NAC
584	G2888	41-61, 120-140	Z-C2H2
586	G2898	62-133	HMG
588	G2907	12-120, 854-923	PCGL
590	G2913	43-127	ARID
592	G2930	53-133	HLH/MYC
594	G2933	65-137	HLH/MYC
596	G2934	37-110	HLH/MYC
598	G2958	88-104, 143-172	IAA
600	G2964	41-63, 201-235	Z-C3H
602	G2967	66-88, 358-385	Z-C2H2
604	G2969	128-150	Z-C2H2
606	G2972	8-32, 129-149, 277-294	Z-C2H2
608	G2979	192-211	E2F

610	G2981	155-173	E2F
612	G2982	107-124	E2F
614	G2983	88-148	HB
616	G2990	54-109, 203-263	ZF-HB
618	G2992	29-84, 159-219	ZF-HB
620	G2993	85-138, 221-285	ZF-HB
622	G2996	75-126, 194-254	ZF-HB
624	G2998	74-127, 243-303	ZF-HB
626	G2999	82-131, 201-261	ZF-HB
628	G3002	6-50, 104-168	ZF-HB
630	G3003	131-280	Z-C2H2
632	G3008	10-275	EIL
634	G3017	133-201	HLH/MYC
636	G3021	110-155	HLH/MYC
638	G3032	285-333	GARP
640	G3044	222-311	HLH/MYC
642	G3054	77-96, 149-168	Z-C3H
644	G3055	97-115, 178-197, 266-287	Z-C3H
646	G3059	219-287	Z-C3H
648	G3060	42-61, 219-237	Z-C3H
650	G3061	73-90, 174-193	Z-C2H2
652	G3067	198-219	Z-C2H2
654	G3070	129-150	Z-C2H2
656	G3076	70-100, 182-209	bZIP-ZW2
658	G3083	75-105, 188-215	bZIP-ZW2
660	G3084	94-110, 148-177	IAA
662	G3086	297-376	HLH/MYC
664	G3091	34-131	PLATZ
666	G3094	7-143	PLATZ
668	G3095	16-151	PLATZ
670	G3111	111-152	RING/C3H2C3

Examples of some of the utilities that may be desirable in plants, and that may be provided by transforming the plants with the presently disclosed sequences, are listed in Table 6. Many of the transcription factors listed in Table 6 may be operably linked with a specific promoter that causes the transcription factor to be expressed in response to environmental, tissue-specific or temporal signals. For example, G370 induces ectopic trichomes on flowers but also produces small plants. The former may be desirable to produce insect or herbivore resistance, or increased cotton yield, but the latter may be undesirable with respect to yield in that it may reduce biomass. However, by operably linking G370 with a flower-specific promoter, one may achieve the desirable benefits of the gene without affecting overall biomass to a significant degree. For examples of flower specific promoters, see Kaiser et al. (supra). For examples of other tissue-specific, temporal-specific or inducible promoters, see the above discussion under the heading "Vectors, Promoters, and Expression Systems".

Table 6. Genes, traits and utilities that affect plant characteristics

Trait Category	Phenotypic alteration(s)	Transcription factor genes that impact traits	Utility
Abiotic stress	Effect of chilling on plants Increased sensitivity Increased tolerance	G2632; G2763; G2790; G2885; G2993 G1274; G1357; G1779; G1928; G2063; G2567; G2579; G2650; G2771; G2930; G2933	Improved growth rate, earlier planting, yield
	Germination in cold Increased sensitivity Increased tolerance	G134; G344; G651; G1808; G2070; G2525; G2543; G2592; G2993 G224; G728; G807; G1274; G1837; G2051; G2317; G2603; G2784	Temperature stress response manipulation Earlier planting; improved survival, yield
	Drought Increased tolerance	G46; G47; G926; G975; G1206; G1274; G1357; G1452; G1792; G2133; G2505; G2717; G2982; G2999; G3076; G3086	Improved survival, vigor, appearance, yield, range
	Freezing	G1206; G2982	Improved survival, vigor, appearance, yield
	Heat Increased sensitivity Increased tolerance	G550 G3086	Improved germination, growth rate, later planting, yield
	Osmotic stress Increased sensitivity Increased tolerance	G155; G370 (KO); G1863; G1938; G2993; G2996 G47; G353; G916; G926; G1033; G1412; G1452; G1730; G1753; G1816; G2207; G2661; G2717; G2776; G2839; G2854; G2969	Abiotic stress response manipulation Improved germination rate, survival, yield
	Salt tolerance Altered response (one line more tolerant, one line more sensitive) Increased tolerance	G2394 G355; G624; G1017; G1037; G1538; G1557; G1660; G1837; G2035; G2041; G2060; G2207; G2317; G2319; G2394; G2404; G2453; G2457; G2691; G2717; G2992; G2998; G2999; G3083; G3086	Improved germination rate, survival, yield; extended growth range
	Nitrogen stress Sensitivity to N limitation Less sensitive to N limitation	G707; G1136; G1483; G1535; G1968; G1995; G2718; G2990; G2992 G153; G200; G581; G839; G916; G1013; G1150; G1274; G1792;	Improved yield and nutrient stress tolerance, decreased fertilizer usage

		G1816; G1988; G2239; G2604; G2718; G2830; G2913; G2981	
	Phosphate stress Sensitivity to PO ₄ limitation Less sensitive to PO ₄ limitation	G1995 G355; G624; G1988; G2142; G2972	Improved yield and nutrient stress tolerance, decreased fertilizer usage
Altered expression	Induced by ABA	G224; G244; G355; G571; G1037; G1482; G1507; G2070; G2085	Modification of seed development, seed dormancy, cold and dehydration tolerance
	Altered by auxin	G151; G153; G224; G244; G550; G807; G1037; G1274; G1384; G1482; G1535; G1923	Regulation of cell division, growth and maturation, particularly at shoot tips
	Induced by salicylic acid	G140; G224; G374; 1037; G1100; G1274; G1507; G1538; G2070	Resilience to heat or physiological conditions that result in high levels of salicylic acid
	After challenge with <i>Erysiphe</i>	G314; G571; G1274; G1923; G2070; G2085	Yield, appearance, survival, extended range
	After challenge with <i>Fusarium</i>	G140; G153; G171; G224; G434; G1384; G1507; G1923	Yield, appearance, survival, extended range
	Induced by heat	G153; G171; G224; G434; G550; G807; G961; G1037; G1384; G1412; G1482; G1507; G1538; G1850; G1923; G2070	Germination, growth rate, later planting
	Cold	G171; G224; G314; G1274; G1730; G2070; G2085; G2597	Improved growth rate, earlier planting, yield
	Osmotic stress	G571; G1274; G1412; G1482; G1730; G1923; G2085	Abiotic stress response manipulation
	Drought	G139; G244; G434; G571; G1100; G1412	Improved survival, vigor, appearance, yield
	Salt	G224; G550; G1037	Improved germination rate, survival, yield; extended growth range
Herbicide	Glyphosate resistance	G2133	Generation of glyphosate resistant plants, and increasing plant resistance to oxidative stress
Hormone sensitivity	Absciscic acid (ABA) sensitivity Reduced sensitivity or insensitive to ABA	G12 (KO); G926; G1357; G1412; G1452; G1893; G2109; G2146; G2207; G2382; G2617; G2717; G2854; G2865; G2969; G2992; G3054; G3055; G3067	Modification of seed development, improved seed dormancy, cold and dehydration tolerance
	1-Aminocyclopropane-1- carboxylate (ACC) sensitivity Increased sensitivity to ACC, the immediate precursor of ethylene	G12	Regulation of oxidative stress and programmed cell death, delay over-ripening of fruit

Disease	<i>Botrytis</i> Increased resistance or tolerance	G1792	Improved yield, appearance, survival, extended range
	<i>Fusarium</i> Increased resistance or tolerance	G1792	Improved yield, appearance, survival, extended range
	<i>Erysiphe</i> Increased resistance or tolerance	G1792	Improved yield, appearance, survival, extended range
Growth regulator	Altered sugar sensing Decreased tolerance to sugars Increased tolerance to sugars	G155; G344; G478; G1420; G2111; G2763 G224; G905; G916; G1033; G1108; G1493; G1535; G1753; G1816; G2661; G2776; G2839; G2854; G2898	Alteration of energy balance, photosynthetic rate, carbohydrate accumulation, biomass production, source-sink relationships, senescence; alteration of storage compound accumulation in seeds
	Altered C/N sensing	G153; G200; G581; G707; G916; G1013; G1150; G1274; G1483; G1535; G1816; G1988; G2239; G2604; G2830; G2913; G2981	Alteration or control of assimilate partitioning
Flowering time	Early flowering	G129; G131; G135; G136; G137; G138; G140; G142; G145; G146; G148; G153; G155; G172; G200; G246; G416; G485 (OE); G549; G600; G627; G1011; G1037 (KO); G1142 (KO); G1538; G1797; G1798; G1823; G1825; G1988; G2071; G2129; G2142; G2184; G2311; G2372; G2443; G2515; G2628; G2633; G2639; G2650; G2754; G2777; G2779; G2802 (antisense clone); G2805; G2832; G2967; G2992; G3002; G3032; G3044; G3060; G3061; G3086	Faster generation time; synchrony of flowering; additional harvests within a growing season, shortening of breeding programs
	Late flowering	G2; G15; G47; G173; G309; G319; G324; G372; G380; G434; G485 (KO); G571 (KO); G581; G624; G707; G738; G744; G752; G839; G852; G905; G1113; G1136; G1142; G1150; G1276; G1357; G1361; G1446; G1451; G1452; G1468; G1474; G1493; G1549; G1554; G1863; G1945;	Increased yield or biomass, alleviate risk of transgenic pollen escape, synchrony of flowering

		G1983; G1998; G1999; G2106; G2146; G2207; G2251; G2269; G2319; G2334; G2432; G2559; G2604; G2694; G2723; G2741; G2743; G2763; G2771; G2802 (sense clone); G2838; G2846; G2964; G2979; G2993; G2998; G3003; G3021; G3060; G3111	
Development and morphology	Altered flower structure	<p>Stamen G15; G129; G133; G1420; G2455; G2694; G2768</p> <p>Sepal G129; G134; G140; G1420; G2694; G2979; G3094</p> <p>Petal G129; G133; G134; G140; G1420; G2768; G3094</p> <p>Pedicel G1420; G1539; G1591; G2839; G2979; G2983</p> <p>Carpel G129; G133; G446; G1539; G1591; G1796; G2455; G2579; G2617; G2694; G2768; G2983</p> <p>Multiple alterations G15; G550; G651; G730; G1013; G1100; G1128; G1420; G1549; G1798; G1825; G1995; G2226; G2457; G2455; G2515; G2575; G2616; G2639; G2640; G2649; G2694; G2743; G2826; G2838; G2859; G2884; G3094</p> <p>Changes in organ identity G129; G133; G134; G140</p> <p>Enlarged floral organs G15; G2979</p> <p>Increase in flower organ number G2768 ;G2979</p> <p>Terminal flowers G1798; G2515</p> <p>Flower organs persisting following fertilization G1011; G1797</p> <p>Siliques G15; G2579; G2884</p> <p>Broad, large rosettes G1274</p> <p>Loss of flower determinacy G131; G135; G2768</p> <p>Reduced fertility G15; G549; G651; G846; G1100; G1798; G2372; G2579; G2616; G2639; G2640; G2649; G2768; G2884</p> <p>Gamete lethal G846</p>	Ornamental modification of plant architecture, improved or reduced fertility to mitigate escape of transgenic pollen, improved fruit size, shape, number or yield

	Altered shoot meristem development	G438 (KO); G916; G1585; G1957; G2636; G2650; G2885	Ornamental modification of plant architecture, manipulation of growth and development, increase leaf numbers, modulation of branching patterns to provide improved yield or biomass
	Inflorescence architectural change Altered inflorescence branching pattern Short internodes/bushy inflorescences Terminal flowers Altered inflorescence determinacy Aerial rosette development Downward pedicels Homeotic transformation Multiple inflorescence alterations	G47; G446; G2571; G2146; G2571; G2694; G2784; G2859 G47; G253; G1274; G1474; G1593; G1743; G1753; G1796; G2146; G2226; G2550; G2251; G2575; G2616; G2639; G2640; G2649; G2958; G3021 G131; G135; G137; G145; G148; G155; G549; G1798; G2372; G2515 G131; G135; G549; G2372; G2515 G1985; G1995; G2826; G2838 G2839 G129, G133, G134; G140 G446; G549; G1798; G2616; G2694; G2784; G2839; G3059	Ornamental modification of flower architecture; timing of flowering; altered plant habit for yield or harvestability benefit; reduction in pollen production of genetically modified plants; manipulation of seasonality and annual or perennial habit; manipulation of determinate vs. indeterminate growth
	Altered branching pattern	G47; G438 (KO)	Ornamental modification of plant architecture, improved lodging resistance
	Stem morphology and altered vascular tissue structure	G47	Modulation of lignin content; improvement of wood, palatability of fruits and vegetables
	Apical dominance Reduced apical dominance	G47	Ornamental modification of plant architecture; , improved lodging resistance
	Altered trichome density; development, or structure Ectopic trichomes Altered trichome development Increased trichome number or density Reduced or no trichomes	G370; G2826 G1539; G2983 G370; G1995; G2085; G2826; G2838 G1452; G1816; G2718	Ornamental modification of plant architecture, increased plant product (e.g., diterpenes, cotton) productivity, insect and herbivore resistance
	Root development Decreased root growth or secondary root development Decreased root branching Increased root branching	G651; G730; G2655; G2747; G2992; G2993 G651; G2993 G2747; G2992	Modification of root architecture and mass Influence uptake of water and nutrients Improved anchorage

	Abnormal gravitropic response	G2983	Manipulation of root development
	Increased root hairs	G1816; G2718; G2983	Improved yield, stress tolerance; anchorage
	Altered cotyledon shape	G916; G1420; G1893; G2432; G2636; G2859; G3059	Ornamental applications
	Altered hypocotyl shape, color, development	G807; G916; G1510; G1988; G2771; G2859; G2884; G2993	Ornamental applications; altered light response (see "Light Response", below)
	Altered seed development, ripening and germination	G961	Modification of seed germination properties and performance
	Slow growth	G652; G1013; G1100; G1468; G1535; G1549; G1779; G1938; G2765; G2784; G2826; G2834; G2851; G3091; G3095	Ornamental applications
	Fast growth	G807; G1476; G2617	Appearance, biomass, yield
	Cell differentiation and cell proliferation	G1539; G1585; G1591; G2885; G2983	Increase in carpel or fruit development; improve regeneration of shoots from callus in transformation or micro-propagation systems
	Cell expansion	G521	Control of cell elongation
	Phase change and floral reversion	G370; G1985; G1995; G2826; G2838	Improved yield, biomass, manipulation of seasonality and annual or perennial habit, developmental plasticity in response to environmental stress
	Senescence Accelerated or premature senescence	G652; G1033; G1128; G1772; G2467; G2574; G2783; G2907; G3059; G3111	Improvement in response to disease, fruit ripening
	Reduced or delayed senescence	G571; G652 (KO); G2536	
	Abnormal embryo development	G2884	
	Embryo lethal when knocked out	G374	Herbicide target
	Gamete lethal	G846	Potential to prevent escape of GMO pollen
	Altered programmed cell death	G12	
	Lethality when overexpressed	G366; G1384; G1556; G1832; G1850; G1957; G1990; G2213; G2298; G2505; G2570; G2587; G2869; G2887	Herbicide target; ablation of specific tissues or organs such as stamen to prevent pollen escape
	Necrosis, formation of necrotic lesions	G12; G1840	Disease resistance
Plant size	Increased plant size or biomass	G46; G268; G287; G314; G319; G324; G438; G624; G852; G1113; G1150; G1451; G1468; G2334; G2536; G2650; G2741; G2979	Improved yield, biomass, appearance
	Large seedlings	G1313; G2679; G2694; G2838	Increased survival and vigor of seedlings, yield

	Dwarfed or more compact plants	G131; G136; G253; G309; G370; G386; G549; G550; G600; G651; G652; G707; G738; G811; G1011; G1100; G1247; G1289; G1340; G1423; G1474; G1483; G1549; G1554; G1593; G1753; G1772; G1779; G1798; G1938; G1983; G1993; G2085; G2226; G2227; G2251; G2372; G2375; G2453; G2456; G2459; G2492; G2515; G2550; G2565; G2574; G2575; G2579; G2616; G2628; G2640; G2649; G2682; G2702; G2757; G2783; G2839; G2846; G2847; G2850; G2884; G2934; G2958; G2979; G2992; G3017; G3059; G3091; G3111	Dwarfism, lodging resistance, manipulation of gibberellin responses
Leaf morphology	Dark green leaves	G30; G253; G309; G707; G811; G957; G1100; G1128; G1327; G1341; G1357; G1389; G1420; G1423; G1452; G1482; G1510; G1535; G1549; G1554; G1593; G1743; G1792; G1796; G1846; G1863; G1932; G1938; G1983; G2085; G2146; G2207; G2226; G2251; G2334; G2371; G2372; G2453; G2456; G2457; G2459; G2550; G2640; G2649; G2661; G2690; G2694; G2771; G2763; G2784; G2837; G2838; G2846; G2847; G2850; G2851; G2958; G2993; G3021; G3059; G3091; G3095; G3111	Increased photosynthesis, biomass, appearance, yield; nutritional value
	Change in leaf shape	G30; G129; G131; G135; G136; G137; G140; G148; G200; G224; G253; G319; G370; G372; G438; G446; G468; G600; G646; G651; G707; G905; G957; G1011; G1013; G1100; G1113; G1128; G1142; G1247; G1341; G1357; G1361; G1389; G1420; G1452; G1468; G1474; G1476; G1493; G1535; G1538; G1549; G1557; G1585; G1593; G1743; G1796;	Ornamental applications

		G1798; G1825; G1846; G1863; G1893; G1917; G1932; G1938; G1945; G1983; G1993; G2084; G2085; G2207; G2226; G2227; G2251; G2334; G2375; G2432; G2453; G2455; G2456; G2457; G2536; G2550; G2565; G2575; G2579; G2604; G2617; G2628; G2636; G2639; G2640; G2649; G2682; G2686; G2690; G2694; G2699; G2702; G2747; G2768; G2771; G2784; G2837; G2839; G2846; G2850; G2851; G2859; G2866; G2888; G2958; G2992; G3021; G3044; G3059; G3084; G3091; G3094; G3095; G3111	
	Increased leaf size and mass	G268; G324; G438; G852; G1113; G1274; G1451; G2536; G2699; G2768; G3008	Increased yield, ornamental applications
	Light green or gray leaves	G351; G600; G651; G1468; G1718; G2565; G2604; G2779; G2859; G3044; G3070	Ornamental applications
	Glossy leaves	G30; G370 (KO); G975; G1792; G2640; G2649	Ornamental applications, manipulation of wax composition, amount, or distribution
	Altered abaxial/adaxial polarity	G730	Modification of plant growth and form
Seed morphology	Altered seed coloration	G581; G961; G2085; G2371	Appearance
	Seed size and shape		
	Altered seed shape	G652; G916; G961	Appearance
	Large seed	G151; G581; G2085; G2585; G2933	
Leaf biochemistry	Increased leaf wax	G975	Insect, pathogen resistance
	Leaf fatty acids		
	Increase in leaf fatty acids	G975	
Seed biochemistry	Seed oil content		
	Increased oil content	G961 (KO); G1451 (KO); G2830 (KO)	Improved oil yield, increased caloric content of food and animal feed
	Seed prenyl lipids	G652 (KO)	Increase in alpha-tocopherol (vitamin E)
Light response/shade avoidance	Altered cotyledon	G30; G2754; G2859	Increased planting densities and yield enhancement
	Altered hypocotyl	G30; G807; G916; G1082; G1510; G1988; G2650; G2754; G2771; G2859; G2884; G2993	

	Altered leaf orientation	G351; G1013; G2650; G2694; G2993; G3032	
	Altered petiole	G478; G807; G1988; G2650; G2694; G2754	
	Shade avoidance	G30; G246; G353; G354; G2432; G2650; G2754	
Pigment	Increased anthocyanin levels	G253; G386; G707; G1482; G2453; G2456; G2459	Enhanced health benefits, improved ornamental appearance, increased stress resistance, attraction of pollinating and seed- dispersing animals
	Decreased anthocyanin levels	G581; G2604; G2718	

Abbreviations: N=nitrogen P=phosphate ABA=abscisic acid C/N=carbon/nitrogen balance

Detailed description of genes, traits and utilities that affect plant characteristics

- 5 The following descriptions of traits and utilities associated with the present transcription factors offer a more comprehensive description than that provided in Table 6.

Abiotic stress, general considerations

- 10 Plant transcription factors can modulate gene expression, and, in turn, be modulated by the environmental experience of a plant. Significant alterations in a plant's environment invariably result in a change in the plant's transcription factor gene expression pattern. Altered transcription factor expression patterns generally result in phenotypic changes in the plant. Transcription factor gene product(s) in transgenic plants then differ(s) in amounts or proportions from that found in wild-type or non-transformed plants, and those transcription factors likely represent polypeptides that are used to alter the
- 15 response to the environmental change. By way of example, it is well accepted in the art that analytical methods based on altered expression patterns may be used to screen for phenotypic changes in a plant far more effectively than can be achieved using traditional methods.

- 20 Abiotic stress: adult stage chilling. Enhanced chilling tolerance produced by modifying expression levels of transcription factors such as G1274, G1357, G1779, G1928, G2063, G2567, G2579, G2650, G2771, G2930, or G2933, for example, in plants may extend the effective growth range of chilling sensitive crop species by allowing earlier planting or later harvest. Improved chilling tolerance may be conferred by increased expression of glycerol-3-phosphate acetyltransferase in chloroplasts (see, for example, Wolter et al. (1992) *EMBO J.* 4685-4692, and Murata et al. (1992) *Nature* 356: 710-713).

- 25 Chilling tolerance could also serve as a model for understanding how plants adapt to water deficit. Both chilling and water stress share similar signal transduction pathways and tolerance/adaptation mechanisms. For example, acclimation to chilling temperatures can be induced by water stress or treatment with abscisic acid. Genes induced by low temperature include dehydrins (or LEA proteins).

Dehydrins are also induced by salinity, abscisic acid, water stress and during the late stages of embryogenesis.

Another large impact of chilling occurs during post-harvest storage. For example, some fruits and vegetables do not store well at low temperatures (for example, bananas, avocados, melons, and tomatoes). The normal ripening process of the tomato is impaired if it is exposed to cool temperatures. Genes conferring resistance to chilling temperatures may enhance tolerance during post-harvest storage.

Abiotic stress: cold germination. The potential utility of presently disclosed transcription factor genes that increase tolerance to cold is to confer better germination and growth in cold conditions. Plants with modified expression levels of G224, G728, G807, G1274, G1837, G2051, G2317, G2603, or G2784 show less sensitivity to germination in cold conditions, indicating a role in regulation of cold responses. These genes might be engineered to manipulate the response to low temperature stress. Genes that would allow germination and seedling vigor in the cold would have highly significant utility in allowing seeds to be planted earlier in the season with a high rate of survival. Transcription factor genes that confer better survival in cooler climates allow a grower to move up planting time in the spring and extend the growing season further into autumn for higher crop yields. Germination of seeds and survival at temperatures significantly below that of the mean temperature required for germination of seeds and survival of non-transformed plants would increase the potential range of a crop plant into regions in which it would otherwise fail to thrive.

Abiotic stress: salt and drought tolerance

Plants are subject to a range of environmental challenges. Several of these, including salt stress, general osmotic stress, drought stress and freezing stress, have the ability to impact whole plant and cellular water availability. Not surprisingly, then, plant responses to this collection of stresses are related. In a recent review, Zhu notes that (Zhu (2002) *Ann. Rev. Plant Biol.* 53: 247-273) "most studies on water stress signaling have focused on salt stress primarily because plant responses to salt and drought are closely related and the mechanisms overlap". Many examples of similar responses (i.e., genetic pathways to this set of stresses have been documented. For example, the CBF transcription factors have been shown to condition resistance to salt, freezing and drought (Kasuga et al. (1999) *Nature Biotech.* 17: 287-291). The *Arabidopsis rd29B* gene is induced in response to both salt and dehydration stress, a process that is mediated largely through an ABA signal transduction process (Uno et al. (2000) *Proc. Natl. Acad. Sci. USA* 97: 11632-11637), resulting in altered activity of transcription factors that bind to an upstream element within the *rd29B* promoter. In *Mesembryanthemum crystallinum* (ice plant), Patharker and Cushman have shown that a calcium-dependent protein kinase (McCDPK1) is induced by exposure to both drought and salt stresses (Patharker and Cushman (2000) *Plant J.* 24: 679-691). The stress-induced kinase was also shown to phosphorylate a transcription factor, presumably altering its activity, although transcript levels of the target transcription factor are not altered in response to salt or drought stress. Similarly, Saijo et al. demonstrated that a rice salt/drought-induced calmodulin-dependent protein kinase

(OsCDPK7) conferred increased salt and drought tolerance to rice when overexpressed (Saijo et al. (2000) *Plant J.* 23: 319-327).

Exposure to dehydration invokes similar survival strategies in plants as does freezing stress (see, for example, Yelenosky (1989) *Plant Physiol* 89: 444-451) and drought stress induces freezing tolerance (see, for example, Siminovitch et al. (1982) *Plant Physiol* 69: 250-255; and Guy et al. (1992) *Planta* 188: 265-270). In addition to the induction of cold-acclimation proteins, strategies that allow plants to survive in low water conditions may include, for example, reduced surface area, or surface oil or wax production.

Consequently, one skilled in the art would expect that some pathways involved in resistance to one of these stresses, and hence regulated by an individual transcription factor, will also be involved in resistance to another of these stresses, regulated by the same or homologous transcription factors. Of course, the overall resistance pathways are related, not identical, and therefore not all transcription factors controlling resistance to one stress will control resistance to the other stresses. Nonetheless, if a transcription factor conditions resistance to one of these stresses, it would be apparent to one skilled in the art to test for resistance to these related stresses. Modifying the expression of a number of presently disclosed transcription factor genes shown to confer increased tolerance to drought, e.g., G46, G47, G926, G975, G1206, G1274, G1357, G1452, G1792, G2133, G2505, G2717, G2982, G2999, G3076, and G3086, and increased tolerance to salt, e.g., G355, G624, G1017, G1037, G1538, G1557, G1660, G1837, G2035, G2041, G2060, G2207, G2317, G2319, G2404, G2453, G2457, G2691, G2717, G2992, G2998, G2999, G3083, and G3086, during germination, the seedling stage, and throughout a plant's life cycle, may thus be used to increase a plant's tolerance to low water conditions and provide the benefits of improved survival, increased yield and an extended geographic and temporal planting range.

Abiotic stress: freezing tolerance and osmotic stress. Modification of the expression of a number of presently disclosed transcription factor genes, , G47, G353, G916, G926, G1033, G1206, G1412, G1452, G1730, G1753, G1816, G2207, G2661, G2717, G2776, G2839, G2854, G2969, or G2982, for example, may be used to increase germination rate or growth under adverse osmotic conditions, which could impact survival and yield of seeds and plants. Osmotic stresses may be regulated by specific molecular control mechanisms that include genes controlling water and ion movements, functional and structural stress-induced proteins, signal perception and transduction, and free radical scavenging, and many others (Wang et al. (2001) *Acta Hort.* (ISHS) 560: 285-292). Instigators of osmotic stress include freezing, drought and high salinity, each of which are discussed in more detail below.

In many ways, freezing, high salt and drought have similar effects on plants, not the least of which is the induction of common polypeptides that respond to these different stresses. For example, freezing is similar to water deficit in that freezing reduces the amount of water available to a plant. Exposure to freezing temperatures may lead to cellular dehydration as water leaves cells and forms ice crystals in intercellular spaces (Buchanan, *supra*). As with high salt concentration and freezing, the problems for plants caused by low water availability include mechanical stresses caused by the

withdrawal of cellular water. Thus, the incorporation of transcription factors that modify a plant's response to osmotic stress into, for example, a crop or ornamental plant, may be useful in reducing damage or loss. Specific effects caused by freezing, high salt and drought are addressed below.

5 Abiotic stress: heat stress tolerance. The germination of many crops is also sensitive to high temperatures. Presently disclosed transcription factor genes, including, for example, G3086, that provide increased heat tolerance, are generally useful in producing plants that germinate and grow in hot conditions, may find particular use for crops that are planted late in the season, or extend the range of a plant by allowing growth in relatively hot climates.

10

Nutrient uptake and utilization: nitrogen and phosphorus. Presently disclosed transcription factor genes introduced into plants provide a means to improve uptake of essential nutrients, including nitrogenous compounds, phosphates, potassium, and trace minerals. The enhanced performance of, for example, G153, G200, G581, G839, G916, G1013, G1150, G1274, G1792, G1816, G1988, G2239,
15 G2604, G2718, G2830, G2913, and G2981, and other overexpressing lines under low nitrogen conditions or G355, G624, G1988, G2142, and G2972 under low phosphorus conditions indicate that these genes and their homologs could be used to engineer crops that could thrive under conditions of reduced nutrient availability. Phosphorus, in particular, tends to be a limiting nutrient in soils and is generally added as a component in fertilizers. Young plants have a rapid intake of phosphate and sufficient phosphate is
20 important for yield of root crops such as carrot, potato and parsnip.

 The effect of these modifications is to increase the seedling germination and range of ornamental and crop plants. The utilities of presently disclosed transcription factor genes conferring tolerance to conditions of low nutrients also include cost savings to the grower by reducing the amounts of fertilizer needed, environmental benefits of reduced fertilizer runoff into watersheds; and improved yield and
25 stress tolerance. In addition, by providing improved nitrogen uptake capability, these genes can be used to alter seed protein amounts and/or composition in such a way that could impact yield as well as the nutritional value and production of various food products.

Decreased herbicide sensitivity. Presently disclosed transcription factor genes, including G2133
30 and its equivalents that confer resistance or tolerance to herbicides (e.g., glyphosate) will find use in providing means to increase herbicide applications without detriment to desirable plants. This would allow for the increased use of a particular herbicide in a local environment, with the effect of increased detriment to undesirable species and less harm to transgenic, desirable cultivars.

 Knockouts of a number of the presently disclosed transcription factor genes have been shown to
35 be lethal to developing embryos. Thus, these genes are potentially useful as herbicide targets.

Altered expression and hormone sensitivity: abscisic acid and auxin. Altering the expression levels of a number of the presently disclosed transcription factor genes, including G12, G224, G244, G355, G571, G926, G1037, G1357, G1412, G1452, G1482, G1507, G1893, G2070, G2085, G2109, G2146, G2207, G2382, G2617, G2717, G2854, G2865, G2969, G2992, G3054, G3055, or G3067, may be used to reduce a plant's sensitivity to ABA or render a plant insensitive to ABA exposure. ABA plays regulatory roles in a host of physiological processes in all higher as well as in lower plants (Davies et al. (1991) Absciscic Acid: Physiology and Biochemistry. Bios Scientific Publishers, Oxford, UK; Zeevaart et al. (1988) *Ann. Rev. Plant Physiol. Plant Mol. Biol.* 49: 439-473; Shimizu-Sato et al. (2001) *Plant Physiol* 127: 1405-1413). ABA mediates stress tolerance responses in higher plants, is a key signal compound that regulates stomatal aperture and, in concert with other plant signaling compounds, is implicated in mediating responses to pathogens and wounding or oxidative damage (for example, see Larkindale et al. (2002) *Plant Physiol.* 128: 682-695). In seeds, ABA promotes seed development, embryo maturation, synthesis of storage products (proteins and lipids), desiccation tolerance, and is involved in maintenance of dormancy (inhibition of germination), and apoptosis (Zeevaart et al. (1988) *Ann. Rev. Plant Physiol. Plant Mol. Biol.* 49: 439-473; Davies (1991), *supra*; Thomas (1993) *Plant Cell* 5: 1401-1410; and Bethke et al. (1999) *Plant Cell* 11: 1033-1046). ABA also affects plant architecture, including root growth and morphology and root-to-shoot ratios. ABA action and metabolism is modulated not only by environmental signals but also by endogenous signals generated by metabolic feedback, transport, hormonal cross-talk and developmental stage. Manipulation of ABA levels, and hence by extension the sensitivity to ABA, has been described as a very promising means to improve productivity, performance and architecture in plants Zeevaart (1999) in: Biochemistry and Molecular Biology of Plant Hormones, Hooykaas et al. eds, Elsevier Science pp 189-207; and Cutler et al. (1999) *Trends Plant Sci.* 4: 472-478).

A number of genes have been shown to be induced by cold acclimation in higher plants, including, for example, G171, G224, G1274, G1730, G2085, and G2597, and the proteins encoded by these genes are thought to play a role in protecting plant cells from injury, including freezing (Nagao et al. (2002) *Plant Cell Physiol.* 43: S168-S168). Since ABA mediates conversion of apical meristems into dormant buds, altered expression to ABA may increase protection of the buds from mechanical damage during winter. A plant's response to ABA also affects sprouting inhibition during premature warm spells. ABA is also important in protecting plants from drought tolerance. Thus, by affecting ABA sensitivity, introduced transcription factor genes may affect cold sensitivity, yield and survival, and plants with G12 knocked-out or plants overexpressing G926, G1357, G1412, G1452, G1893, G2109, G2146, G2207, G2382, G2617, G2717, G2854, G2865, G2969, G2992, G3054, G3055, and G3067, may have modified ABA responses that influence seed development and dormancy, as well as cold and dehydration tolerance, and survival.

"Auxin" refers to a class of plant hormones, including indoleacetic acid (IAA), having a variety of effects, such as phototropic response through the stimulation of cell elongation, stimulation of

secondary growth, and the development of leaf traces and fruit. Specifically, auxin is involved in the regulation of cell division, particularly at shoot tips. Transcription factors genes that regulate a plant's response to auxin thus provide a means for controlling shoot tip development and secondary growth, which in turn can be used to manipulate plant growth and development.

5

Disease resistance or tolerance: *Erysiphe*, *Fusarium*, *Botrytis*, and other pathogens. A number of the presently disclosed transcription factor genes have been induced to be expressed (e.g., G140, G171, G224, G434, G571, G1100, G1274, G1384, G1507, G1538, G1923, and G2085), or have been shown to provide resistance or tolerance (e.g., G1792) after challenge with more than one pathogen, including fungal pathogens *Fusarium oxysporum*, *Botrytis cinerea* and *Erysiphe orontii*. Modification of the expression levels of one or more transcription factor genes may provide some benefit to the plant to help prevent or overcome infestation. The mechanisms by which the transcription factors work could include changing surface characteristics such as waxes, oils, or cell wall composition and thickness, or by the activation of signal transduction pathways that regulate plant defenses in response to attacks by pathogens (including, for example, reactive oxygen species, anti-fungal proteins, defensins, thionins, glucanases, and chitinases). Another means to combat fungal and other pathogens is by accelerating local cell death or senescence, mechanisms used to impair the spread of pathogenic microorganisms throughout a plant. For instance, the best known example of accelerated cell death is the resistance gene-mediated hypersensitive response, which causes localized cell death at an infection site and initiates a systemic defense response. Because many defenses, signaling molecules, and signal transduction pathways are common to defense against different pathogens and pests, such as fungal, bacterial, oomycete, nematode, and insect, transcription factors that are implicated in defense responses against the fungal pathogens tested may also function in defense against other pathogens and pests.

25

Growth regulator: sugar sensing.

In addition to their important role as an energy source and structural component of the plant cell, sugars are central regulatory molecules that control several aspects of plant physiology, metabolism and development (Hsieh et al. (1998) *Proc. Natl. Acad. Sci.* 95: 13965-13970). It is thought that this control is achieved by regulating gene expression and, in higher plants, sugars have been shown to repress or activate plant genes involved in many essential processes such as photosynthesis, glyoxylate metabolism, respiration, starch and sucrose synthesis and degradation, pathogen response, wounding response, cell cycle regulation, pigmentation, flowering and senescence. The mechanisms by which sugars control gene expression are not understood.

Several sugar-sensing mutants have turned out to be allelic to abscisic acid (ABA) and ethylene mutants. ABA is found in all photosynthetic organisms and acts as a key regulator of transpiration, stress responses, embryogenesis, and seed germination. Most ABA effects are related to the compound acting as a signal of decreased water availability, whereby it triggers a reduction in water loss, slows growth,

35

and mediates adaptive responses. However, ABA also influences plant growth and development via interactions with other phytohormones. Physiological and molecular studies indicate that maize and *Arabidopsis* have almost identical pathways with regard to ABA biosynthesis and signal transduction. For further review, see Finkelstein and Rock ((2002) Absciscic acid biosynthesis and response (In The
5 Arabidopsis Book, Editors: Somerville and Meyerowitz (American Society of Plant Biologists, Rockville, MD).

This potentially implicates G155, G224, G344, G478, G905, G916, G1033, G1108, G1420, G1493, G1535, G1753, G1816, G2111, G2661, G2763, G2776, G2839, G2854, G2898 and related transcription factors in hormone signaling based on the sucrose sugar sensing phenotype of transgenic
10 lines overexpressing these polypeptides. On the other hand, the sucrose treatment used in these experiments (9.5% w/v) could also be an osmotic stress. Therefore, one could interpret these data as an indication that these transgenic lines overexpressing are more tolerant to osmotic stress. However, it is well known that plant responses to ABA, osmotic and other stress may be linked, and these different treatments may even act in a synergistic manner to increase the degree of a response. For example,
15 Xiong, Ishitani, and Zhu ((1999) *Plant Physiol.* 119: 205-212) have shown that genetic and molecular studies may be used to show extensive interaction between osmotic stress, temperature stress, and ABA responses in plants. These investigators analyzed the expression of *RD29A-LUC* in response to various treatment regimes in *Arabidopsis*. The *RD29A* promoter contains both the ABA-responsive and the dehydration-responsive element - also termed the C-repeat - and can be activated by osmotic stress, low
20 temperature, or ABA treatment; transcription of the *RD29A* gene in response to osmotic and cold stresses is mediated by both ABA-dependent and ABA-independent pathways (Xiong, Ishitani, and Zhu (1999) *supra*). *LUC* refers to the firefly luciferase coding sequence, which, in this case, was driven by the stress responsive *RD29A* promoter. The results revealed both positive and negative interactions, depending on the nature and duration of the treatments. Low temperature stress was found to impair osmotic signaling
25 but moderate heat stress strongly enhanced osmotic stress induction, thus acting synergistically with osmotic signaling pathways. In this study, the authors reported that osmotic stress and ABA could act synergistically by showing that the treatments simultaneously induced transgene and endogenous gene expression. Similar results were reported by Bostock and Quatrano ((1992) *Plant Physiol.* 98: 1356-1363), who found that osmotic stress and ABA act synergistically and induce maize *Em* gene expression.
30 Ishitani et al (1997) *Plant Cell* 9: 1935-1949) isolated a group of *Arabidopsis* single-gene mutations that confer enhanced responses to both osmotic stress and ABA. The nature of the recovery of these mutants from osmotic stress and ABA treatment indicated that although separate signaling pathways exist for osmotic stress and ABA, the pathways share a number of components; these common components may mediate synergistic interactions between osmotic stress and ABA. Thus, contrary to the previously held
35 belief that ABA-dependent and ABA-independent stress signaling pathways act in a parallel manner, our data reveal that these pathways cross talk and converge to activate stress gene expression.

Because sugars are important signaling molecules, the ability to control either the concentration of a signaling sugar or how the plant perceives or responds to a signaling sugar could be used to control plant development, physiology or metabolism. For example, the flux of sucrose (a disaccharide sugar used for systemically transporting carbon and energy in most plants) has been shown to affect gene expression and alter storage compound accumulation in seeds. Manipulation of the sucrose-signaling pathway in seeds may therefore cause seeds to have more protein, oil or carbohydrate, depending on the type of manipulation. Similarly, in tubers, sucrose is converted to starch which is used as an energy store. It is thought that sugar signaling pathways may partially determine the levels of starch synthesized in the tubers. The manipulation of sugar signaling in tubers could lead to tubers with a higher starch content.

Thus, the presently disclosed transcription factor genes that manipulate the sugar signal transduction pathway may lead to altered gene expression to produce plants with desirable traits. In particular, manipulation of sugar signal transduction pathways could be used to alter source-sink relationships in seeds, tubers, roots and other storage organs leading to increase in yield.

Growth regulator: carbon and nitrogen balance. A number of the transcription factor-overexpressing lines, including G153, G200, G581, G707, G916, G1013, G1150, G1274, G1483, G1535, G1816, G1988, G2239, G2604, G2830, G2913, and G2981, may be used to produce plants with altered C/N sensing. These plants may, for example, make less anthocyanin on high sucrose plus glutamine, indicating that these genes can be used to modify carbon and nitrogen status, and hence assimilate partitioning (assimilate partitioning refers to the manner in which an essential element, such as nitrogen, is distributed among different pools inside a plant, generally in a reduced form, for the purpose of transport to various tissues).

Flowering time: early and late flowering. Presently disclosed transcription factor genes that accelerate flowering, which include G129, G131, G135, G136, G137, G138, G140, G142, G145, G146, G148, G153, G155, G172, G200, G246, G416, G485, G549, G600, G627, G1011, G1037, G1142, G1538, G1797, G1798, G1823, G1825, G1988, G2071, G2129, G2142, G2184, G2311, G2372, G2443, G2515, G2628, G2633, G2639, G2650, G2754, G2777, G2779, G2802, G2805, G2832, G2967, G2992, G3002, G3032, G3044, G3060, G3061, and G3086, could have valuable applications in such programs, since they allow much faster generation times. In a number of species, for example, broccoli, cauliflower, where the reproductive parts of the plants constitute the crop and the vegetative tissues are discarded, it would be advantageous to accelerate time to flowering. Accelerating flowering could shorten crop and tree breeding programs. Additionally, in some instances, a faster generation time would allow additional harvests of a crop to be made within a given growing season. A number of *Arabidopsis* genes have already been shown to accelerate flowering when constitutively expressed. These include LEAFY, APETALA1 and CONSTANS (Mandel et al. (1995) *Nature* 377: 522-524; Weigel and Nilsson (1995) *Nature* 377: 495-500; Simon et al. (1996) *Nature* 384: 59-62).

By regulating the expression of potential flowering using inducible promoters, flowering could be triggered by application of an inducer chemical. This would allow flowering to be synchronized across a crop and facilitate more efficient harvesting. Such inducible systems could also be used to tune the flowering of crop varieties to different latitudes. At present, species such as soybean and cotton are available as a series of maturity groups that are suitable for different latitudes on the basis of their flowering time (which is governed by day-length). A system in which flowering could be chemically controlled would allow a single high-yielding northern maturity group to be grown at any latitude. In southern regions such plants could be grown for longer periods before flowering was induced, thereby increasing yields. In more northern areas, the induction would be used to ensure that the crop flowers prior to the first winter frosts.

In a sizeable number of species, for example, root crops, where the vegetative parts of the plants constitute the crop and the reproductive tissues are discarded, it is advantageous to identify and incorporate transcription factor genes that delay or prevent flowering in order to prevent resources being diverted into reproductive development. For example, G2, G15, G47, G173, G309, G319, G324, G372, G380, G434, G485, G571, G581, G624, G707, G738, G744, G752, G839, G852, G905, G1113, G1136, G1142, G1150, G1276, G1357, G1361, G1446, G1451, G1452, G1468, G1474, G1493, G1549, G1554, G1863, G1945, G1983, G1998, G1999, G2106, G2146, G2207, G2251, G2269, G2319, G2334, G2432, G2559, G2604, G2694, G2723, G2741, G2743, G2763, G2771, G2802, G2838, G2846, G2964, G2979, G2993, G2998, G3003, G3021, G3060, and G3111 have been shown to delay flowering time in plants. Extending vegetative development with presently disclosed transcription factor genes could thus bring about large increases in yields. Prevention of flowering can help maximize vegetative yields and prevent escape of genetically modified organism (GMO) pollen.

Presently disclosed transcription factors that extend flowering time have utility in engineering plants with longer-lasting flowers for the horticulture industry, and for extending the time in which the plant is fertile.

Altered flower structure and inflorescence: aerial rosettes, architecture, branching, short internodes, terminal flowers and phase change. Presently disclosed transgenic transcription factors such as G15, G129, G131, G133, G134, G135, G140, G446, G549, G550, G651, G730, G846, G1011, G1013, G1100, G1128, G1274, G1420, G1539, G1549, G1591, G1796, G1797, G1798, G1825, G1995, G2226, G2372, G2455, G2457, G2515, G2575, G2579, G2616, G2617, G2639, G2640, G2649, G2694, G2743, G2768, G2826, G2838, G2839, G2859, G2884, G2979, G2983, and G3094 have been used to create plants with larger flowers or arrangements of flowers that are distinct from wild-type or non-transformed cultivars. This would likely have the most value for the ornamental horticulture industry, where larger flowers or interesting floral configurations are generally preferred and command the highest prices.

Flower structure may have advantageous or deleterious effects on fertility, and could be used, for example, to decrease fertility by the absence, reduction or screening of reproductive components. In fact,

plants that overexpress a sizable number of the presently disclosed transcription factor genes, including G15, G549, G651, G846, G1100, G1798, G2372, G2579, G2616, G2639, G2640, G2649, G2768, and G2884, have been shown to possess reduced fertility compared with control plants. These could be desirable traits, as low fertility could be exploited to prevent or minimize the escape of the pollen of genetically modified organisms (GMOs) into the environment.

The alterations in shoot architecture seen in the lines in which the expression G47, G446, G2571, G2146, G2571, G2694, G2784, or G2859, for example, was modified indicates that these genes can be used to manipulate inflorescence branching patterns. This could influence yield and offer the potential for more effective harvesting techniques. For example, a "self pruning" mutation of tomato results in a determinate growth pattern and facilitates mechanical harvesting (Pnueli et al. (2001) *Plant Cell* 13(12): 2687-702).

Although the fertility of plants overexpressing some of the lines in which the present transcription factors (e.g., G2579) expression levels were poor, siliques of these plants appeared to grow out fairly extensively in many instances, indication that these genes may be producing parthenocarpic effects (fruit development in the absence of seed set), and may have utility in producing seedless fruit.

One interesting application for manipulation of flower structure, for example, by introduced transcription factors could be in the increased production of edible flowers or flower parts, including saffron, which is derived from the stigmas of *Crocus sativus*.

A number of the presently disclosed transcription factors may affect the timing of phase changes in plants (e.g., G370, G1985, G1995, G2826, and G2838). Since the timing or phase changes generally affects a plant's eventual size, these genes may prove beneficial by providing means for improving yield and biomass.

General development and morphology: shoot meristem and branching patterns. Presently disclosed transcription factor genes, when introduced into plants, may be used to modify branching patterns (e.g., by knocking-out G438, and overexpression of G916, G1585, G1957, G2636, G2650, and G2885), for example, by causing stem bifurcations in developing shoots in which the shoot meristems split to form two or three separate shoots. These transcription factors and their functional equivalents may thus be used to manipulate branching. This would provide a unique appearance, which may be desirable in ornamental applications, and may be used to modify lateral branching for use in the forestry industry. A reduction in the formation of lateral branches could reduce knot formation. Conversely, increasing the number of lateral branches could provide utility when a plant is used as a view- or windscreen. Transcription factors that cause primary shoots to become 'kinked' at each cوفlorescence node (e.g., G47) may be used to manipulate plant structure and provide for a unique ornamental appearance.

General development and morphology: apical dominance: The modified expression of presently disclosed transcription factors (e.g., G47, and its equivalents) that reduce apical dominance could be used in ornamental horticulture, for example, to modify plant architecture, for example, to produce a shorter, more bushy stature than wild type. The latter form would have ornamental utility as well as provide
5 increased resistance to lodging.

Development and morphology: trichomes. Several of the presently disclosed transcription factor genes have been used to modify trichome number, density, trichome cell fate or amount of trichome products produced by plants. These include G370, G1452, G1539, G1816, G1995, G2085, G2718,
10 G2826, G2838, and G2983. In most cases where the metabolic pathways are impossible to engineer, increasing trichome density or size on leaves may be the only way to increase plant productivity. Thus, by increasing trichome density, size or type, trichome-affecting genes and their homologs would have profound utilities in molecular farming practices and increasing the yield of cotton fibers.

If the effects on trichome patterning reflect a general change in heterochronic processes,
15 trichome-affecting transcription factors or their homologs can be used to modify the way meristems and/or cells develop during different phases of the plant life cycle. In particular, altering the timing of phase changes could afford positive effects on yield and biomass production.

General development and morphology: stem morphology and altered vascular tissue structure.
20 Plants in which expression of transcription factor gene that modify stem morphology or lignin content is modified may be used to affect overall plant architecture and the distribution of lignified fiber cells within the stem.

Modulating lignin content might allow the quality of wood used for furniture or construction to be improved. Lignin is energy rich; increasing lignin composition could therefore be valuable in raising
25 the energy content of wood used for fuel. Conversely, the pulp and paper industries seek wood with a reduced lignin content. Currently, lignin must be removed in a costly process that involves the use of many polluting chemicals. Consequently, lignin is a serious barrier to efficient pulp and paper production (Tzfira et al. (1998) *TIBTECH* 16: 439-446; Robinson (1999) *Nature Biotechnology* 17: 27-30). In addition to forest biotechnology applications, changing lignin content by selectively expressing or
30 repressing transcription factors in fruits and vegetables might increase their palatability.

Transcription factors that modify stem structure, including G47 and its equivalents, may also be used to achieve reduction of higher-order shoot development, resulting in significant plant architecture modification. Overexpression of the genes that encode these transcription factors in woody plants might result in trees that lack side branches, and have fewer knots in the wood. Altering branching patterns
35 could also have applications amongst ornamental and agricultural crops. For example, applications might exist in any species where secondary shoots currently have to be removed manually, or where changes in branching pattern could increase yield or facilitate more efficient harvesting.

General development and morphology: altered root development. By modifying the structure or development of roots by modifying expression levels of one or more of the presently disclosed transcription factor genes, including G651, G730, G1816, G2655, G2718, G2747, G2983, G2992, G2993, and their equivalents, plants may be produced that have the capacity to thrive in otherwise unproductive soils. For example, grape roots extending further into rocky soils would provide greater anchorage, greater coverage with increased branching, or would remain viable in waterlogged soils, thus increasing the effective planting range of the crop and/or increasing yield and survival. It may be advantageous to manipulate a plant to produce short roots, as when a soil in which the plant will be growing is occasionally flooded, or when pathogenic fungi or disease-causing nematodes are prevalent.

In addition, presently disclosed transcription factors including G1816, G2718, G2983 and their equivalents, may be used to increase root hair density and thus increase tolerance to abiotic stresses, thereby improving yield and quality.

Development and morphology: cotyledon, hypocotyl. The morphological phenotypes shown by plants overexpressing several of the transcription factor genes in Table 6 indicate that these genes, including those that produce altered cotyledons (e.g., G916, G1420, G1893, G2432, G2636, G2859, and G3059) and hypocotyls (G807, G916, G1510, G1988, G2771, G2859, G2884, G2993), can be used to manipulate light responses such as shade avoidance. As these genes also alter plant architecture, they may find use in the ornamental horticulture industry.

Development and morphology: seed development, ripening and germination rate. A number of the presently disclosed transcription factor genes (e.g., G961) have been shown to modify seed development and germination rate, including when the seeds are in conditions normally unfavorable for germination (e.g., cold, heat or salt stress, or in the presence of ABA), and may, along with functional equivalents, thus be used to modify and improve germination rates under adverse conditions.

Growth rate and development: fast growth. A number of the presently disclosed transcription factor genes, including G807, G1476, and G2617, could be used to accelerate seedling growth, and thereby allow a crop to become established faster. This would minimize exposure to stress conditions at early stages of growth when the plants are most sensitive. Additionally, it can allow a crop to grow faster than competing weed species.

A number of these transcription factors have also been shown to increase growth rate of mature plants to a significant extent, including more rapid growth and development of reproductive organs. This provides utility for regions with short growing seasons. Accelerating plant growth would also improve early yield or increase biomass at an earlier stage, when such is desirable (for example, in producing vegetable crops or forestry products).

General development and morphology: slow growth rate. A number of the presently disclosed transcription factor genes, including G652, G1013, G1100, G1468, G1535, G1549, G1779, G1938, G2765, G2784, G2826, G2834, G2851, G3091, and G3095, have been shown to have significant effects on retarding plant growth rate and development. These observations have included, for example, delayed growth and development of reproductive organs. Slow growing plants may be highly desirable to ornamental horticulturists, both for providing house plants that display little change in their appearance over time, or outdoor plants for which wild-type or rapid growth is undesirable (e.g., ornamental palm trees). Slow growth may also provide for a prolonged fruiting period, thus extending the harvesting season, particularly in regions with long growing seasons. Slow growth could also provide a prolonged period in which pollen is available for improved self- or cross-fertilization, or cross-fertilization of cultivars that normally flower over non-overlapping time periods. The latter aspect may be particularly useful to plants comprising two or more distinct grafted cultivars (e.g., fruit trees) with normally non-overlapping flowering periods.

General development and morphology: senescence. Presently disclosed transcription factor genes may be used to alter senescence responses in plants. Although leaf senescence is thought to be an evolutionary adaptation to recycle nutrients, the ability to control senescence in an agricultural setting has significant value. For example, a delay in leaf senescence in some maize hybrids is associated with a significant increase in yields and a delay of a few days in the senescence of soybean plants can have a large impact on yield. In an experimental setting, tobacco plants engineered to inhibit leaf senescence had a longer photosynthetic lifespan, and produced a 50% increase in dry weight and seed yield (Gan and Amasino (1995) *Science* 270: 1986-1988). Delayed flower senescence caused by knocking out G652 or overexpressing G571, G2536, for example, may generate plants that retain their blossoms longer and this may be of potential interest to the ornamental horticulture industry, and delayed foliar and fruit senescence could improve post-harvest shelf-life of produce.

Premature senescence caused by, for example, G652, G1033, G1128, G1772, G2467, G2574, G2783, G2907, G3059, G3111 and their equivalents may be used to improve a plant's response to disease and hasten fruit ripening.

Growth rate and development: lethality and necrosis. Overexpression of transcription factors, for example, G12, G366, G1384, G1556, G1840, G1832, G1840, G1850, G1957, G1990, G2213, G2298, G2505, G2570, G2587, G2869, G2887 and their equivalents that have a role in regulating cell death may be used to induce lethality in specific tissues or necrosis in response to pathogen attack. For example, if a transcription factor gene inducing lethality or necrosis was specifically active in gametes (e.g., (G846), embryos (e.g., G374 knockouts) or reproductive organs, its expression in these tissues would lead to ablation and subsequent male or female sterility. Alternatively, under pathogen-regulated expression, a necrosis-inducing transcription factor can restrict the spread of a pathogen infection through a plant.

Plant size: large plants and increased biomass.

Plants overexpressing G46, G268, G287, G314, G319, G324, G438, G624, G852, G1113, G1150, G1451, G1468, G2334, G2536, G2650, G2741, and G2979, for example, have been shown to be larger than controls. For some ornamental plants, the ability to provide larger varieties with these genes or their equivalents may be highly desirable. More significantly, crop species overexpressing these genes from diverse species would also produce higher yields on larger cultivars, particularly those in which the vegetative portion of the plant is edible.

Overexpression of these genes can confer increased stress tolerance as well as increased biomass, and the increased biomass appears to be related to the particular mechanism of stress tolerance exhibited by these genes. The decision for a lateral organ to continue growth and expansion versus entering late development phases (growth cessation and senescence) is controlled genetically and hormonally, including regulation at an organ size checkpoint (e.g., Mizukami (1001) *Curr Opinion Plant Biol* 4: 533-39; Mizukami and Fisher (2000) *Proc. Natl. Acad. Sci.* 97: 942-47; Hu et al. *Plant Cell* 15: 1591)). Organ size is controlled by the meristematic competence of organ cells, with increased meristematic competence leading to increased organ size (both leaves and stems). Plant hormones can impact plant organ size, with ethylene pathway overexpression leading to reduced organ size. There are also suggestions that auxin plays a determinative role in organ size. Stress responses can impact hormone levels in plant tissues, including ABA and ethylene levels. Thus, overexpression of G1073 appears to alter environmental (e.g., stress) inputs to the organ size checkpoint, thus enhancing organ size

Plant size: large seedlings. Presently disclosed transcription factor genes, that produce large seedlings can be used to produce crops that become established faster. Large seedlings are generally hardier, less vulnerable to stress, and better able to out-compete weed species. Seedlings in which expression of some of the presently disclosed transcription factors, including G1313, G2679, G2694, and G2838, for example, was modified, have been shown to possess larger cotyledons and/or were more developmentally advanced than control plants. Rapid seedling development made possible by manipulating expression of these genes or their equivalents is likely to reduce loss due to diseases particularly prevalent at the seedling stage (e.g., damping off) and is thus important for survivability of plants germinating in the field or in controlled environments.

Plant size: dwarfed plants. Presently disclosed transcription factor genes, including G131, G136, G253, G309, G370, G386, G549, G550, G600, G651, G652, G707, G738, G811, G1011, G1100, G1247, G1289, G1340, G1423, G1474, G1483, G1549, G1554, G1593, G1753, G1772, G1779, G1798, G1938, G1983, G1993, G2085, G2226, G2227, G2251, G2372, G2375, G2453, G2456, G2459, G2492, G2515, G2550, G2565, G2574, G2575, G2579, G2616, G2628, G2640, G2649, G2682, G2702, G2757, G2783, G2839, G2846, G2847, G2850, G2884, G2934, G2958, G2979, G2992, G3017, G3059, G3091, and G3111 and their equivalents can be used to decrease plant stature and may produce plants that are more

resistant to damage by wind and rain, have improved lodging resistance, or more resistant to heat or low humidity or water deficit. Dwarf plants are also of significant interest to the ornamental horticulture industry, and particularly for home garden applications for which space availability may be limited.

5 Growth rate and development: Cell proliferation and differentiation. Transcription factors may be used regulate cell proliferation and/or differentiation in plants. Control of these processes could have valuable applications in plant transformation, cell culture or micro-propagation systems, as well as in control of the proliferation of particular useful tissues or cell types. Transcription factors that induce the proliferation of undifferentiated cells, such as G1539, G1585, G1591, G2885, and G2983, can be
10 operably linked with an inducible promoter to promote the formation of callus that can be used for transformation or production of cell suspension cultures. Transcription factors that promote differentiation of shoots could be used in transformation or micro-propagation systems, where regeneration of shoots from callus is currently problematic. In addition, transcription factors that regulate the differentiation of specific tissues could be used to increase the proportion of these tissues in a plant.
15 Transcription factors may promote the differentiation of carpel tissue, and these genes could be applied to commercial species to induce formation of increased numbers of carpels or fruits. A particular application might exist in saffron, one of the world's most expensive spices. Saffron filaments, or threads, are actually the dried stigmas of the saffron flower, *Crocus sativus Linneaus*. Each flower contains only three stigmas, and more than 75,000 of these flowers are needed to produce just one pound of saffron
20 filaments. An increase in carpel number would increase the quantity of stigmatic tissue and improve yield.

Growth rate and development: cell expansion. Plant growth results from a combination of cell division and cell expansion. Transcription factors may be useful in regulation of cell expansion. Altered
25 regulation of cell expansion (for example, by G521) could affect stem length, an important agronomic characteristic. For instance, short cultivars of wheat contributed to the Green Revolution, because plants that put fewer resources into stem elongation allocate more resources into developing seed and produce higher yield. These plants are also less vulnerable to wind and rain damage. These cultivars were found to be altered in their sensitivity to gibberellins, hormones that regulate stem elongation through control of
30 both cell expansion and cell division. Altered cell expansion in leaves could also produce novel and ornamental plant forms.

Leaf morphology: dark leaves. Color-affecting components in leaves include chlorophylls (generally green), anthocyanins (generally red to blue) and carotenoids (generally yellow to red).
35 Transcription factor genes that increase these pigments in leaves, including G30, G253, G309, G707, G811, G957, G1100, G1128, G1327, G1341, G1357, G1389, G1420, g1423, G1452, G1482, G1510, G1535, G1549, G1554, G1593, G1743, G1792, G1796, G1846, G1863, G1932, G1938, G1983, G2085, G2146, G2207, G2226, G2251, G2334, G2371, G2372, G2453, G2456, G2457, G2459, G2550, G2640,

G2649, G2661, G2690, G2694, G2771, G2763, G2784, G2837, G2838, G2846, G2847, G2850, G2851, G2958, G2993, G3021, G3059, G3091, G3095, and G3111, may positively affect a plant's value to the ornamental horticulture industry. Variegated varieties, in particular, would show improved contrast. Other uses that result from overexpression of transcription factor genes include improvements in the nutritional value of foodstuffs. For example, lutein is an important nutraceutical; lutein-rich diets have been shown to help prevent age-related macular degeneration (ARMD), the leading cause of blindness in elderly people. Consumption of dark green leafy vegetables has been shown in clinical studies to reduce the risk of ARMD.

Enhanced chlorophyll and carotenoid levels could also improve yield in crop plants. Lutein, like other xanthophylls such as zeaxanthin and violaxanthin, is an essential component in the protection of the plant against the damaging effects of excessive light. Specifically, lutein contributes, directly or indirectly, to the rapid rise of non-photochemical quenching in plants exposed to high light. Crop plants engineered to contain higher levels of lutein could therefore have improved photo-protection, leading to less oxidative damage and better growth under high light (e.g., during long summer days, or at higher altitudes or lower latitudes than those at which a non-transformed plant would thrive). Additionally, elevated chlorophyll levels increases photosynthetic capacity.

Leaf morphology: changes in leaf shape. Presently disclosed transcription factors produce marked and diverse effects on leaf development and shape, and include G30 and many others (see Table 6, "Change in leaf shape"). At early stages of growth, transgenic seedlings have developed narrow, upward pointing leaves with long petioles, possibly indicating a disruption in circadian-clock controlled processes or nyctinastic movements. Other transcription factor genes can be used to alter leaf shape in a significant manner from wild-type, some of which may find use in ornamental applications.

Leaf morphology: altered leaf size. Large leaves, such as those produced in plants overexpressing G268, G324, G438, G852, G1113, G1274, G1451, G2536, G2699, G2768, and G3008, generally increase plant biomass. This provides benefit for crops where the vegetative portion of the plant is the marketable portion.

Leaf morphology: light green and gray leaves. Transcription factor genes such as G351, G600, G651, G1468, G1718, G2565, G2604, G2779, G2859, G3044, and G3070 that provide an altered appearance may positively affect a plant's value to the ornamental horticulture industry.

Leaf morphology: glossy leaves. Transcription factor genes such as G30, G370 (when knocked-out), G975, G1792, G2640, G2649 and their equivalents that induce the formation of glossy leaves generally do so by elevating levels of epidermal wax. Thus, the genes could be used to engineer changes in the composition and amount of leaf surface components, including waxes. The ability to manipulate wax composition, amount, or distribution could modify plant tolerance to drought and low humidity, or

resistance to insects or pathogens. Additionally, wax may be a valuable commodity in some species, and altering its accumulation and/or composition could enhance yield.

Seed morphology: altered seed coloration. Presently disclosed transcription factor genes, including G581, G961, G2085, and G2371, have been used to modify seed color, which, along with the equivalents of these genes, could provide added appeal to seeds or seed products.

Seed morphology: altered seed size and shape. The introduction of presently disclosed transcription factor genes, including G151, G581, G2085, G2585, or G2933, into plants that increase the size of seeds may have a significant impact on yield and appearance, particularly when the product is the seed itself (e.g., in the case of grains, legumes, nuts, etc.). Seed size, in addition to seed coat integrity, thickness and permeability, seed water content and a number of other components including antioxidants and oligosaccharides, also affects seed longevity in storage, with larger seeds often being more desirable for prolonged storage.

Transcription factor genes that alter seed shape, including G652, G916, G961 and their equivalents may have both ornamental applications and improve or broaden the appeal of seed products.

Leaf and seed biochemistry. Overexpression of transcription factors genes, including G975 and its equivalents, which results in increased leaf wax could be used to manipulate wax composition, amount, or distribution. These transcription factors can improve yield in those plants and crops from which wax is a valuable product. The genes may also be used to modify plant tolerance to drought and/or low humidity or resistance to insects, as well as plant appearance (glossy leaves). The effect of increased wax deposition on leaves of a plant like may improve water use efficiency. Manipulation of these genes may reduce the wax coating on sunflower seeds; this wax fouls the oil extraction system during sunflower seed processing for oil. For the latter purpose or any other where wax reduction is valuable, antisense or co-suppression of the transcription factor genes in a tissue-specific manner would be valuable.

Prenyl lipids play a role in anchoring proteins in membranes or membranous organelles. Thus modifying the prenyl lipid content of seeds and leaves could affect membrane integrity and function. One important group of prenyl lipids, the tocopherols, have both anti-oxidant and vitamin E activity. Transcription factor genes (e.g., a G652 knockout) have been shown to modify the prenyl lipid content of leaves in plants, and these genes and their equivalents may thus be used to alter prenyl lipid content of leaves.

Overexpression of transcription factors have resulted in plants with altered leaf insoluble sugar content. These transcription factors and their equivalents that alter plant cell wall composition have several potential applications including altering food digestibility, plant tensile strength, wood quality, pathogen resistance and in pulp production. In particular, hemicellulose is not desirable in paper pulps

because of its lack of strength compared with cellulose. Thus modulating the amounts of cellulose vs. hemicellulose in the plant cell wall is desirable for the paper/lumber industry. Increasing the insoluble carbohydrate content in various fruits, vegetables, and other edible consumer products will result in enhanced fiber content. Increased fiber content would not only provide health benefits in food products, but might also increase digestibility of forage crops. In addition, the hemicellulose and pectin content of fruits and berries affects the quality of jam and catsup made from them. Changes in hemicellulose and pectin content could result in a superior consumer product.

A number of the presently disclosed transcription factor genes have been shown to alter the fatty acid composition in plants (e.g., G975), and seeds and leaves in particular. This modification suggests several utilities, including improving the nutritional value of seeds or whole plants. Dietary fatty acid ratios have been shown to have an effect on, for example, bone integrity and remodeling (see, for example, Weiler (2000) *Pediatr. Res.* 47:5 692-697). The ratio of dietary fatty acids may alter the precursor pools of long-chain polyunsaturated fatty acids that serve as precursors for prostaglandin synthesis. In mammalian connective tissue, prostaglandins serve as important signals regulating the balance between resorption and formation in bone and cartilage. Thus dietary fatty acid ratios altered in seeds may affect the etiology and outcome of bone loss.

Transcription factors that reduce leaf fatty acids, for example, 16:3 fatty acids, may be used to control thylakoid membrane development, including proplastid to chloroplast development. The genes that encode these transcription factors might thus be useful for controlling the transition from proplastid to chromoplast in fruits and vegetables. It may also be desirable to change the expression of these genes to prevent cotyledon greening in *Brassica napus* or *B. campestris* to avoid green oil due to early frost.

Transcription factor genes that increase leaf fatty acid production, including G975 and its equivalents could potentially be used to manipulate seed composition, which is very important for the nutritional value and production of various food products. A number of transcription factor genes are involved in mediating an aspect of the regulatory response to temperature. These genes may be used to alter the expression of desaturases that lead to production of 18:3 and 16:3 fatty acids, the balance of which affects membrane fluidity and mitigates damage to cell membranes and photosynthetic structures at high and low temperatures.

The G652 knockout line had a reproducible increase in the leaf glucosinolate M39480. It also showed a reproducible increase in seed alpha-tocopherol. A number of glucosinolates have been shown to have anti-cancer activity; thus, increasing the levels or composition of these compounds by modifying the expression of transcription factors (e.g., G652), can have a beneficial effect on human diet.

Glucosinolates are undesirable components of the oilseeds used in animal feed since they produce toxic effects. Low-glucosinolate varieties of canola, for example, have been developed to combat this problem. Glucosinolates form part of a plant's natural defense against insects. Modification of glucosinolate composition or quantity by introducing transcription factors that affect these characteristics can therefore afford increased protection from herbivores. Furthermore, in edible crops,

tissue specific promoters can be used to ensure that these compounds accumulate specifically in tissues, such as the epidermis, which are not taken for consumption.

Presently disclosed transcription factor genes that modify levels of phytosterols in plants may have at least two utilities. First, phytosterols are an important source of precursors for the manufacture of human steroid hormones. Thus, regulation of transcription factor expression or activity could lead to elevated levels of important human steroid precursors for steroid semi-synthesis. For example, transcription factors that cause elevated levels of campesterol in leaves, or sitosterols and stigmasterols in seed crops, would be useful for this purpose. Phytosterols and their hydrogenated derivatives phytostanols also have proven cholesterol-lowering properties, and transcription factor genes that modify the expression of these compounds in plants would thus provide health benefits.

The composition of seeds, particularly with respect to seed oil amounts and/or composition, is very important for the nutritional and caloric value and production of various food and feed products. Modifying the expression of transcription factor genes that alter seed oil content could be used to improve the heat stability of oils or to improve the nutritional quality of seed oil, by, for example, reducing the number of calories in seed by decreasing oil or fatty acid content, OR increasing the number of calories in animal feeds by increasing fatty acid or seed oil content (e.g., by knocking out G961, G1451, or G2830).

As with seed oils, the composition of seeds, particularly with respect to protein amounts and/or composition, is very important for the nutritional value and production of various food and feed products. Transcription factor genes may be used to modify protein concentrations in seeds, which would modify the caloric content of seeds or provide nutritional benefits, and may be used to prolong storage, increase seed pest or disease resistance, or modify germination rates.

Prenyl lipids play a role in anchoring proteins in membranes or membranous organelles. Thus, presently disclosed transcription factor genes, including G652 and equivalents, that modify the prenyl lipid content of seeds and leaves (in the case of G652, when this gene is knocked out) could affect membrane integrity and function. Transcription factor genes have been shown to modify the tocopherol composition of plants. α -Tocopherol is better known as vitamin E. Tocopherols such as α - and γ -tocopherol both have anti-oxidant activity.

Light response/shade avoidance: altered cotyledon, hypocotyl, petiole development, altered leaf orientation, constitutive photomorphogenesis, photomorphogenesis in low light. Presently disclosed transcription factor genes, including G30; G246; G351, G353; G354; G478, G807, G916, G1013, G1082, G1510, G1988, G2432; G2650; G2694, G2754, G2771, G2859, G2884, G2993, G3032 and their equivalents that can modify a plant's response to light may be useful for modifying plant growth or development, for example, photomorphogenesis in poor light, or accelerating flowering time in response to various light intensities, quality or duration to which a non-transformed plant would not similarly respond. Examples of such responses that have been demonstrated include leaf number and arrangement,

and early flower bud appearances. Elimination of shading responses may lead to increased planting densities with subsequent yield enhancement. As these genes may also alter plant architecture, they may find use in the ornamental horticulture industry.

5 Pigment: increased anthocyanin level in various plant organs and tissues.

G253, G386, G581, G707, G1482, G2453, G2456, G2459, G2604, G2718 and equivalents can be used to alter anthocyanin levels in one or more tissues, depending on the organ in which these genes are expressed may be used to alter anthocyanin production in numerous plant species. Expression of presently disclosed transcription factor genes that increase flavonoid production in plants, including
 10 anthocyanins and condensed tannins, may be used to alter in pigment production for horticultural purposes, and possibly increasing stress resistance. A number of flavonoids have been shown to have antimicrobial activity and could be used to engineer pathogen resistance. Several flavonoid compounds have health promoting effects such as inhibition of tumor growth, prevention of bone loss and prevention of the oxidation of lipids. Increased levels of condensed tannins, in forage legumes would be an
 15 important agronomic trait because they prevent pasture bloat by collapsing protein foams within the rumen. For a review on the utilities of flavonoids and their derivatives, refer to Dixon et al. (1999) *Trends Plant Sci.* 4: 394-400.

Antisense and Co-suppression

20 In addition to expression of the nucleic acids of the invention as gene replacement or plant phenotype modification nucleic acids, the nucleic acids are also useful for sense and anti-sense suppression of expression, e.g. to down-regulate expression of a nucleic acid of the invention, e.g. as a further mechanism for modulating plant phenotype. That is, the nucleic acids of the invention, or subsequences or anti-sense sequences thereof, can be used to block expression of naturally occurring
 25 homologous nucleic acids. A variety of sense and anti-sense technologies are known in the art, e.g. as set forth in Lichtenstein and Nellen (1997) Antisense Technology: A Practical Approach IRL Press at Oxford University Press, Oxford, U.K. Antisense regulation is also described in Crowley et al. (1985) *Cell* 43: 633-641; Rosenberg et al. (1985) *Nature* 313: 703-706; Preiss et al. (1985) *Nature* 313: 27-32; Melton (1985) *Proc. Natl. Acad. Sci.* 82: 144-148; Izant and Weintraub (1985) *Science* 229: 345-352;
 30 and Kim and Wold (1985) *Cell* 42: 129-138. Additional methods for antisense regulation are known in the art. Antisense regulation has been used to reduce or inhibit expression of plant genes in, for example in European Patent Publication No. 271988. Antisense RNA may be used to reduce gene expression to produce a visible or biochemical phenotypic change in a plant (Smith et al. (1988) *Nature*, 334: 724-726; Smith et al. (1990) *Plant Mol. Biol.* 14: 369-379). In general, sense or anti-sense sequences are
 35 introduced into a cell, where they are optionally amplified, e.g. by transcription. Such sequences include both simple oligonucleotide sequences and catalytic sequences such as ribozymes.

For example, a reduction or elimination of expression (i.e., a “knock-out”) of a transcription factor or transcription factor homolog polypeptide in a transgenic plant, e.g., to modify a plant trait, can be obtained by introducing an antisense construct corresponding to the polypeptide of interest as a cDNA. For antisense suppression, the transcription factor or homolog cDNA is arranged in reverse orientation (with respect to the coding sequence) relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length cDNA or gene, and need not be identical to the cDNA or gene found in the plant type to be transformed. Typically, the antisense sequence need only be capable of hybridizing to the target gene or RNA of interest. Thus, where the introduced sequence is of shorter length, a higher degree of homology to the endogenous transcription factor sequence will be needed for effective antisense suppression. While antisense sequences of various lengths can be utilized, preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous transcription factor gene in the plant cell.

Suppression of endogenous transcription factor gene expression can also be achieved using RNA interference, or RNAi. RNAi is a post-transcriptional, targeted gene-silencing technique that uses double-stranded RNA (dsRNA) to incite degradation of messenger RNA (mRNA) containing the same sequence as the dsRNA (Constans, (2002) *The Scientist* 16:36). Small interfering RNAs, or siRNAs are produced in at least two steps: an endogenous ribonuclease cleaves longer dsRNA into shorter, 21-23 nucleotide-long RNAs. The siRNA segments then mediate the degradation of the target mRNA (Zamore, (2001) *Nature Struct. Biol.*, 8:746-50). RNAi has been used for gene function determination in a manner similar to antisense oligonucleotides (Constans, (2002) *The Scientist* 16:36). Expression vectors that continually express siRNAs in transiently and stably transfected have been engineered to express small hairpin RNAs (shRNAs), which get processed in vivo into siRNAs-like molecules capable of carrying out gene-specific silencing (Brummelkamp et al., (2002) *Science* 296:550-553, and Paddison, et al. (2002) *Genes & Dev.* 16:948-958). Post-transcriptional gene silencing by double-stranded RNA is discussed in further detail by Hammond et al. (2001) *Nature Rev Gen* 2: 110-119, Fire et al. (1998) *Nature* 391: 806-811 and Timmons and Fire (1998) *Nature* 395: 854. Vectors in which RNA encoded by a transcription factor or transcription factor homolog cDNA is over-expressed can also be used to obtain co-suppression of a corresponding endogenous gene, e.g., in the manner described in US Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire transcription factor cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous transcription factor gene of interest. However, as with antisense suppression, the suppressive efficiency will be enhanced as specificity of hybridization is

increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity between the introduced sequence and the endogenous transcription factor gene is increased.

Vectors expressing an untranslatable form of the transcription factor mRNA, e.g., sequences comprising one or more stop codon, or nonsense mutation) can also be used to suppress expression of an endogenous transcription factor, thereby reducing or eliminating its activity and modifying one or more traits. Methods for producing such constructs are described in US Patent No. 5,583,021. Preferably, such constructs are made by introducing a premature stop codon into the transcription factor gene.

Alternatively, a plant trait can be modified by gene silencing using double-strand RNA (Sharp (1999)

Genes and Development 13: 139-141). Another method for abolishing the expression of a gene is by

insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a transcription factor or transcription factor homolog gene. Plants containing a single transgene insertion event at the desired gene can be crossed to generate homozygous plants for the mutation. Such methods are well known to those of skill in the art (See for example Koncz et al. (1992) Methods in Arabidopsis Research, World Scientific Publishing Co. Pte. Ltd., River Edge, NJ).

Alternatively, a plant phenotype can be altered by eliminating an endogenous gene, such as a transcription factor or transcription factor homolog, e.g., by homologous recombination (Kempin et al. (1997) *Nature* 389: 802-803).

A plant trait can also be modified by using the Cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome can be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the intervening DNA sequence between the two sites is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention can also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the endogenous gene by other means, such as, for example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al. (1997) *Nature* 390 698-701; Kakimoto et al. (1996) *Science* 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery in a plant can be modified so as to increase transcription levels of a polynucleotide of the invention (See, e.g., PCT Publications WO 96/06166 and WO 98/53057 which describe the modification of the DNA-binding specificity of zinc finger proteins by changing particular amino acids in the DNA-binding motif).

The transgenic plant can also include the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example, by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

Transgenic plants (or plant cells, or plant explants, or plant tissues) incorporating the polynucleotides of the invention and/or expressing the polypeptides of the invention can be produced by a variety of well established techniques as described above. Following construction of a vector, most typically an expression cassette, including a polynucleotide, e.g., encoding a transcription factor or transcription factor homolog, of the invention, standard techniques can be used to introduce the polynucleotide into a plant, a plant cell, a plant explant or a plant tissue of interest. Optionally, the plant cell, explant or tissue can be regenerated to produce a transgenic plant.

The plant can be any higher plant, including gymnosperms, monocotyledonous and dicotyledonous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover, etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcubitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al., eds., (1984) Handbook of Plant Cell Culture—Crop Species, Macmillan Publ. Co., New York, NY; Shimamoto et al. (1989) *Nature* 338: 274-276; Fromm et al. (1990) *Bio/Technol.* 8: 833-839; and Vasil et al. (1990) *Bio/Technol.* 8: 429-434.

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable methods can include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumefaciens* mediated transformation. Transformation means introducing a nucleotide sequence into a plant in a manner to cause stable or transient expression of the sequence.

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: US Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait can be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention can be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

Integrated Systems – Sequence Identity

Additionally, the present invention may be an integrated system, computer or computer readable medium that comprises an instruction set for determining the identity of one or more sequences in a database. In addition, the instruction set can be used to generate or identify sequences that meet any specified criteria. Furthermore, the instruction set may be used to associate or link certain functional benefits, such improved characteristics, with one or more identified sequence.

For example, the instruction set can include, e.g., a sequence comparison or other alignment program, e.g., an available program such as, for example, the Wisconsin Package Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madison, WI). Public sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PHYTOSEQ sequence database (Incyte Genomics, Palo Alto, CA) can be searched.

Alignment of sequences for comparison can be conducted by the local homology algorithm of Smith and Waterman (1981) *Adv. Appl. Math.* 2: 482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48: 443-453, by the search for similarity method of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci.* 85: 2444-2448, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence similarity. The comparison window can be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al. *supra*.

A variety of methods for determining sequence relationships can be used, including manual alignment and computer assisted sequence alignment and analysis. This later approach is a preferred approach in the present invention, due to the increased throughput afforded by computer assisted methods. As noted above, a variety of computer programs for performing sequence alignment are available, or can be produced by one of skill.

One example algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. (1990) *J. Mol. Biol.* 215: 403-410. Software for performing BLAST analyses is publicly available, e.g., through the National Library of Medicine's National Center for Biotechnology Information (ncbi.nlm.nih; see at world wide web (www) National Institutes of Health US government (gov) website). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al. *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide

sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1992) *Proc. Natl. Acad. Sci.* 89: 10915-10919). Unless otherwise indicated, "sequence identity" here refers to the % sequence identity generated from a tblastx using the NCBI version of the algorithm at the default settings using gapped alignments with the filter "off" (see, for example, NIH NLM NCBI website at ncbi.nlm.nih, *supra*).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g. Karlin and Altschul (1993) *Proc. Natl. Acad. Sci.* 90: 5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence (and, therefore, in this context, homologous) if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, or less than about 0.01, and or even less than about 0.001. An additional example of a useful sequence alignment algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. The program can align, e.g., up to 300 sequences of a maximum length of 5,000 letters.

The integrated system, or computer typically includes a user input interface allowing a user to selectively view one or more sequence records corresponding to the one or more character strings, as well as an instruction set which aligns the one or more character strings with each other or with an additional character string to identify one or more region of sequence similarity. The system may include a link of one or more character strings with a particular phenotype or gene function. Typically, the system includes a user readable output element that displays an alignment produced by the alignment instruction set.

The methods of this invention can be implemented in a localized or distributed computing environment. In a distributed environment, the methods may implemented on a single computer comprising multiple processors or on a multiplicity of computers. The computers can be linked, e.g. through a common bus, but more preferably the computer(s) are nodes on a network. The network can be a generalized or a dedicated local or wide-area network and, in certain preferred embodiments, the computers may be components of an intra-net or an internet.

Thus, the invention provides methods for identifying a sequence similar or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant phenotype or gene function with a sequence. In the methods, a sequence database is provided (locally or
5 across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

Any sequence herein can be entered into the database, before or after querying the database. This provides for both expansion of the database and, if done before the querying step, for insertion of control sequences into the database. The control sequences can be detected by the query to ensure the general
10 integrity of both the database and the query. As noted, the query can be performed using a web browser based interface. For example, the database can be a centralized public database such as those noted herein, and the querying can be done from a remote terminal or computer across an internet or intranet.

Any sequence herein can be used to identify a similar, homologous, paralogous, or orthologous sequence in another plant. This provides means for identifying endogenous sequences in other plants that
15 may be useful to alter a trait of progeny plants, which results from crossing two plants of different strain. For example, sequences that encode an ortholog of any of the sequences herein that naturally occur in a plant with a desired trait can be identified using the sequences disclosed herein. The plant is then crossed with a second plant of the same species but which does not have the desired trait to produce progeny which can then be used in further crossing experiments to produce the desired trait in the second plant.
20 Therefore the resulting progeny plant contains no transgenes; expression of the endogenous sequence may also be regulated by treatment with a particular chemical or other means, such as EMR. Some examples of such compounds well known in the art include: ethylene; cytokinins; phenolic compounds, which stimulate the transcription of the genes needed for infection; specific monosaccharides and acidic environments which potentiate vir gene induction; acidic polysaccharides which induce one or more
25 chromosomal genes; and opines; other mechanisms include light or dark treatment (for a review of examples of such treatments, see, Winans (1992) *Microbiol. Rev.* 56: 12-31; Eyal et al. (1992) *Plant Mol. Biol.* 19: 589-599; Chrispeels et al. (2000) *Plant Mol. Biol.* 42: 279-290; Piazza et al. (2002) *Plant Physiol.* 128: 1077-1086).

Table 7 lists sequences discovered to be orthologous to a number of representative transcription
30 factors of the present invention. The column headings include the transcription factors listed by (a) the SEQ ID NO: of the *Arabidopsis* sequence that was used to discover the non-*Arabidopsis* orthologous sequence; (b) the GID sequence identifier of the *Arabidopsis* sequence; (c) the Sequence Identifier or GenBank Accession Number of the orthologous sequence; (d) the species from which the orthologous sequence is derived; (e) the SEQ ID NO: of the non-*Arabidopsis* orthologous sequence, and (e) the
35 smallest sum probability pairwise comparison of each orthologous sequence to the similar *Arabidopsis* sequence determined by BLAST analysis.

Table 7. Orthologs of Representative *Arabidopsis* Transcription Factor Genes

SEQ ID NO: of <i>Arabidopsis</i> Sequence Used to Discover Ortholog	GID No.	Species from Which Ortholog is Derived	Sequence Identifier or Accession Number	SEQ ID NO: of Orthologous Sequence	Smallest Sum Probability to Ortholog, When Known
2	G2	<i>Petunia x hybrida</i>	AF132001		1.00E-122
2	G2	<i>Pisum sativum</i>	AF325506		1.00E-121
2	G2	<i>Antirrhinum majus</i>	AY223518		1.00E-120
2	G2	<i>Malus x domestica</i>	AF332215		1.00E-119
2	G2	<i>Lycopersicon esculentum</i>	BM412075		1.00E-105
2	G2	<i>Picea abies</i>	AF253970		1.00E-103
2	G2	<i>Solanum tuberosum</i>	BQ120583		3.00E-98
2	G2	<i>Oryza sativa</i> (japonica cultivar-group)	CB649669		1.00E-96
2	G2	<i>Lactuca sativa</i>	BU000526		1.00E-93
2	G2	<i>Oryza sativa</i> (indica cultivar-group)	CB624207		5.00E-92
2	G2	<i>Petunia x hybrida</i>	gi5081555		2.70E-123
2	G2	<i>Pisum sativum</i>	gi13173164		1.50E-117
2	G2	<i>Antirrhinum majus</i>	gi28894443		8.20E-113
2	G2	<i>Malus x domestica</i>	gi21717332		2.00E-111
2	G2	<i>Oryza sativa</i> (japonica cultivar-group)	gi32483001		6.90E-105
2	G2	<i>Picea abies</i>	gi11181610		8.20E-102
2	G2	<i>Hordeum vulgare</i>	gi18476518		3.00E-85
2	G2	<i>Zea mays</i>	gi2944040		1.00E-84
2	G2	<i>Hyacinthus orientalis</i>	gi5360996		1.90E-79
2	G2	<i>Glycine max</i>	gi25898745		2.60E-46
3	G12	<i>Glycine max</i>	BG045111.1	671	
3	G12	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER22720_1	672	
3	G12	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER22720_2	673	
3	G12	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER272_47	674	
3	G12	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER272_51	675	
3	G12	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER59385_1	676	
3	G12	<i>Glycine max</i>	LIB3093-031-Q1-K1-C10	677	
3	G12	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER160586_1	678	
3	G12	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER76674_1	679	
3	G12	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER76674_4	680	
3	G12	<i>Oryza sativa</i>	OSC102287.C1.p11.fg	681	

3	G12	<i>Oryza sativa</i>	OSC15346.C1.p71.fg	682	
3	G12	<i>Oryza sativa</i>	OSC32395.C1.p3.fg	683	
3	G12	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER88196 1	684	
3	G12	<i>Oryza sativa</i>	Os_S32369	1557	
3	G12	<i>Oryza sativa</i>	Os_S80194	1558	
3	G12	<i>Glycine max</i>	Gma_S5071803	1632	
3	G12	<i>Medicago truncatula</i>	Mtr_S5349908	1690	
3	G12	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-49683	1937	
3	G12	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-54594	1938	
3	G12	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-47313	1939	
4	G12	<i>Brassica oleracea</i>	BH429963		4.00E-85
4	G12	<i>Gossypium arboreum</i>	BQ405872		3.00E-51
4	G12	<i>Medicago truncatula</i>	BG648561		2.00E-47
4	G12	<i>Thellungiella halophila</i>	BM985484		5.00E-47
4	G12	<i>Brassica napus</i>	CD834636		6.00E-46
4	G12	<i>Glycine max</i>	BG046836		5.00E-40
4	G12	<i>Lupinus albus</i>	CA526351		1.00E-39
4	G12	<i>Oryza sativa</i>	OSJN00057		1.00E-39
4	G12	<i>Oryza sativa</i> (japonica cultivar-group)	AK061095		1.00E-39
4	G12	<i>Helianthus argophyllus</i>	CF089073		2.00E-39
4	G12	<i>Oryza sativa</i> (japonica cultivar-group)	gi21740879		8.40E-40
4	G12	<i>Oryza sativa</i>	gi5091503		1.30E-38
4	G12	<i>Glycine max</i>	gi31324058		2.60E-36
4	G12	<i>Lycopersicon esculentum</i>	gi27436378		7.30E-22
4	G12	<i>Zea mays</i>	gi21908034		7.30E-22
4	G12	<i>Catharanthus roseus</i>	gi8980313		3.40E-20
4	G12	<i>Stylosanthes hamata</i>	gi4099921		4.80E-19
4	G12	<i>Fagus sylvatica</i>	gi18496063		2.70E-18
4	G12	<i>Hordeum vulgare</i>	gi27960757		8.40E-18
4	G12	<i>Nicotiana tabacum</i>	gi10798644		9.30E-18
6	G15	<i>Brassica napus</i>	BD274518		1.0e-999
6	G15	<i>Glycine max</i>	AX555216		1.00E-131
6	G15	<i>Oryza sativa</i> (japonica cultivar-group)	AK106306		1.00E-116
6	G15	<i>Oryza sativa</i>	AX555220		1.00E-116
6	G15	<i>Nuphar advena</i>	CD475882		1.00E-91
6	G15	<i>Zea mays</i>	AY109146		5.00E-89
6	G15	<i>Brassica oleracea</i>	BZ056530		1.00E-88
6	G15	<i>Physcomitrella patens</i> subsp. <i>patens</i>	BJ188928		3.00E-84
6	G15	<i>Lactuca sativa</i>	BQ864461		1.00E-76

6	G15	<i>Triticum aestivum</i>	BJ312281		6.00E-73
6	G15	<i>Glycine max</i>	gi25898745		1.50E-132
6	G15	<i>Oryza sativa</i> (japonica cultivar-group)	gi28201307		1.70E-122
6	G15	<i>Oryza sativa</i>	gi25898752		6.90E-118
6	G15	<i>Brassica napus</i>	gi21069051		1.00E-88
6	G15	<i>Zea mays</i>	gi2652938		7.00E-84
6	G15	<i>Malus x domestica</i>	gi21717332		1.50E-45
6	G15	<i>Picea abies</i>	gi11181612		1.70E-45
6	G15	<i>Pisum sativum</i>	gi13173164		1.90E-45
6	G15	<i>Hordeum vulgare</i>	gi18476518		3.40E-43
6	G15	<i>Antirrhinum majus</i>	gi28894443		9.10E-43
7	G30	<i>Oryza sativa</i>	G3381	2126	5.00E-33
7	G30	<i>Glycine max</i>	AW308784.1	685	
7	G30	<i>Glycine max</i>	BG790680.1	686	
7	G30	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER602185_1	687	
7	G30	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER91218_1	688	
7	G30	<i>Glycine max</i>	LIB5118-009-Q1-PF1-F2	689	
7	G30	<i>Oryza sativa</i>	OSC20174.C1.p2.fg	690	
7	G30	<i>Zea mays</i>	LIB4756-134-A1-K1- G10	691	
7	G30	<i>Oryza sativa</i>	Os_S102414	1559	
7	G30	<i>Glycine max</i>	Gma_S5001644	1633	
7	G30	<i>Zea mays</i>	Zm_S11513768	1754	
7	G30	<i>Triticum aestivum</i>	Ta_S274849	1834	
8	G30	<i>Brassica oleracea</i>	BH517030		1.00E-37
8	G30	<i>Lycopersicon esculentum</i>	AI776626		2.00E-35
8	G30	<i>Triticum aestivum</i>	BT009060		2.00E-33
8	G30	<i>Sorghum bicolor</i>	BZ337899		1.00E-32
8	G30	<i>Eucalyptus grandis</i>	CB967722		1.00E-31
8	G30	<i>Zea mays</i>	CC349655		1.00E-31
8	G30	<i>Oryza sativa</i> (japonica cultivar-group)	AP004623		3.00E-31
8	G30	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01005323		3.00E-31
8	G30	<i>Oryza sativa</i>	AP003891		3.00E-31
8	G30	<i>Glycine max</i>	BG790680		4.00E-29
8	G30	<i>Oryza sativa</i> (japonica cultivar-group)	gi28071302		3.60E-32
8	G30	<i>Lycopersicon esculentum</i>	gi2213783		7.90E-26
8	G30	<i>Catharanthus roseus</i>	gi8980313		4.70E-24
8	G30	<i>Matricaria chamomilla</i>	gi17385636		1.10E-23
8	G30	<i>Oryza sativa</i>	gi12597874		1.80E-23
8	G30	<i>Mesembryanthemu m crystallinum</i>	gi32401273		3.70E-23
8	G30	<i>Nicotiana tabacum</i>	gi1732406		5.20E-23
8	G30	<i>Nicotiana glauca</i>	gi8809571		8.70E-22

8	G30	<i>Cicer arietinum</i>	gi24817250		1.10E-21
8	G30	<i>Glycine max</i>	gi21304712		1.40E-21
9	G46	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER15812 1	692	
9	G46	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER15812 2	693	
9	G46	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER164789 1	694	
9	G46	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER164789 2	695	
9	G46	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER2315 2	696	
9	G46	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER605 217	697	
9	G46	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER605 219	698	
9	G46	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER91242 1	699	
9	G46	<i>Oryza sativa</i>	OSC101836.C1.p4.fg	700	
9	G46	<i>Zea mays</i>	LIB3062-015-Q1-K1-F11	701	
9	G46	<i>Lycopersicon esculentum</i>	Les_S5295471	1925	
9	G46	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-44432	1940	
9	G46	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-49046	1941	
9	G46	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-49310	1942	
10	G46	<i>Brassica oleracea</i>	BH970151		3.00E-83
10	G46	<i>Brassica napus</i>	CD834612		3.00E-70
10	G46	<i>Lycopersicon esculentum</i>	AY192370		3.00E-38
10	G46	<i>Solanum tuberosum</i>	BG592132		2.00E-37
10	G46	<i>Medicago truncatula</i>	BF637755		4.00E-32
10	G46	<i>Glycine max</i>	BQ740307		7.00E-31
10	G46	<i>Lotus japonicus</i>	AV423260		4.00E-30
10	G46	<i>Populus tremula</i> x: <i>Populus tremuloides</i>	BU814218		8.00E-30
10	G46	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU871861		8.00E-30
10	G46	<i>Vitis vinifera</i>	BM436925		2.00E-29
10	G46	<i>Brassica oleracea</i>	gi15054374		2.50E-47
10	G46	<i>Lycopersicon esculentum</i>	gi28274834		4.20E-38
10	G46	<i>Nicotiana tabacum</i>	gi1208497		5.90E-31
10	G46	<i>Nicotiana sylvestris</i>	gi8809575		3.50E-29
10	G46	<i>Oryza sativa</i>	gi14140141		4.50E-29
10	G46	<i>Matricaria chamomilla</i>	gi17385636		1.80E-28
10	G46	<i>Mesembryanthemum crystallinum</i>	gi32401273		5.00E-28
10	G46	<i>Oryza sativa</i> (japonica cultivar-group)	gi31433532		1.00E-27
10	G46	<i>Catharanthus roseus</i>	gi8980313		1.20E-24

10	G46	<i>Glycine max</i>	gi21304712		6.80E-22
11	G47	<i>Glycine max</i>	G3643	2225	2.00E-29
11	G47	<i>Oryza sativa</i>	G3644	2227	3.00E-25
11	G47	<i>Brassica rapa</i>	G3645	2229	1.00E-63
11	G47	<i>Brassica oleracea</i>	G3646	2231	2.00E-46
11	G47	<i>Zinnia elegans</i>	G3647	2233	3.00E-33
11	G47	<i>Oryza sativa</i>	G3649	2235	4.00E-23
11	G47	<i>Oryza sativa</i>	G3651	2237	3.00E-20
11	G47	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER115749_1	702	
11	G47	<i>Oryza sativa</i>	OSC21268.C1.p12.fg	703	
11	G47	<i>Hordeum vulgare</i>	Hv_S7318	1718	
12	G47	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BG543936		2.00E-60
12	G47	<i>Brassica oleracea</i>	BH420519		4.00E-43
12	G47	<i>Zinnia elegans</i>	AU292603		5.00E-30
12	G47	<i>Medicago truncatula</i>	BE320193		2.00E-24
12	G47	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01000718		2.00E-22
12	G47	<i>Oryza sativa</i>	AP003379		2.00E-22
12	G47	<i>Oryza sativa</i> (japonica cultivar-group)	AC124836		1.00E-20
12	G47	<i>Zea mays</i>	BZ403609		2.00E-20
12	G47	<i>Solanum tuberosum</i>	BQ513932		7.00E-17
12	G47	<i>Pinus taeda</i>	BQ698717		1.00E-16
12	G47	<i>Oryza sativa</i> (japonica cultivar-group)	gi20161239		8.50E-24
12	G47	<i>Oryza sativa</i>	gi14140155		8.30E-17
12	G47	<i>Lycopersicon esculentum</i>	gi25992102		2.80E-16
12	G47	<i>Glycine max</i>	gi31324058		2.80E-16
12	G47	<i>Zea mays</i>	gi21908034		8.60E-15
12	G47	<i>Brassica napus</i>	gi20303011		2.30E-14
12	G47	<i>Atriplex hortensis</i>	gi8571476		3.70E-14
12	G47	<i>Catharanthus roseus</i>	gi8980313		2.60E-13
12	G47	<i>Hordeum vulgare</i>	gi19071243		5.40E-13
12	G47	<i>Matricaria chamomilla</i>	gi17385636		1.40E-12
14	G129	<i>Brassica napus</i>	BNABAG1X		1.00E-133
14	G129	<i>Vitis vinifera</i>	CB969483		3.00E-94
14	G129	<i>Silene latifolia</i>	SLSLM1		1.00E-93
14	G129	<i>Panax ginseng</i>	PGORFGAG2		1.00E-92
14	G129	<i>Gossypium hirsutum</i>	AY083173		3.00E-92
14	G129	<i>Malus x domestica</i>	MDO251118		5.00E-92
14	G129	<i>Corylus avellana</i>	AF027376		2.00E-91
14	G129	<i>Lycopersicon esculentum</i>	TOMTAG1A		3.00E-91
14	G129	<i>Betula pendula</i>	BPE252071		2.00E-90
14	G129	<i>Nicotiana tabacum</i>	TOBNAG1A		3.00E-90
14	G129	<i>Brassica napus</i>	gi167126		3.30E-125
14	G129	<i>Populus</i>	gi2981131		1.00E-89

		<i>balsamifera</i> subsp. <i>trichocarpa</i>			
14	G129	<i>Silene latifolia</i>	gi602900		2.20E-89
14	G129	<i>Panax ginseng</i>	gi3913005		9.30E-89
14	G129	<i>Malus x domestica</i>	gi16973298		2.50E-88
14	G129	<i>Gossypium</i> <i>hirsutum</i>	gi19743774		2.50E-88
14	G129	<i>Corylus avellana</i>	gi4103757		6.60E-88
14	G129	<i>Lycopersicon</i> <i>esculentum</i>	gi3913004		1.70E-87
14	G129	<i>Betula pendula</i>	gi8745072		3.60E-87
14	G129	<i>Helianthus annuus</i>	gi27657747		9.60E-87
16	G131	<i>Brassica oleracea</i>	BOU67452		1.00E-139
16	G131	<i>Brassica oleracea</i> var. <i>botrytis</i>	BOL505845		1.00E-139
16	G131	<i>Sinapis alba</i>	SAAP1		1.00E-137
16	G131	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BCA251300		1.00E-109
16	G131	<i>Pisum sativum</i>	PSA279089		4.00E-97
16	G131	<i>Betula pendula</i>	BPMADS3GN		1.00E-95
16	G131	<i>Populus tremuloides</i>	AF034094		3.00E-92
16	G131	<i>Daucus carota</i>	DCA271147		2.00E-90
16	G131	<i>Malus x domestica</i>	MDAJ759		3.00E-90
16	G131	<i>Heuchera</i> <i>americana</i>	AY306148		2.00E-88
16	G131	<i>Brassica oleracea</i>	gi1561780		6.20E-131
16	G131	<i>Brassica oleracea</i> var. <i>botrytis</i>	gi23304680		6.20E-131
16	G131	<i>Sinapis alba</i>	gi1076477		3.90E-129
16	G131	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi6469345		8.30E-104
16	G131	<i>Pisum sativum</i>	gi13446154		2.30E-92
16	G131	<i>Betula pendula</i>	gi1483228		2.10E-91
16	G131	<i>Populus tremuloides</i>	gi28381537		4.00E-88
16	G131	<i>Antirrhinum majus</i>	gi16052		3.30E-86
16	G131	<i>Daucus carota</i>	gi22091473		5.30E-86
16	G131	<i>Heuchera</i> <i>americana</i>	gi32478021		3.40E-84
18	G133	<i>Brassica oleracea</i>	BOU67453		1.00E-125
18	G133	<i>Brassica napus</i>	AF124814		1.00E-118
18	G133	<i>Petunia x hybrida</i>	PHGP		2.00E-74
18	G133	<i>Antirrhinum majus</i>	AJ559554		8.00E-74
18	G133	<i>Nicotiana tabacum</i>	NTMADSBOX		8.00E-73
18	G133	<i>Vitis vinifera</i>	CB971393		1.00E-71
18	G133	<i>Solanum tuberosum</i>	STPD4		5.00E-70
18	G133	<i>Medicago sativa</i>	ALFMBP		1.00E-69
18	G133	<i>Glycine max</i>	AX478039		1.00E-69
18	G133	<i>Chrysanthemum x</i> <i>morifolium</i>	AY173060		2.00E-68
18	G133	<i>Brassica oleracea</i>	gi1561782		5.30E-118
18	G133	<i>Brassica napus</i>	gi6841082		1.50E-111
18	G133	<i>Brassica oleracea</i> var. <i>botrytis</i>	gi7446540		1.20E-109
18	G133	<i>Petunia x hybrida</i>	gi22665		4.00E-72
18	G133	<i>Antirrhinum majus</i>	gi100479		1.70E-71

18	G133	<i>Nicotiana tabacum</i>	gi1370276	1.20E-70
18	G133	<i>Solanum tuberosum</i>	gi431226	1.60E-68
18	G133	<i>Medicago sativa</i>	gi1870206	8.90E-68
18	G133	<i>Chrysanthemum x morifolium</i>	gi27804367	1.00E-66
18	G133	<i>Gerbera hybrida</i>	gi4218171	2.10E-66
20	G134	<i>Cucumis sativus</i>	AF043255	2.00E-67
20	G134	<i>Malus x domestica</i>	MDO291490	2.00E-66
20	G134	<i>Petunia x hybrida</i>	PHFBP3	6.00E-64
20	G134	<i>Vitis vinifera</i>	CB970125	2.00E-62
20	G134	<i>Lactuca sativa</i>	BU013737	3.00E-62
20	G134	<i>Gerbera hybrida</i>	GHY9726	3.00E-62
20	G134	<i>Betula pendula</i>	BPE488589	3.00E-61
20	G134	<i>Eucalyptus grandis</i>	AF029976	6.00E-61
20	G134	<i>Chrysanthemum x morifolium</i>	AY173061	1.00E-60
20	G134	<i>Silene latifolia</i>	SLSLM2	3.00E-60
20	G134	<i>Cucumis sativus</i>	gi4105097	1.50E-65
20	G134	<i>Malus x domestica</i>	gi12666533	7.40E-64
20	G134	<i>Petunia x hybrida</i>	gi2129971	1.60E-61
20	G134	<i>Gerbera hybrida</i>	gi4218173	6.90E-61
20	G134	<i>Betula pendula</i>	gi28874430	6.20E-60
20	G134	<i>Chrysanthemum x morifolium</i>	gi27804369	2.70E-59
20	G134	<i>Eucalyptus grandis</i>	gi3114586	5.60E-59
20	G134	<i>Tulipa gesneriana</i>	gi30172225	2.40E-58
20	G134	<i>Silene latifolia</i>	gi602902	2.40E-58
20	G134	<i>Helianthus annuus</i>	gi27657749	3.10E-58
22	G135	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BCA251300	1.00E-115
22	G135	<i>Brassica oleracea</i>	BNADBDA	1.00E-109
22	G135	<i>Brassica oleracea</i> var. <i>botrytis</i>	BOL505847	1.00E-109
22	G135	<i>Sinapis alba</i>	SAAP1	1.00E-107
22	G135	<i>Malus x domestica</i>	MDAJ759	3.00E-83
22	G135	<i>Pisum sativum</i>	PSA279089	3.00E-83
22	G135	<i>Nicotiana tabacum</i>	AF009127	5.00E-81
22	G135	<i>Betula pendula</i>	BPMADS3GN	8.00E-80
22	G135	<i>Nicotiana sylvestris</i>	AF068726	8.00E-80
22	G135	<i>Populus tremuloides</i>	AF034093	2.00E-79
22	G135	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi6469345	2.00E-109
22	G135	<i>Brassica oleracea</i>	gi1561784	1.70E-103
22	G135	<i>Brassica oleracea</i> var. <i>botrytis</i>	gi23304680	9.60E-103
22	G135	<i>Sinapis alba</i>	gi1076477	1.20E-102
22	G135	<i>Pisum sativum</i>	gi13446154	8.30E-81
22	G135	<i>Nicotiana tabacum</i>	gi4102113	1.80E-78
22	G135	<i>Betula pendula</i>	gi1483228	1.60E-77
22	G135	<i>Populus tremuloides</i>	gi28381535	1.60E-77
22	G135	<i>Nicotiana sylvestris</i>	gi5070144	2.00E-77
22	G135	<i>Daucus carota</i>	gi22091473	3.00E-76
24	G136	<i>Brassica napus</i>	AY036062	1.00E-126
24	G136	<i>Liquidambar styraciflua</i>	AF103903	1.00E-89

24	G136	<i>Vitis vinifera</i>	AF265562	1.00E-88
24	G136	<i>Rosa rugosa</i>	AB025643	3.00E-88
24	G136	<i>Medicago truncatula</i>	CB066648	4.00E-88
24	G136	<i>Malus x domestica</i>	MDO251117	6.00E-88
24	G136	<i>Gossypium arboreum</i>	BQ411600	4.00E-86
24	G136	<i>Nicotiana tabacum</i>	TOBNAG1A	8.00E-84
24	G136	<i>Panax ginseng</i>	PGORFGAG2	2.00E-83
24	G136	<i>Betula pendula</i>	BPE252071	3.00E-83
24	G136	<i>Brassica napus</i>	gi12655901	1.70E-119
24	G136	<i>Liquidambar styraciflua</i>	gi5031217	9.60E-87
24	G136	<i>Rosa rugosa</i>	gi6970411	3.70E-85
24	G136	<i>Malus x domestica</i>	gi16973296	9.90E-85
24	G136	<i>Vitis vinifera</i>	gi14279306	1.10E-83
24	G136	<i>Nicotiana tabacum</i>	gi3913007	1.30E-80
24	G136	<i>Betula pendula</i>	gi8745072	2.20E-80
24	G136	<i>Panax ginseng</i>	gi3913005	3.60E-80
24	G136	<i>Corylus avellana</i>	gi4103757	5.80E-80
24	G136	<i>Petunia integrifolia</i>	gi848999	5.80E-80
26	G137	<i>Brassica oleracea</i> var. <i>botrytis</i>	BOL508053	1.00E-130
26	G137	<i>Malus domestica</i>	U78947	1.00E-105
26	G137	<i>Malus x domestica</i>	MDAJ1681	1.00E-104
26	G137	<i>Cucumis sativus</i>	AF135962	1.00E-102
26	G137	<i>Vitis vinifera</i>	AF373601	1.00E-100
26	G137	<i>Populus tremuloides</i>	AF185574	1.00E-100
26	G137	<i>Fragaria x ananassa</i>	AF484683	6.00E-93
26	G137	<i>Gossypium arboreum</i>	BG440326	2.00E-90
26	G137	<i>Prunus persica</i>	BU048398	4.00E-89
26	G137	<i>Antirrhinum majus</i>	AMDEFH49G	2.00E-87
26	G137	<i>Brassica oleracea</i> var. <i>botrytis</i>	gi23304688	2.10E-123
26	G137	<i>Malus x domestica</i>	gi3290209	7.70E-101
26	G137	<i>Malus domestica</i>	gi7488622	7.70E-101
26	G137	<i>Cucumis sativus</i>	gi6683777	1.70E-98
26	G137	<i>Populus tremuloides</i>	gi28372802	1.30E-96
26	G137	<i>Vitis vinifera</i>	gi20385584	1.70E-96
26	G137	<i>Fragaria x ananassa</i>	gi28628841	1.90E-90
26	G137	<i>Antirrhinum majus</i>	gi1239961	2.90E-85
26	G137	<i>Lycopersicon esculentum</i>	gi24967143	1.10E-83
26	G137	<i>Petunia x hybrida</i>	gi13384048	3.00E-83
28	G138	<i>Brassica oleracea</i> var. <i>botrytis</i>	BOL508052	1.00E-114
28	G138	<i>Petunia x hybrida</i>	AF335236	2.00E-72
28	G138	<i>Lycopersicon esculentum</i>	AY294329	3.00E-72
28	G138	<i>Nicotiana tabacum</i>	AF068723	5.00E-72
28	G138	<i>Capsicum annuum</i>	AF129875	1.00E-70
28	G138	<i>Malus domestica</i>	U78947	3.00E-70

28	G138	<i>Malus x domestica</i>	MDAJ1681		1.00E-69
28	G138	<i>Pinus radiata</i>	PRU42399		2.00E-69
28	G138	<i>Antirrhinum majus</i>	AMDEFH49G		2.00E-69
28	G138	<i>Daucus carota</i>	DCA271151		8.00E-69
28	G138	<i>Brassica oleracea</i> var. <i>botrytis</i>	gi23304686		4.20E-109
28	G138	<i>Petunia x hybrida</i>	gi13384050		5.90E-71
28	G138	<i>Nicotiana tabacum</i>	gi8567991		1.20E-70
28	G138	<i>Lycopersicon</i> <i>esculentum</i>	gi31747208		2.60E-70
28	G138	<i>Capsicum annuum</i>	gi6651033		4.80E-69
28	G138	<i>Antirrhinum majus</i>	gi1239961		2.10E-68
28	G138	<i>Malus x domestica</i>	gi3290209		4.30E-68
28	G138	<i>Malus domestica</i>	gi7488622		4.30E-68
28	G138	<i>Daucus carota</i>	gi22091481		8.90E-68
28	G138	<i>Pinus radiata</i>	gi1206003		1.50E-67
30	G139	<i>Brassica oleracea</i> var. <i>botrytis</i>	BOL508053		1.00E-115
30	G139	<i>Populus tremuloides</i>	AF185574		1.00E-100
30	G139	<i>Cucumis sativus</i>	AF135962		4.00E-97
30	G139	<i>Malus domestica</i>	U78947		2.00E-96
30	G139	<i>Malus x domestica</i>	MDAJ1681		5.00E-96
30	G139	<i>Vitis vinifera</i>	AF373601		9.00E-92
30	G139	<i>Populus</i> <i>balsamifera</i> subsp. <i>trichocarpa</i>	BU869391		9.00E-89
30	G139	<i>Fragaria x</i> <i>ananassa</i>	AF484683		8.00E-88
30	G139	<i>Prunus persica</i>	BU048398		1.00E-86
30	G139	<i>Antirrhinum majus</i>	AMDEFH49G		8.00E-85
30	G139	<i>Brassica oleracea</i> var. <i>botrytis</i>	gi23304688		6.00E-110
30	G139	<i>Populus tremuloides</i>	gi28372802		2.20E-96
30	G139	<i>Cucumis sativus</i>	gi6683777		2.00E-93
30	G139	<i>Malus x domestica</i>	gi3290209		2.60E-93
30	G139	<i>Malus domestica</i>	gi7488622		2.60E-93
30	G139	<i>Vitis vinifera</i>	gi20385584		1.00E-89
30	G139	<i>Fragaria x</i> <i>ananassa</i>	gi28628841		6.80E-86
30	G139	<i>Antirrhinum majus</i>	gi1239961		1.30E-82
30	G139	<i>Petunia x hybrida</i>	gi13384048		2.00E-79
30	G139	<i>Lycopersicon</i> <i>esculentum</i>	gi24967143		2.30E-78
32	G140	<i>Brassica napus</i>	CD818823		1.00E-112
32	G140	<i>Liquidambar</i> <i>styraciflua</i>	AF103903		7.00E-88
32	G140	<i>Vitis vinifera</i>	AF265562		9.00E-88
32	G140	<i>Medicago</i> <i>truncatula</i>	CB066648		2.00E-87
32	G140	<i>Gossypium</i> <i>arboreum</i>	BQ411600		2.00E-85
32	G140	<i>Malus x domestica</i>	MDO251117		4.00E-83
32	G140	<i>Rosa rugosa</i>	AB025643		5.00E-83
32	G140	<i>Nicotiana tabacum</i>	TOBNAG1A		1.00E-80
32	G140	<i>Petunia integrifolia</i>	PETFHPP		1.00E-80
32	G140	<i>Citrus sinensis</i>	CB290594		2.00E-80

32	G140	<i>Brassica napus</i>	gi12655901		4.10E-102
32	G140	<i>Liquidambar styraciflua</i>	gi5031217		6.10E-85
32	G140	<i>Vitis vinifera</i>	gi14279306		8.00E-83
32	G140	<i>Rosa rugosa</i>	gi6970411		3.10E-81
32	G140	<i>Malus x domestica</i>	gi16973296		4.60E-80
32	G140	<i>Nicotiana tabacum</i>	gi3913007		3.70E-78
32	G140	<i>Petunia integrifolia</i>	gi848999		2.00E-77
32	G140	<i>Petunia x hybrida</i>	gi2129972		5.40E-77
32	G140	<i>Panax ginseng</i>	gi3913005		5.40E-77
32	G140	<i>Lycopersicon esculentum</i>	gi3913004		8.80E-77
34	G142	<i>Brassica oleracea</i> var. <i>botrytis</i>	BOL508409		1.00E-127
34	G142	<i>Vitis vinifera</i>	AF373602		1.00E-88
34	G142	<i>Malus domestica</i>	MDAJ763		3.00E-84
34	G142	<i>Petunia x hybrida</i>	AB031035		2.00E-77
34	G142	<i>Agapanthus praecox</i>	AB079261		1.00E-76
34	G142	<i>Chrysanthemum x morifolium</i>	AY173062		8.00E-75
34	G142	<i>Oryza sativa</i>	OSU78782		6.00E-74
34	G142	<i>Oryza sativa</i> (japonica cultivar-group)	AK069103		6.00E-74
34	G142	<i>Zea mays</i>	MZEMADSB		3.00E-73
34	G142	<i>Triticum aestivum</i>	AB007505		3.00E-72
34	G142	<i>Brassica oleracea</i> var. <i>botrytis</i>	gi23304710		6.50E-120
34	G142	<i>Vitis vinifera</i>	gi20385586		3.30E-86
34	G142	<i>Malus domestica</i>	gi3646340		1.20E-81
34	G142	<i>Petunia x hybrida</i>	gi7544096		1.60E-75
34	G142	<i>Agapanthus praecox</i>	gi29467050		1.50E-74
34	G142	<i>Oryza sativa</i>	gi2286109		2.20E-73
34	G142	<i>Chrysanthemum x morifolium</i>	gi27804371		4.50E-73
34	G142	<i>Zea mays</i>	gi7446515		1.50E-72
34	G142	<i>Lolium perenne</i>	gi28630959		8.40E-72
34	G142	<i>Triticum aestivum</i>	gi3688591		2.20E-71
36	G145	<i>Sinapis alba</i>	SAMADSD		1.00E-127
36	G145	<i>Vitis vinifera</i>	CB980340		5.00E-98
36	G145	<i>Lycopersicon esculentum</i>	AY294330		5.00E-97
36	G145	<i>Nicotiana glauca</i>	AF068722		8.00E-96
36	G145	<i>Pisum sativum</i>	PSAJ3318		1.00E-95
36	G145	<i>Brassica napus</i>	CD814473		2.00E-95
36	G145	<i>Petunia x hybrida</i>	PETTRNSFB		2.00E-95
36	G145	<i>Antirrhinum majus</i>	AMDEFH200		3.00E-95
36	G145	<i>Gossypium hirsutum</i>	AF538965		5.00E-95
36	G145	<i>Populus tremuloides</i>	AY235222		7.00E-95
36	G145	<i>Sinapis alba</i>	gi1617211		7.30E-121
36	G145	<i>Vitis vinifera</i>	gi20385588		6.00E-94
36	G145	<i>Lycopersicon esculentum</i>	gi31747210		2.00E-93
36	G145	<i>Pisum sativum</i>	gi3184054		6.90E-93

36	G145	<i>Nicotiana sylvestris</i>	gi5070138		2.30E-92
36	G145	<i>Petunia x hybrida</i>	gi1181186		4.80E-92
36	G145	<i>Populus tremuloides</i>	gi30314024		7.90E-92
36	G145	<i>Antirrhinum majus</i>	gi1239959		1.60E-91
36	G145	<i>Gossypium hirsutum</i>	gi23194451		2.10E-91
36	G145	<i>Chrysanthemum x morifolium</i>	gi27804361		1.50E-88
38	G146	<i>Brassica napus</i>	CD818636		1.00E-104
38	G146	<i>Gossypium hirsutum</i>	AF538966		1.00E-91
38	G146	<i>Gossypium arboreum</i>	BG441292		1.00E-90
38	G146	<i>Medicago truncatula</i>	BI311053		3.00E-89
38	G146	<i>Cucumis sativus</i>	AF022377		4.00E-89
38	G146	<i>Vitis vinifera</i>	CB975703		1.00E-88
38	G146	<i>Momordica charantia</i>	AY178837		1.00E-87
38	G146	<i>Glycine max</i>	AW184799		2.00E-82
38	G146	<i>Phaseolus coccineus</i>	CA902463		5.00E-79
38	G146	<i>Malus domestica</i>	MDAJ762		7.00E-79
38	G146	<i>Gossypium hirsutum</i>	gi23194453		8.40E-88
38	G146	<i>Cucumis sativus</i>	gi4103342		1.40E-85
38	G146	<i>Vitis vinifera</i>	gi20385590		2.60E-84
38	G146	<i>Momordica charantia</i>	gi27763670		8.90E-84
38	G146	<i>Agapanthus praecox</i>	gi29467048		1.30E-75
38	G146	<i>Petunia x hybrida</i>	gi1568513		1.00E-73
38	G146	<i>Hyacinthus orientalis</i>	gi21955182		6.60E-72
38	G146	<i>Panax ginseng</i>	gi3913005		7.50E-71
38	G146	<i>Lycopersicon esculentum</i>	gi24967137		1.60E-70
38	G146	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	gi2981133		8.70E-70
39	G148	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER24877 1	704	
39	G148	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER99362 1	705	
39	G148	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER865 1	706	
39	G148	<i>Oryza sativa</i>	OSC101589.C1.p14.fg	707	
39	G148	<i>Zea mays</i>	LIB4766-083-R1-K1-A9	708	
39	G148	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER914 1	709	
39	G148	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER914 14	710	
39	G148	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER914 2	711	
39	G148	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER914 3	712	
39	G148	<i>Oryza sativa</i>	Os_S31752	1560	
39	G148	<i>Oryza sativa</i>	Os_S63871	1561	

39	G148	<i>Oryza sativa</i>	Os S65486	1562	
39	G148	<i>Zea mays</i>	Zm S11418374	1755	
39	G148	<i>Zea mays</i>	Zm S11418375	1756	
39	G148	<i>Triticum aestivum</i>	Ta S66204	1835	
39	G148	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-44128	1943	
39	G148	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-42436	1944	
40	G148	<i>Brassica oleracea var. botrytis</i>	BOL508409		3.00E-74
40	G148	<i>Malus domestica</i>	MDAJ763		2.00E-65
40	G148	<i>Vitis vinifera</i>	AF373602		3.00E-64
40	G148	<i>Petunia x hybrida</i>	AB031035		1.00E-59
40	G148	<i>Chrysanthemum x morifolium</i>	AY173062		1.00E-58
40	G148	<i>Oryza sativa</i>	OSU78782		3.00E-57
40	G148	<i>Oryza sativa (japonica cultivar- group)</i>	AK069103		3.00E-57
40	G148	<i>Triticum aestivum</i>	AB007505		1.00E-56
40	G148	<i>Lolium perenne</i>	AY198329		1.00E-55
40	G148	<i>Poa annua</i>	AF372840		5.00E-55
40	G148	<i>Brassica oleracea var. botrytis</i>	gi23304710		1.70E-73
40	G148	<i>Malus domestica</i>	gi3646340		6.50E-65
40	G148	<i>Vitis vinifera</i>	gi20385586		7.40E-64
40	G148	<i>Petunia x hybrida</i>	gi7544096		7.10E-59
40	G148	<i>Chrysanthemum x morifolium</i>	gi27804371		2.20E-57
40	G148	<i>Triticum aestivum</i>	gi3688591		3.50E-57
40	G148	<i>Oryza sativa</i>	gi2286109		4.50E-57
40	G148	<i>Lolium perenne</i>	gi28630959		5.20E-56
40	G148	<i>Poa annua</i>	gi13958339		8.40E-56
40	G148	<i>Agapanthus praecox</i>	gi29467050		9.70E-55
42	G151	<i>Brassica napus</i>	BNU22681		1.00E-94
42	G151	<i>Selaginella remotifolia</i>	AB086021		5.00E-39
42	G151	<i>Lycopodium annotinum</i>	AF425598		5.00E-37
42	G151	<i>Helianthus annuus</i>	BQ970680		2.00E-36
42	G151	<i>Pinus radiata</i>	PRU42400		9.00E-36
42	G151	<i>Gnetum parvifolium</i>	AB022665		1.00E-35
42	G151	<i>Gnetum gnemon</i>	GGN132215		1.00E-35
42	G151	<i>Pinus resinosa</i>	PRMADS1		2.00E-35
42	G151	<i>Oryza sativa (japonica cultivar- group)</i>	AY177696		6.00E-35
42	G151	<i>Oryza sativa</i>	OSU78782		8.00E-35
42	G151	<i>Brassica napus</i>	gi3831486		9.40E-96
42	G151	<i>Selaginella remotifolia</i>	gi29467138		2.20E-39
42	G151	<i>Lycopodium annotinum</i>	gi21396795		1.80E-37
42	G151	<i>Pinus radiata</i>	gi1206005		1.60E-36
42	G151	<i>Gnetum gnemon</i>	gi5019456		2.60E-36
42	G151	<i>Gnetum parvifolium</i>	gi6092009		2.60E-36

42	G151	<i>Pinus resinosa</i>	gi1702951		3.40E-36
42	G151	<i>Oryza sativa</i>	gi2286109		5.50E-36
42	G151	<i>Zea mays</i>	gi7446514		5.50E-36
42	G151	<i>Lolium perenne</i>	gi28630959		1.10E-35
43	G153	<i>Oryza sativa</i>	G3479	2189	2.00E-59
43	G153	<i>Glycine max</i>	G3484	2191	3.00E-77
43	G153	<i>Glycine max</i>	G3485	2193	9.00E-63
43	G153	<i>Zea mays</i>	G3487	2195	5.00E-63
43	G153	<i>Zea mays</i>	G3488	2197	2.00E-61
43	G153	<i>Zea mays</i>	G3489	2199	6.00E-66
43	G153	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER393266_1	713	
43	G153	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER84992_1	714	
43	G153	<i>Oryza sativa</i>	OSC19180.C1.p14.fg	715	
43	G153	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER124_1	716	
43	G153	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER226078_2	717	
43	G153	<i>Zea mays</i>	uC-zmflMo17202h01	718	
43	G153	<i>Glycine max</i>	Gma_S5139103	1634	
43	G153	<i>Zea mays</i>	Zm_S11418691	1757	
43	G153	<i>Zea mays</i>	Zm_S11433900	1758	
43	G153	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-362903	1945	
43	G153	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-8562	1946	
44	G153	<i>Antirrhinum majus</i>	AMDEFH125		1.00E-67
44	G153	<i>Zea mays</i>	AF112149		8.00E-63
44	G153	<i>Oryza sativa</i> (japonica cultivar-group)	AY177696		1.00E-62
44	G153	<i>Glycine max</i>	AW706936		5.00E-59
44	G153	<i>Medicago truncatula</i>	BQ164807		5.00E-59
44	G153	<i>Lycopersicon esculentum</i>	AW218280		5.00E-56
44	G153	<i>Solanum tuberosum</i>	BM405213		2.00E-55
44	G153	<i>Medicago sativa</i>	MSU91964		6.00E-54
44	G153	<i>Triticum aestivum</i>	AX658813		3.00E-49
44	G153	<i>Mesembryanthemum crystallinum</i>	BE034403		3.00E-48
44	G153	<i>Antirrhinum majus</i>	gi1816459		2.10E-66
44	G153	<i>Oryza sativa</i> (japonica cultivar-group)	gi30313677		2.90E-62
44	G153	<i>Zea mays</i>	gi29611976		7.70E-62
44	G153	<i>Medicago sativa</i>	gi1928874		1.30E-52
44	G153	<i>Ipomoea batatas</i>	gi15081463		6.90E-45
44	G153	<i>Oryza sativa</i>	gi7592642		9.10E-43
44	G153	<i>Lolium perenne</i>	gi28630953		8.20E-42
44	G153	<i>Lolium temulentum</i>	gi4204232		1.70E-41
44	G153	<i>Triticum aestivum</i>	gi30721847		2.80E-41
44	G153	<i>Hordeum vulgare</i>	gi9367313		2.80E-41
45	G155	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER112511_1	719	

45	G155	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER2290_5	720	
45	G155	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER24178_1	721	
45	G155	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER24178_4	722	
45	G155	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER862_1	723	
45	G155	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER862_2	724	
45	G155	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER862_3	725	
45	G155	<i>Glycine max</i>	LIB4127-088-Q1-N1-F3	726	
45	G155	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER117_2	727	
45	G155	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER397_1	728	
45	G155	<i>Oryza sativa</i>	OSC101428.C1.p6.fg	729	
45	G155	<i>Oryza sativa</i>	OSC22851.C1.p5.fg	730	
45	G155	<i>Oryza sativa</i>	OSC23163.C1.p8.fg	731	
45	G155	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER444_10	732	
45	G155	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER444_17	733	
45	G155	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER444_19	734	
45	G155	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER444_20	735	
45	G155	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER444_25	736	
45	G155	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER444_29	737	
45	G155	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER444_38	738	
45	G155	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER49_1	739	
45	G155	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER49_2	740	
45	G155	<i>Oryza sativa</i>	Os_S60917	1563	
45	G155	<i>Oryza sativa</i>	Os_S65478	1564	
45	G155	<i>Oryza sativa</i>	Os_S65480	1565	
45	G155	<i>Oryza sativa</i>	Os_S81123	1566	
45	G155	<i>Glycine max</i>	Gma_S5001655	1635	
45	G155	<i>Hordeum vulgare</i>	Hv_S74097	1719	
45	G155	<i>Hordeum vulgare</i>	Hv_S74098	1720	
45	G155	<i>Hordeum vulgare</i>	Hv_S74100	1721	
45	G155	<i>Zea mays</i>	Zm_S11355421	1759	
45	G155	<i>Zea mays</i>	Zm_S11374058	1760	
45	G155	<i>Zea mays</i>	Zm_S11418377	1761	
45	G155	<i>Zea mays</i>	Zm_S11418747	1762	
45	G155	<i>Zea mays</i>	Zm_S11435147	1763	
45	G155	<i>Zea mays</i>	Zm_S11527666	1764	
45	G155	<i>Triticum aestivum</i>	Ta_S185481	1836	
45	G155	<i>Triticum aestivum</i>	Ta_S210240	1837	
45	G155	<i>Triticum aestivum</i>	Ta_S66203	1838	
45	G155	<i>Lycopersicon esculentum</i>	Les_S5931544	1926	

45	G155	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-44980	1947	
45	G155	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-45332	1948	
45	G155	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-329711	1949	
45	G155	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-457556	1950	
45	G155	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-477293	1951	
45	G155	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-67345	1952	
46	G155	<i>Brassica oleracea var. botrytis</i>	BOL505844		1.00E-123
46	G155	<i>Sinapis alba</i>	SAU25695		1.00E-120
46	G155	<i>Brassica napus</i>	CD841921		1.00E-119
46	G155	<i>Betula pendula</i>	BPMADS5GN		3.00E-82
46	G155	<i>Nicotiana sylvestris</i>	AF068725		1.00E-79
46	G155	<i>Nicotiana tabacum</i>	AF385746		2.00E-79
46	G155	<i>Malus x domestica</i>	MDU78948		3.00E-78
46	G155	<i>Capsicum annuum</i>	AF130118		4.00E-78
46	G155	<i>Petunia x hybrida</i>	AF176783		1.00E-77
46	G155	<i>Lycopersicon esculentum</i>	AW442282		1.00E-77
46	G155	<i>Brassica oleracea var. botrytis</i>	gi23304678		2.00E-116
46	G155	<i>Sinapis alba</i>	gi1049024		2.40E-113
46	G155	<i>Betula pendula</i>	gi1483232		2.00E-79
46	G155	<i>Nicotiana sylvestris</i>	gi5070142		5.40E-77
46	G155	<i>Nicotiana tabacum</i>	gi27373049		8.80E-77
46	G155	<i>Capsicum annuum</i>	gi14518447		7.90E-76
46	G155	<i>Petunia x hybrida</i>	gi6606306		1.30E-75
46	G155	<i>Malus x domestica</i>	gi3947985		3.40E-75
46	G155	<i>Petunia sp.</i>	gi6731756		7.10E-75
46	G155	<i>Lycopersicon esculentum</i>	gi23428887		1.90E-74
48	G171	<i>Brassica oleracea</i>	BZ059285		2.00E-86
48	G171	<i>Lotus japonicus</i>	AG231874		1.00E-15
48	G171	<i>Glycine max</i>	BE610209		1.00E-11
48	G171	<i>Medicago truncatula</i>	AC135316		3.00E-10
48	G171	<i>Zea mays</i>	CC654475		6.00E-10
48	G171	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01000422		1.00E-09
48	G171	<i>Oryza sativa</i>	AP002480		1.00E-09
48	G171	<i>Vitis vinifera</i>	CB980345		2.00E-09
48	G171	<i>Oryza sativa (japonica cultivar- group)</i>	AP006531		9.00E-08
48	G171	<i>Lycopersicon esculentum</i>	BI930829		2.00E-07
48	G171	<i>Oryza sativa</i>	gi8096379		4.10E-11
48	G171	<i>Oryza sativa (japonica cultivar- group)</i>	gi15623935		6.90E-09
48	G171	<i>Malus x domestica</i>	gi32452884		5.60E-07

48	G171	<i>Petunia x hybrida</i>	gi13384058	5.60E-07
48	G171	<i>Lycopodium annotinum</i>	gi30525823	8.10E-07
48	G171	<i>Ceratopteris richardii</i>	gi2252482	1.40E-06
48	G171	<i>Cichorium intybus</i>	gi3986689	3.00E-06
48	G171	<i>Brassica napus</i>	gi3831486	3.60E-06
48	G171	<i>Ipomoea nil</i>	gi27372827	3.80E-06
48	G171	<i>Rosa rugosa</i>	gi9857312	5.30E-06
50	G172	<i>Brassica oleracea</i>	BH583694	9.00E-52
50	G172	<i>Medicago truncatula</i>	AC144481	5.00E-09
50	G172	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01005416	3.00E-08
50	G172	<i>Oryza sativa</i>	AC098572	3.00E-08
50	G172	<i>Lotus japonicus</i>	AP006142	5.00E-08
50	G172	<i>Lotus corniculatus</i> var. <i>japonicus</i>	AP006379	1.00E-06
50	G172	<i>Lycopersicon esculentum</i>	BH014401	9.00E-06
50	G172	<i>Zea mays</i>	CC690653	2.00E-05
50	G172	<i>Oryza sativa (japonica cultivar-group)</i>	AP004784	4.00E-05
50	G172	<i>Sorghum bicolor</i>	BZ627051	6.00E-05
50	G172	<i>Brassica rapa</i>	gi30523366	5.60E-06
50	G172	<i>Brassica napus</i>	gi17933454	1.00E-05
50	G172	<i>Brassica oleracea</i> var. <i>capitata</i>	gi30523252	1.00E-05
50	G172	<i>Zea mays</i>	gi1076827	1.10E-05
50	G172	<i>Oryza sativa (japonica cultivar-group)</i>	gi30313673	2.10E-05
50	G172	<i>Lolium perenne</i>	gi28630955	6.40E-05
50	G172	<i>Lolium temulentum</i>	gi4204234	6.40E-05
50	G172	<i>Oryza sativa</i>	gi15290141	7.10E-05
50	G172	<i>Raphanus sativus</i>	gi30523250	0.0001
50	G172	<i>Cucumis sativus</i>	gi8216957	0.00014
52	G173	<i>Brassica oleracea</i>	BZ519961	3.00E-20
52	G173	<i>Zea mays</i>	AX540653	8.00E-17
52	G173	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01022896	1.00E-07
52	G173	<i>Oryza sativa</i>	AC093312	5.00E-07
52	G173	<i>Medicago truncatula</i>	AC135316	3.00E-06
52	G173	<i>Glycine max</i>	AW508033	1.00E-05
52	G173	<i>Physcomitrella patens</i>	PPA419330	3.00E-05
52	G173	<i>Oryza sativa (japonica cultivar-group)</i>	AP005734	2.00E-04
52	G173	<i>Triticum aestivum</i>	BJ303010	7.00E-04
52	G173	<i>Lotus japonicus</i>	AG231874	0.001
52	G173	<i>Physcomitrella patens</i>	gi22474466	1.30E-08
52	G173	<i>Ipomoea batatas</i>	gi13448658	1.40E-08

52	G173	<i>Oryza sativa</i>	gi8096379		1.90E-08
52	G173	<i>Magnolia praecocissima</i>	gi16549058		1.40E-06
52	G173	<i>Sinapis alba</i>	gi1617211		1.90E-06
52	G173	<i>Gnetum gnemon</i>	gi27151621		1.90E-06
52	G173	<i>Physcomitrella patens</i> subsp. <i>patens</i>	gi22090622		3.00E-06
52	G173	<i>Cichorium intybus</i>	gi3986689		3.30E-06
52	G173	<i>Nicotiana glauca</i>	gi5070144		4.70E-06
52	G173	<i>Papaver nudicaule</i>	gi3170500		4.70E-06
53	G200	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER46239_2	741	
53	G200	<i>Oryza sativa</i>	1945280	742	
53	G200	<i>Oryza sativa</i>	OSC1073.C1.p11.fg	743	
53	G200	<i>Oryza sativa</i>	rsicem_4884.y1.abd	744	
53	G200	<i>Zea mays</i>	LIB4980-049-R1-K1-C12	745	
53	G200	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER286_1	746	
53	G200	<i>Oryza sativa</i>	Os_S60479	1567	
53	G200	<i>Medicago truncatula</i>	Mtr_S5340749	1691	
53	G200	<i>Zea mays</i>	Zm_S11327053	1765	
53	G200	<i>Zea mays</i>	Zm_S11454145	1766	
53	G200	<i>Zea mays</i>	Zm_S11529138	1767	
53	G200	<i>Zea mays</i>	Zm_S11529143	1768	
53	G200	<i>Zea mays</i>	Zm_S11529165	1769	
53	G200	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-57276	1953	
53	G200	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-385670	1954	
54	G200	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU876112		8.00E-79
54	G200	<i>Beta vulgaris</i>	BQ587622		8.00E-73
54	G200	<i>Gossypium arboreum</i>	BG441590		6.00E-70
54	G200	<i>Oryza sativa</i> (japonica cultivar-group)	AK061437		1.00E-68
54	G200	<i>Oryza sativa</i>	OSMYB1308		1.00E-68
54	G200	<i>Poncirus trifoliata</i>	CD576612		3.00E-68
54	G200	<i>Nuphar advena</i>	CD474802		2.00E-66
54	G200	<i>Brassica oleracea</i>	BH976962		4.00E-66
54	G200	<i>Lycopersicon esculentum</i>	LETHM6		5.00E-65
54	G200	<i>Zea mays</i>	AY107969		5.00E-65
54	G200	<i>Oryza sativa</i>	gi1945281		5.80E-68
54	G200	<i>Antirrhinum majus</i>	gi256828		6.00E-62
54	G200	<i>Oryza sativa</i> (japonica cultivar-group)	gi33087065		7.50E-62
54	G200	<i>Lycopersicon esculentum</i>	gi1430848		1.00E-59
54	G200	<i>Zea mays</i>	gi19072744		8.40E-56
54	G200	<i>Dendrobium sp. XMW-2002-1</i>	gi28628947		1.60E-53

54	G200	<i>Lotus corniculatus</i> var. <i>japonicus</i>	gi30024598		5.90E-50
54	G200	<i>Petunia x hybrida</i>	gi20561		1.20E-49
54	G200	<i>Nicotiana tabacum</i>	gi6552389		2.40E-49
54	G200	<i>Glycine max</i>	gi5139802		8.60E-47
56	G224	<i>Brassica oleracea</i>	BH442040		2.00E-38
56	G224	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01016190		4.00E-08
56	G224	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AP005575		5.00E-08
56	G224	<i>Lotus japonicus</i>	AP004985		9.00E-07
56	G224	<i>Medicago</i> <i>truncatula</i>	AC135101		2.00E-06
56	G224	<i>Prunus persica</i>	BU040633		6.00E-06
56	G224	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BQ791286		2.00E-05
56	G224	<i>Oryza sativa</i>	OSJN00182		2.00E-05
56	G224	<i>Brassica napus</i>	CD832269		2.00E-05
56	G224	<i>Vitis vinifera</i>	CB345908		5.00E-05
56	G224	<i>Oryza sativa</i>	gi8096405		1.40E-06
56	G224	<i>Antirrhinum</i> <i>hispanicum</i>	gi13161528		3.60E-06
56	G224	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi31433564		8.80E-06
56	G224	<i>Prunus mume</i>	gi29420809		0.0019
56	G224	<i>Prunus dulcis</i>	gi28866899		0.014
56	G224	<i>Lycopersicon</i> <i>esculentum</i>	gi9858770		0.91
56	G224	<i>Daucus carota</i>	gi20066308		0.99
56	G224	<i>Lotus japonicus</i>	gi28624856		1
58	G244	<i>Brassica oleracea</i>	BH667251		1.00E-120
58	G244	<i>Oryza sativa</i>	AX755614		5.00E-88
58	G244	<i>Hordeum vulgare</i>	BI959020		6.00E-88
58	G244	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01009672		7.00E-79
58	G244	<i>Sorghum bicolor</i>	AF474126		6.00E-69
58	G244	<i>Vitis vinifera</i>	CB971781		8.00E-68
58	G244	<i>Lycopersicon</i> <i>esculentum</i>	AW624307		3.00E-54
58	G244	<i>Solanum tuberosum</i>	BG592600		3.00E-53
58	G244	<i>Mesembryanthemu</i> <i>m crystallinum</i>	BG269414		1.00E-52
58	G244	<i>Populus x</i> <i>canescens</i>	AY129246		2.00E-52
58	G244	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi32487951		2.60E-90
58	G244	<i>Sorghum bicolor</i>	gi19073322		7.20E-66
58	G244	<i>Oryza sativa</i>	gi1946267		1.20E-55
58	G244	<i>Populus x</i> <i>canescens</i>	gi22795039		3.40E-52
58	G244	<i>Gossypium</i> <i>hirsutum</i>	gi13346188		4.30E-52
58	G244	<i>Antirrhinum majus</i>	gi485867		3.20E-51
58	G244	<i>Lotus corniculatus</i>	gi30024600		8.00E-51

		var. japonicus			
58	G244	<i>Petunia x hybrida</i>	gi20563		1.70E-50
58	G244	<i>Zea mays</i>	gi127582		3.50E-50
58	G244	<i>Boea crassifolia</i>	gi30575840		5.70E-50
60	G246	<i>Lycopersicon esculentum</i>	AW624217		3.00E-36
60	G246	<i>Brassica napus</i>	CD841933		1.00E-35
60	G246	<i>Oryza sativa (japonica cultivar- group)</i>	AK107461		1.00E-34
60	G246	<i>Solanum tuberosum</i>	BQ514458		2.00E-34
60	G246	<i>Oryza sativa</i>	AX699697		2.00E-33
60	G246	<i>Physcomitrella patens</i>	AX288143		6.00E-33
60	G246	<i>Medicago truncatula</i>	BQ165917		3.00E-32
60	G246	<i>Zinnia elegans</i>	AU287803		4.00E-32
60	G246	<i>Citrus sinensis</i>	BQ623005		5.00E-32
60	G246	<i>Populus tremula x Populus tremuloides</i>	POP567345		1.00E-31
60	G246	<i>Oryza sativa</i>	gi6539552		1.50E-35
60	G246	<i>Populus tremula x Populus tremuloides</i>	gi31980093		8.30E-33
60	G246	<i>Oryza sativa (japonica cultivar- group)</i>	gi21321780		3.60E-32
60	G246	<i>Solanum tuberosum</i>	gi9954112		1.00E-25
60	G246	<i>Nicotiana tabacum</i>	gi27529846		2.20E-25
60	G246	<i>Papaver rhoeas</i>	gi7230673		1.10E-22
60	G246	<i>Physcomitrella patens</i>	gi8745321		1.30E-22
60	G246	<i>Adiantum raddianum</i>	gi7677136		3.30E-22
60	G246	<i>Hordeum vulgare</i>	gi8745325		1.80E-21
60	G246	<i>Secale cereale</i>	gi7677132		3.80E-21
62	G253	<i>Brassica napus</i>	CD841933		3.00E-26
62	G253	<i>Lycopersicon esculentum</i>	AW624217		3.00E-26
62	G253	<i>Solanum tuberosum</i>	BQ514458		2.00E-25
62	G253	<i>Medicago truncatula</i>	BQ165917		4.00E-25
62	G253	<i>Citrus sinensis</i>	BQ623005		6.00E-25
62	G253	<i>Triticum aestivum</i>	BQ838360		2.00E-24
62	G253	<i>Oryza sativa (japonica cultivar- group)</i>	AK107461		2.00E-24
62	G253	<i>Physcomitrella patens</i>	AX288143		4.00E-24
62	G253	<i>Zinnia elegans</i>	AU287803		8.00E-24
62	G253	<i>Papaver rhoeas</i>	AF236059		2.00E-23
62	G253	<i>Oryza sativa (japonica cultivar- group)</i>	gi21321780		1.50E-28
62	G253	<i>Oryza sativa</i>	gi6979341		7.10E-27
62	G253	<i>Papaver rhoeas</i>	gi7230673		3.20E-24
62	G253	<i>Populus tremula x Populus tremuloides</i>	gi31980093		4.10E-24

62	G253	<i>Adiantum raddianum</i>	gi7677136		9.70E-23
62	G253	<i>Solanum tuberosum</i>	gi9954114		1.10E-22
62	G253	<i>Nicotiana tabacum</i>	gi16326137		2.40E-22
62	G253	<i>Physcomitrella patens</i>	gi8745321		2.00E-21
62	G253	<i>Craterostigma plantagineum</i>	gi1002800		7.80E-21
62	G253	<i>Hordeum vulgare</i>	gi8745325		1.00E-20
64	G268	<i>Oryza sativa</i> (japonica cultivar-group)	AK070193		1.0e-999
64	G268	<i>Zea mays</i>	AY104480		1.00E-146
64	G268	<i>Oryza sativa</i>	AX654858		1.00E-125
64	G268	<i>Malus domestica</i>	AF220204		1.00E-116
64	G268	<i>Glycine max</i>	CA785038		1.00E-112
64	G268	<i>Solanum tuberosum</i>	BM406566		1.00E-111
64	G268	<i>Lactuca sativa</i>	BQ863563		1.00E-101
64	G268	<i>Lycopersicon esculentum</i>	BI936015		1.00E-101
64	G268	<i>Medicago truncatula</i>	BE203572		1.00E-100
64	G268	<i>Oryza sativa</i> (indica cultivar-group)	CB621547		1.00E-100
64	G268	<i>Oryza sativa</i>	gi15408875		4.90E-250
64	G268	<i>Oryza sativa</i> (japonica cultivar-group)	gi20160625		4.90E-250
64	G268	<i>Malus x domestica</i>	gi6752888		2.40E-113
64	G268	<i>Narcissus pseudonarcissus</i>	gi18419598		8.90E-52
64	G268	<i>Pinus pinaster</i>	gi20218829		1.70E-09
64	G268	<i>Nicotiana glauca</i>	gi1247388		0.00015
64	G268	<i>Bromheadia finlaysoniana</i>	gi2108256		0.00025
64	G268	<i>Lycopersicon esculentum</i>	gi1345539		0.00031
64	G268	<i>Antirrhinum majus</i>	gi16029		0.00064
64	G268	<i>Volvox carterii</i>	gi21992		0.0024
66	G287	<i>Vicia faba</i>	VFPTF2		5.00E-99
66	G287	<i>Oryza sativa</i> (japonica cultivar-group)	AK069464		1.00E-80
66	G287	<i>Brassica oleracea</i>	BZ074994		6.00E-63
66	G287	<i>Lactuca sativa</i>	BQ869065		1.00E-61
66	G287	<i>Oryza sativa</i> (indica cultivar-group)	CB620939		1.00E-58
66	G287	<i>Amborella trichopoda</i>	CD482217		2.00E-52
66	G287	<i>Solanum tuberosum</i>	BG599712		1.00E-40
66	G287	<i>Medicago truncatula</i>	BG648535		2.00E-32
66	G287	<i>Triticum aestivum</i>	CD897359		1.00E-29
66	G287	<i>Oryza sativa</i>	AP002536		2.00E-14
66	G287	<i>Vicia faba</i>	gi2104683		5.80E-99
66	G287	<i>Oryza sativa</i> (japonica cultivar-group)	gi28301944		3.90E-09

		group)			
66	G287	<i>Oryza sativa</i>	gi15451572		0.004
66	G287	<i>Lycopersicon esculentum</i>	gi13620220		0.47
66	G287	<i>Brassica nigra</i>	gi20148766		0.47
66	G287	<i>Nicotiana tabacum</i>	gi119714		0.57
66	G287	<i>Spermatozopsis similis</i>	gi4584086		0.75
66	G287	<i>Prunus armeniaca</i>	gi2688826		0.99
66	G287	<i>Petunia x hybrida</i>	gi21105740		1
68	G309	<i>Gossypium hirsutum</i>	AY208992		1.00E-180
68	G309	<i>Vitis vinifera</i>	AF378125		1.00E-176
68	G309	<i>Lycopersicon esculentum</i>	AY269087		1.00E-175
68	G309	<i>Brassica napus</i>	AX081276		1.00E-164
68	G309	<i>Zea mays</i>	ZMA242530		1.00E-158
68	G309	<i>Hordeum vulgare</i>	AF460219		1.00E-157
68	G309	<i>Triticum aestivum</i>	BD074479		1.00E-157
68	G309	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01015042		1.00E-137
68	G309	<i>Oryza sativa</i>	AC087797		1.00E-137
68	G309	<i>Zea mays</i> subsp. <i>mays</i>	AF413202		1.00E-137
68	G309	<i>Vitis vinifera</i>	gi20334379		2.10E-170
68	G309	<i>Calycadenia multiglandulosa</i>	gi20257451		1.10E-155
68	G309	<i>Brassica napus</i>	gi13170126		2.30E-155
68	G309	<i>Hordeum vulgare</i>	gi18254373		5.30E-153
68	G309	<i>Triticum aestivum</i>	gi5640157		1.10E-152
68	G309	<i>Carlquistia muirii</i>	gi20257447		1.20E-151
68	G309	<i>Argyroxiphium kauense</i>	gi20257461		1.50E-151
68	G309	<i>Madia sativa</i>	gi20257442		5.00E-151
68	G309	<i>Argyroxiphium sandwicense</i> subsp. <i>macrocephalum</i>	gi20257457		5.00E-151
68	G309	<i>Dubautia raillardoides</i>	gi20257473		1.30E-150
70	G314	<i>Lotus japonicus</i>	AP006085		7.00E-94
70	G314	<i>Medicago truncatula</i>	AC137703		1.00E-90
70	G314	<i>Oryza sativa</i>	AP003823		8.00E-82
70	G314	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01000614		8.00E-82
70	G314	<i>Oryza sativa (japonica cultivar- group)</i>	AP005149		8.00E-82
70	G314	<i>Brassica oleracea</i>	BZ432637		1.00E-72
70	G314	<i>Solanum tuberosum</i>	BF052580		1.00E-47
70	G314	<i>Lycopersicon esculentum</i>	BG123921		2.00E-47
70	G314	<i>Glycine max</i>	BH152995		2.00E-35
70	G314	<i>Zea mays</i>	CC732802		4.00E-22
70	G314	<i>Oryza sativa (japonica cultivar- group)</i>	gi28564823		7.40E-80

70	G314	<i>Oryza sativa</i>	gi14719333		1.30E-26
70	G314	<i>Lycopersicon esculentum</i>	gi13620224		1.60E-25
70	G314	<i>Brassica napus</i>	gi13170126		2.00E-19
70	G314	<i>Zea mays</i> subsp. <i>mays</i>	gi15866286		7.40E-18
71	G319	<i>Oryza sativa</i>	Os_S76767	1568	
71	G319	<i>Zea mays</i>	Zm_S11428226	1770	
71	G319	<i>Triticum aestivum</i>	Ta_S281561	1839	
71	G319	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-50683	1955	
72	G319	<i>Brassica oleracea</i>	BZ004068		4.00E-37
72	G319	<i>Oryza sativa</i> (japonica cultivar- group)	AK098865		3.00E-14
72	G319	<i>Oryza minuta</i>	CB211383		3.00E-14
72	G319	<i>Oryza sativa</i>	AB001888		6.00E-14
72	G319	<i>Oryza sativa</i> (indica cultivar-group)	CA763406		8.00E-14
72	G319	<i>Triticum aestivum</i>	AX658811		8.00E-14
72	G319	<i>Sorghum bicolor</i>	CD208331		1.00E-13
72	G319	<i>Zea mays</i>	CD650991		2.00E-13
72	G319	<i>Glycine max</i>	BE058171		4.00E-13
72	G319	<i>Beta vulgaris</i>	BQ589272		7.00E-13
72	G319	<i>Oryza sativa</i>	gi3618320		1.40E-17
72	G319	<i>Oryza sativa</i> (japonica cultivar- group)	gi23589949		1.90E-11
72	G319	<i>Malus x domestica</i>	gi4091804		2.20E-10
72	G319	<i>Brassica nigra</i>	gi22854920		5.80E-10
72	G319	<i>Hordeum vulgare</i>	gi21667475		1.90E-09
72	G319	<i>Raphanus sativus</i>	gi3341723		4.90E-09
72	G319	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi21655156		8.70E-09
72	G319	<i>Brassica napus</i>	gi30984027		1.30E-08
72	G319	<i>Pinus radiata</i>	gi4557093		4.10E-08
72	G319	<i>Ipomoea nil</i>	gi10946337		4.80E-08
74	G324	<i>Oryza sativa</i> (japonica cultivar- group)	AK068618		1.00E-157
74	G324	<i>Oryza sativa</i>	AP004141		9.00E-95
74	G324	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01001748		2.00E-94
74	G324	<i>Brassica oleracea</i>	BH487952		2.00E-91
74	G324	<i>Brassica napus</i>	CD837146		5.00E-89
74	G324	<i>Lycopersicon esculentum</i>	AW979372		5.00E-87
74	G324	<i>Phaseolus coccineus</i>	CA906556		1.00E-72
74	G324	<i>Medicago truncatula</i>	CB892723		3.00E-71
74	G324	<i>Solanum tuberosum</i>	BG889245		4.00E-70
74	G324	<i>Triticum aestivum</i>	BJ245931		1.00E-69
74	G324	<i>Oryza sativa</i> (japonica cultivar- group)	gi21742100		2.20E-06

74	G324	<i>Populus x canescens</i>	gi22795037		0.00055
74	G324	<i>Oryza sativa</i>	gi15289911		0.0058
74	G324	<i>Rosa hybrid cultivar</i>	gi15029364		0.084
74	G324	<i>Ipomoea nil</i>	gi11127996		0.087
74	G324	<i>Oryza sativa</i> subsp. <i>japonica</i>	gi7592844		0.088
74	G324	<i>Lycopersicon esculentum</i>	gi4090943		0.17
74	G324	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi27357054		0.18
74	G324	<i>Brassica oleracea</i>	gi1418353		0.22
74	G324	<i>Zea diploperennis</i>	gi1076786		0.25
76	G344	<i>Brassica oleracea</i>	BZ490921		2.00E-42
76	G344	<i>Medicago truncatula</i>	BE124805		3.00E-40
76	G344	<i>Lactuca sativa</i>	BQ865907		2.00E-37
76	G344	<i>Vitis vinifera</i>	BQ800135		5.00E-36
76	G344	<i>Populus tremula x Populus tremuloides</i>	BU836743		4.00E-33
76	G344	<i>Glycine max</i>	BI470689		9.00E-33
76	G344	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU876397		1.00E-30
76	G344	<i>Lycopersicon esculentum</i>	AW030365		1.00E-29
76	G344	<i>Zea mays</i>	CC605963		1.00E-29
76	G344	<i>Helianthus annuus</i>	CD855694		2.00E-29
76	G344	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi32488102		1.00E-38
76	G344	<i>Oryza sativa</i>	gi14165317		6.10E-35
76	G344	<i>Nicotiana tabacum</i>	gi12711287		1.70E-27
76	G344	<i>Nicotiana glauca</i>	gi1076609		4.30E-20
76	G344	<i>Atropa belladonna</i>	gi14329812		0.93
76	G344	<i>Glycine max</i>	gi26522778		0.99
76	G344	<i>Ricinus communis</i>	gi112762		1
78	G351	<i>Brassica oleracea</i>	BH552655		2.00E-51
78	G351	<i>Brassica napus</i>	BQ704580		1.00E-47
78	G351	<i>Lotus japonicus</i>	AP004523		6.00E-43
78	G351	<i>Vitis aestivalis</i>	CB288865		6.00E-42
78	G351	<i>Datisca glomerata</i>	AF119050		1.00E-41
78	G351	<i>Petunia x hybrida</i>	PETZFP4		2.00E-39
78	G351	<i>Vitis vinifera</i>	BM437679		2.00E-38
78	G351	<i>Medicago sativa</i>	MSY18788		4.00E-38
78	G351	<i>Glycine max</i>	GMU68763		3.00E-37
78	G351	<i>Lycopersicon esculentum</i>	BI421491		3.00E-37
78	G351	<i>Petunia x hybrida</i>	gi439493		3.10E-41
78	G351	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi28849865		3.00E-35
78	G351	<i>Datisca glomerata</i>	gi4666360		2.70E-34
78	G351	<i>Brassica rapa</i>	gi2058506		6.70E-32
78	G351	<i>Glycine max</i>	gi1763063		3.70E-30

78	G351	<i>Medicago sativa</i>	gi7228329		3.40E-27
78	G351	<i>Triticum aestivum</i>	gi485814		1.90E-25
78	G351	<i>Oryza sativa</i>	gi12698882		7.70E-25
78	G351	<i>Nicotiana tabacum</i>	gi2981169		9.00E-20
78	G351	<i>Pisum sativum</i>	gi2129892		3.40E-14
79	G355	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER22443_1	747	
79	G355	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER22443_2	748	
79	G355	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER23033_1	749	
79	G355	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER32665_1	750	
79	G355	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER32665_2	751	
79	G355	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER69201_1	752	
79	G355	<i>Oryza sativa</i>	Os_S97951	1569	
79	G355	<i>Glycine max</i>	Gma_S5045942	1636	
79	G355	<i>Medicago truncatula</i>	Mtr_S5425959	1692	
79	G355	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-46187	1956	
79	G355	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-47520	1957	
79	G355	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-6966	1958	
80	G355	<i>Brassica oleracea</i>	BH566556		6.00E-59
80	G355	<i>Medicago truncatula</i>	AC125368		2.00E-36
80	G355	<i>Glycine max</i>	BI967719		4.00E-31
80	G355	<i>Petunia x hybrida</i>	AB006599		6.00E-31
80	G355	<i>Populus tremula x Populus tremuloides</i>	BU862641		5.00E-29
80	G355	<i>Lycopersicon esculentum</i>	BI422808		1.00E-28
80	G355	<i>Vitis vinifera</i>	CA818230		4.00E-28
80	G355	<i>Solanum tuberosum</i>	BQ121106		6.00E-27
80	G355	<i>Lotus japonicus</i>	AP006100		1.00E-24
80	G355	<i>Populus balsamifera</i> subsp. <i>trichocarpa x Populus deltoides</i>	CB239372		2.00E-22
80	G355	<i>Petunia x hybrida</i>	gi2346974		6.50E-33
80	G355	<i>Pisum sativum</i>	gi2129892		1.20E-23
80	G355	<i>Oryza sativa</i> (japonica cultivar-group)	gi29124132		2.70E-20
80	G355	<i>Oryza sativa</i>	gi18652814		4.00E-17
80	G355	<i>Nicotiana tabacum</i>	gi2981169		1.40E-15
80	G355	<i>Medicago sativa</i>	gi7228329		2.00E-15
80	G355	<i>Datisca glomerata</i>	gi4666360		2.90E-14
80	G355	<i>Triticum aestivum</i>	gi485814		8.60E-14
80	G355	<i>Glycine max</i>	gi1763063		2.10E-13
80	G355	<i>Brassica rapa</i>	gi2058504		1.10E-07
82	G366	<i>Brassica oleracea</i>	BZ046051		8.00E-40
82	G366	<i>Oryza sativa</i>	AP005415		2.00E-10

		(japonica cultivar-group)			
82	G366	<i>Oryza sativa</i> (indica cultivar-group)	AAAAA01000097		3.00E-10
82	G366	<i>Hordeum vulgare</i>	BI960158		4.00E-10
82	G366	<i>Lycopersicon esculentum</i>	AW035599		5.00E-10
82	G366	<i>Zea mays</i>	CC701812		5.00E-10
82	G366	<i>Medicago truncatula</i>	BI308410		8.00E-10
82	G366	<i>Vitis vinifera</i>	CB979728		1.00E-09
82	G366	<i>Glycine max</i>	CA784474		1.00E-09
82	G366	<i>Phaseolus coccineus</i>	CA902532		1.00E-09
82	G366	<i>Oryza sativa</i> (japonica cultivar-group)	gi29027767		6.20E-12
82	G366	<i>Sorghum bicolor</i>	gi18390109		5.40E-09
82	G366	<i>Oryza sativa</i>	gi15528588		1.20E-08
82	G366	<i>Petunia x hybrida</i>	gi2346978		2.70E-05
82	G366	<i>Zea ramosa</i>	gi18674684		0.012
82	G366	<i>Triticum aestivum</i>	gi485814		0.09
82	G366	<i>Brassica rapa</i>	gi2058504		0.27
82	G366	<i>Medicago sativa</i>	gi7228329		0.27
82	G366	<i>Glycine max</i>	gi1763063		0.35
82	G366	<i>Pisum sativum</i>	gi2129892		0.44
83	G370	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER166362_1	753	
83	G370	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER180202_1	754	
83	G370	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER726571_1	755	
83	G370	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER74662_1	756	
83	G370	<i>Glycine max</i>	uC-gmflminsoy032f06b1	757	
83	G370	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER173260_2	758	
83	G370	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER200967_1	759	
83	G370	<i>Oryza sativa</i>	OSC100895.C1.p14.fg	760	
83	G370	<i>Oryza sativa</i>	OSC23411.C1.p1.fg	761	
83	G370	<i>Oryza sativa</i>	OSC2409.C1.p2.fg	762	
83	G370	<i>Oryza sativa</i>	OSC25680.C1.p1.fg	763	
83	G370	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER436044_1	764	
83	G370	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER518126_1	765	
83	G370	<i>Oryza sativa</i>	Os_S111189	1570	
83	G370	<i>Glycine max</i>	Gma_S5146649	1637	
83	G370	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-54039	1959	
83	G370	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-54252	1960	
83	G370	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-392715	1961	
84	G370	<i>Brassica oleracea</i>	BZA73777		1.00E-98
84	G370	<i>Vitis vinifera</i>	CD714231		5.00E-32

84	G370	<i>Oryza sativa</i> (japonica cultivar-group)	AK068762		4.00E-31
84	G370	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01009505		6.00E-30
84	G370	<i>Lycopersicon esculentum</i>	BG123251		8.00E-30
84	G370	<i>Oryza sativa</i>	AC105732		4.00E-26
84	G370	<i>Gossypium arboreum</i>	BF272143		3.00E-25
84	G370	<i>Hordeum vulgare</i>	BF616974		8.00E-25
84	G370	<i>Sorghum bicolor</i>	BE357942		1.00E-23
84	G370	<i>Zea mays</i>	BH875187		4.00E-23
84	G370	<i>Sorghum bicolor</i>	gi18390109		6.80E-22
84	G370	<i>Oryza sativa</i>	gi15528588		1.10E-09
84	G370	<i>Oryza sativa</i> (japonica cultivar-group)	gi29027767		1.90E-07
84	G370	<i>Petunia x hybrida</i>	gi14275902		3.10E-05
84	G370	<i>Glycine max</i>	gi5524682		0.0016
84	G370	<i>Solanum tuberosum</i>	gi13161908		0.0016
84	G370	<i>Medicago sativa</i>	gi7228329		0.0072
84	G370	<i>Datisca glomerata</i>	gi4666360		0.018
84	G370	<i>Zea ramosa</i>	gi18674684		0.05
84	G370	<i>Petroselinum crispum</i>	gi9650824		0.15
85	G372	<i>Oryza sativa</i>	OSC5500.C1.p4.fg	766	
85	G372	<i>Oryza sativa</i>	OSC5501.C1.p10.fg	767	
86	G372	<i>Cucurbita pepo</i>	CD726821		1.00E-76
86	G372	<i>Brassica oleracea</i>	BH426533		5.00E-63
86	G372	<i>Medicago truncatula</i>	CB892663		6.00E-49
86	G372	<i>Glycine max</i>	CA800122		4.00E-48
86	G372	<i>Solanum tuberosum</i>	BG596951		4.00E-45
86	G372	<i>Lactuca sativa</i>	BQ853373		1.00E-38
86	G372	<i>Prunus persica</i>	BU040110		8.00E-38
86	G372	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BI120429		3.00E-36
86	G372	<i>Lotus japonicus</i>	AV411356		4.00E-36
86	G372	<i>Helianthus annuus</i>	BU025620		2.00E-35
86	G372	<i>Oryza sativa</i> (japonica cultivar-group)	gi28564640		3.30E-25
86	G372	<i>Oryza sativa</i>	gi15289911		6.80E-21
86	G372	<i>Populus x canescens</i>	gi22795037		6.50E-19
86	G372	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi27357054		0.00023
86	G372	<i>Triticum aestivum</i>	gi32400766		0.00056
86	G372	<i>Cicer arietinum</i>	gi10334499		0.0007
86	G372	<i>Ipomoea nil</i>	gi11127996		0.0015
86	G372	<i>Rosa hybrid cultivar</i>	gi15029364		0.0015
86	G372	<i>Arabis gemmifera</i>	gi22775495		0.0023
86	G372	<i>Pinus pinaster</i>	gi18129286		0.0041
88	G374	<i>Oryza sativa</i>	AK069434		1.0e-999

		(japonica cultivar-group)			
88	G374	<i>Zea mays</i>	AY109632		1.00E-176
88	G374	<i>Brassica napus</i>	CD831794		1.00E-108
88	G374	<i>Lactuca sativa</i>	BQ852311		1.00E-103
88	G374	<i>Helianthus annuus</i>	BQ968130		1.00E-97
88	G374	<i>Medicago truncatula</i>	BG646959		2.00E-90
88	G374	<i>Solanum tuberosum</i>	BI177742		3.00E-90
88	G374	<i>Lycopersicon esculentum</i>	BG128229		9.00E-84
88	G374	<i>Hordeum vulgare</i>	BG344938		2.00E-79
88	G374	<i>Beta vulgaris</i>	BQ592292		5.00E-77
88	G374	<i>Viola cornuta</i>	gi31540598		0.42
88	G374	<i>Oryza sativa</i> (japonica cultivar-group)	gi29371983		0.83
90	G380	<i>Oryza sativa</i> (japonica cultivar-group)	AK071468		1.00E-63
90	G380	<i>Oryza sativa</i>	AX652813		2.00E-62
90	G380	<i>Medicago truncatula</i>	BG581311		2.00E-60
90	G380	<i>Solanum tuberosum</i>	BG592404		7.00E-58
90	G380	<i>Lycopersicon esculentum</i>	AW625867		1.00E-56
90	G380	<i>Lactuca sativa</i>	BQ993132		4.00E-54
90	G380	<i>Gossypium arboreum</i>	BQ411449		8.00E-54
90	G380	<i>Ipomoea nil</i>	BJ578890		2.00E-53
90	G380	<i>Glycine max</i>	BM143561		8.00E-51
90	G380	<i>Brassica napus</i>	CD827948		4.00E-49
90	G380	<i>Oryza sativa</i> (japonica cultivar-group)	gi21740878		5.50E-60
90	G380	<i>Pisum sativum</i>	gi4240031		1.20E-33
90	G380	<i>Glycine max</i>	gi1076498		1.40E-30
90	G380	<i>Oryza sativa</i>	gi8570055		1.10E-25
90	G380	<i>Lotus japonicus</i>	gi1086225		2.30E-25
90	G380	<i>Cicer arietinum</i>	gi10334499		5.00E-16
90	G380	<i>Oryza sativa</i> (indica cultivar-group)	gi29164825		1.40E-10
90	G380	<i>Thellungiella halophila</i>	gi20340241		3.30E-08
90	G380	<i>Triticum aestivum</i>	gi32400766		1.40E-06
90	G380	<i>Zea mays</i>	gi21645888		0.00012
92	G386	<i>Picea abies</i>	AF328842		1.0e-999
92	G386	<i>Oryza sativa</i> (japonica cultivar-group)	AB101648		1.0e-999
92	G386	<i>Oryza sativa</i>	AX658854		1.0e-999
92	G386	<i>Zea mays</i>	ZMA17898		1.0e-999
92	G386	<i>Malus domestica</i>	AF067961		1.0e-999
92	G386	<i>Phalaenopsis</i> sp. SM9108	PSU34743		1.0e-999
92	G386	<i>Oryza sativa</i> (indica	AAAA01007245		1.0e-999

		cultivar-group)			
92	G386	<i>Gossypium hirsutum</i>	AF530913		1.00E-179
92	G386	<i>Helianthus annuus</i>	HNNHAHR		1.00E-145
92	G386	<i>Sorghum bicolor</i>	AF466200		1.00E-142
92	G386	<i>Picea abies</i>	gi19070143		1.20E-253
92	G386	<i>Zea mays</i>	gi5531484		3.60E-240
92	G386	<i>Malus x domestica</i>	gi3925363		2.40E-232
92	G386	<i>Oryza sativa</i> (japonica cultivar-group)	gi32482878		1.00E-218
92	G386	<i>Phalaenopsis</i> sp. SM9108	gi1173622		1.20E-210
92	G386	<i>Phalaenopsis</i> sp.	gi2147484		1.20E-210
92	G386	<i>Oryza sativa</i>	gi19072102		3.70E-197
92	G386	<i>Sorghum bicolor</i>	gi18481701		5.00E-177
92	G386	<i>Gossypium hirsutum</i>	gi22475195		5.20E-159
92	G386	<i>Helianthus annuus</i>	gi1208940		7.30E-121
94	G416	<i>Oryza sativa</i> (japonica cultivar-group)	AK098855		1.00E-83
94	G416	<i>Vitis vinifera</i>	CB341898		2.00E-72
94	G416	<i>Zea mays</i>	ZMHOX2AGN		3.00E-64
94	G416	<i>Hedyotis terminalis</i>	CB076461		5.00E-62
94	G416	<i>Petroselinum crispum</i>	PUMPRHPA		5.00E-55
94	G416	<i>Oryza sativa</i>	CA753304		7.00E-54
94	G416	<i>Hordeum vulgare</i>	BG365916		8.00E-52
94	G416	<i>Sorghum propinquum</i>	BF704605		4.00E-48
94	G416	<i>Glycine max</i>	BM086637		3.00E-47
94	G416	<i>Lotus japonicus</i>	AP004517		2.00E-44
94	G416	<i>Zea mays</i>	gi1170434		1.30E-78
94	G416	<i>Oryza sativa</i> (japonica cultivar-group)	gi22830607		1.40E-66
94	G416	<i>Petroselinum crispum</i>	gi1346791		1.10E-59
94	G416	<i>Nicotiana tabacum</i>	gi8096269		3.70E-08
94	G416	<i>Lycopersicon esculentum</i>	gi9858781		2.70E-05
94	G416	<i>Oryza sativa</i>	gi25172773		4.30E-05
94	G416	<i>Cicer arietinum</i>	gi3129939		5.90E-05
94	G416	<i>Medicago sativa</i>	gi1279563		8.10E-05
94	G416	<i>Cucurbita maxima</i>	gi17221648		9.00E-05
94	G416	<i>Raphanus sativus</i>	gi9049359		0.00024
96	G434	<i>Zea mays</i>	ZMA17898		1.00E-126
96	G434	<i>Oryza sativa</i> (japonica cultivar-group)	AB101648		1.00E-125
96	G434	<i>Oryza sativa</i>	AX658854		1.00E-124
96	G434	<i>Picea abies</i>	AF328842		1.00E-122
96	G434	<i>Phalaenopsis</i> sp. SM9108	PSU34743		1.00E-117
96	G434	<i>Malus domestica</i>	AF067961		1.00E-111

96	G434	<i>Gossypium hirsutum</i>	AF530913		1.00E-103
96	G434	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01007245		1.00E-96
96	G434	<i>Helianthus annuus</i>	HNNHAHR		4.00E-82
96	G434	<i>Gossypium arboreum</i>	BG444723		7.00E-61
96	G434	<i>Oryza sativa</i> (japonica cultivar-group)	gi31339103		1.90E-123
96	G434	<i>Zea mays</i>	gi5531484		1.70E-122
96	G434	<i>Oryza sativa</i>	gi19072102		6.70E-115
96	G434	<i>Phalaenopsis</i> sp. SM9108	gi1173622		1.80E-114
96	G434	<i>Phalaenopsis</i> sp.	gi2147484		1.80E-114
96	G434	<i>Malus x domestica</i>	gi3925363		1.10E-110
96	G434	<i>Picea abies</i>	gi12002853		1.40E-110
96	G434	<i>Gossypium hirsutum</i>	gi22475195		2.90E-101
96	G434	<i>Sorghum bicolor</i>	gi18481701		6.50E-100
96	G434	<i>Helianthus annuus</i>	gi1208940		5.40E-77
97	G438	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER24488 2	768	
97	G438	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER26184 1	769	
97	G438	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER26184 2	770	
97	G438	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER26184 4	771	
97	G438	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER501573 1	772	
97	G438	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER5380 1	773	
97	G438	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER5380 2	774	
97	G438	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER75018 1	775	
97	G438	<i>Glycine max</i>	LIB4164-014-Q1-K1-A6	776	
97	G438	<i>Glycine max</i>	LIB4390-042-R1-K2-D5	777	
97	G438	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER146698 1	778	
97	G438	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER146698 2	779	
97	G438	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER270598 1	780	
97	G438	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER42938 1	781	
97	G438	<i>Oryza sativa</i>	OSC14111.C1.p2.fg	782	
97	G438	<i>Oryza sativa</i>	OSC18647.C1.p19.fg	783	
97	G438	<i>Oryza sativa</i>	OSC19346.C1.p14.fg	784	
97	G438	<i>Oryza sativa</i>	OSC19540.C1.p1.fg	785	
97	G438	<i>Oryza sativa</i>	rsicek_3640.y1.abd	786	
97	G438	<i>Oryza sativa</i>	rsicek_9941.y1.abd	787	
97	G438	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER301 638	788	
97	G438	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER301 668	789	

97	G438	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER47950 1	790	
97	G438	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER495 335	791	
97	G438	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER495 404	792	
97	G438	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER495 514	793	
97	G438	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER745568 1	794	
97	G438	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER83671 1	795	
97	G438	<i>Zea mays</i>	uC-zmflteosinte083g09b1	796	
97	G438	<i>Zea mays</i>	uC-zmrob73075f05b1	797	
97	G438	<i>Oryza sativa</i>	Os_S120953	1571	
97	G438	<i>Oryza sativa</i>	Os_S19524	1572	
97	G438	<i>Oryza sativa</i>	Os_S23391	1573	
97	G438	<i>Oryza sativa</i>	Os_S42908	1574	
97	G438	<i>Glycine max</i>	Gma_S4876016	1638	
97	G438	<i>Glycine max</i>	Gma_S4999094	1639	
97	G438	<i>Glycine max</i>	Gma_S5075763	1640	
97	G438	<i>Medicago truncatula</i>	Mtr_S5308980	1693	
97	G438	<i>Medicago truncatula</i>	Mtr_S5411708	1694	
97	G438	<i>Hordeum vulgare</i>	Hv_S197562	1722	
97	G438	<i>Hordeum vulgare</i>	Hv_S224721	1723	
97	G438	<i>Hordeum vulgare</i>	Hv_S69222	1724	
97	G438	<i>Zea mays</i>	Zm_S11477054	1771	
97	G438	<i>Zea mays</i>	Zm_S11521524	1772	
97	G438	<i>Zea mays</i>	Zm_S11522470	1773	
97	G438	<i>Zea mays</i>	Zm_S11523253	1774	
97	G438	<i>Zea mays</i>	Zm_S11526859	1775	
97	G438	<i>Triticum aestivum</i>	Ta_S130807	1840	
97	G438	<i>Triticum aestivum</i>	Ta_S131992	1841	
97	G438	<i>Triticum aestivum</i>	Ta_S132089	1842	
97	G438	<i>Triticum aestivum</i>	Ta_S25579	1843	
97	G438	<i>Triticum aestivum</i>	Ta_S50749	1844	
97	G438	<i>Triticum aestivum</i>	Ta_S6425	1845	
97	G438	<i>Lycopersicon esculentum</i>	Les_S5289520	1927	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-50207	1962	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-50208	1963	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-50279	1964	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-50602	1965	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-50986	1966	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-52670	1967	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-53069	1968	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-54002	1969	

97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-54245	1970	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-58239	1971	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-58887	1972	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-333165	1973	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-333872	1974	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-340997	1975	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-388971	1976	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-401049	1977	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-451497	1978	
97	G438	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-452871	1979	
98	G438	<i>Zinnia elegans</i>	ZEL312053		1.0e-999
98	G438	<i>Oryza sativa (japonica cultivar- group)</i>	AK102830		1.0e-999
98	G438	<i>Physcomitrella patens</i>	AB032182		1.0e-999
98	G438	<i>Zea mays</i>	AY105765		1.0e-999
98	G438	<i>Oryza sativa</i>	AX699680		1.0e-999
98	G438	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01006159		1.00E-165
98	G438	<i>Medicago truncatula</i>	CB894606		1.00E-128
98	G438	<i>Lactuca sativa</i>	BU002601		1.00E-120
98	G438	<i>Poncirus trifoliata</i>	CD574584		1.00E-113
98	G438	<i>Mesembryanthemu m crystallinum</i>	BE035416		1.00E-106
98	G438	<i>Zinnia elegans</i>	gi18076736		1.0e-999
98	G438	<i>Oryza sativa</i>	gi13384370		1.0e-999
98	G438	<i>Oryza sativa (japonica cultivar- group)</i>	gi31432701		1.0e-999
98	G438	<i>Physcomitrella patens</i>	gi7209912		6.00E-238
98	G438	<i>Ceratopteris richardii</i>	gi3868829		4.20E-35
98	G438	<i>Sorghum bicolor</i>	gi18481701		5.00E-21
98	G438	<i>Phalaenopsis sp. SM9108</i>	gi1173622		1.00E-20
98	G438	<i>Phalaenopsis sp.</i>	gi2147484		1.00E-20
98	G438	<i>Picea abies</i>	gi12002853		1.80E-20
98	G438	<i>Zea mays</i>	gi8920427		4.00E-20
100	G446	<i>Oryza sativa (japonica cultivar- group)</i>	AK103312		1.0e-999
100	G446	<i>Oryza sativa</i>	AX654320		1.00E-168
100	G446	<i>Mangifera indica</i>	AY255705		1.00E-116
100	G446	<i>Medicago truncatula</i>	CB894037		1.00E-114

100	G446	<i>Prunus persica</i>	AF467900		1.00E-102
100	G446	<i>Zea mays</i>	AY105215		9.00E-99
100	G446	<i>Beta vulgaris</i>	BQ594500		6.00E-87
100	G446	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	AI166599		8.00E-84
100	G446	<i>Oryza sativa</i> (indica cultivar-group)	CB631221		8.00E-81
100	G446	<i>Pinus pinaster</i>	BX250119		1.00E-80
100	G446	<i>Prunus persica</i>	gi27450533		2.70E-277
100	G446	<i>Oryza sativa</i>	gi19352037		4.80E-203
100	G446	<i>Oryza sativa</i> (japonica cultivar-group)	gi32489051		5.70E-198
100	G446	<i>Mangifera indica</i>	gi30027167		5.50E-121
100	G446	<i>Oryza sativa</i> (indica cultivar-group)	gi26251300		2.50E-115
100	G446	<i>Mirabilis jalapa</i>	gi23343944		5.10E-20
100	G446	<i>Marchantia polymorpha</i>	gi25272004		7.40E-11
100	G446	<i>Pisum sativum</i>	gi871511		1.90E-06
100	G446	<i>Lycopersicon esculentum</i>	gi1217664		8.30E-06
100	G446	<i>Zea mays</i>	gi18697008		9.10E-06
102	G468	<i>Populus tremula</i> x <i>Populus tremuloides</i>	PTR306827		1.00E-37
102	G468	<i>Glycine max</i>	BU965031		4.00E-33
102	G468	<i>Medicago truncatula</i>	BF649039		9.00E-26
102	G468	<i>Oryza sativa</i> (japonica cultivar-group)	AK103865		4.00E-25
102	G468	<i>Hordeum vulgare</i>	BG301068		2.00E-19
102	G468	<i>Triticum aestivum</i>	BJ228821		5.00E-19
102	G468	<i>Zea mays</i>	BF727992		7.00E-18
102	G468	<i>Helianthus annuus</i>	BU018212		1.00E-17
102	G468	<i>Lycopersicon esculentum</i>	BI209073		3.00E-17
102	G468	<i>Cycas rumphii</i>	CB089859		3.00E-17
102	G468	<i>Populus tremula</i> x <i>Populus tremuloides</i>	gi20269055		4.70E-39
102	G468	<i>Oryza sativa</i>	gi8096369		7.90E-26
102	G468	<i>Triticum aestivum</i>	gi32400272		2.70E-20
102	G468	<i>Oryza sativa</i> (indica cultivar-group)	gi30962267		3.40E-20
102	G468	<i>Vitis vinifera</i>	gi29465672		6.20E-20
102	G468	<i>Glycine max</i>	gi2388689		8.10E-20
102	G468	<i>Cucumis sativus</i>	gi6136832		1.50E-19
102	G468	<i>Pinus taeda</i>	gi32396293		3.80E-19
102	G468	<i>Mirabilis jalapa</i>	gi23343936		1.00E-18
102	G468	<i>Pisum sativum</i>	gi1352057		1.70E-18
104	G478	<i>Brassica napus</i>	CD839423		1.00E-81
104	G478	<i>Antirrhinum majus</i>	AMA011621		5.00E-75
104	G478	<i>Poncirus trifoliata</i>	CD574568		1.00E-66
104	G478	<i>Brassica oleracea</i>	BH693623		2.00E-58
104	G478	<i>Capsicum annuum</i>	CA516164		7.00E-56

104	G478	<i>Glycine max</i>	AI443033		2.00E-48
104	G478	<i>Medicago truncatula</i>	BQ146536		4.00E-46
104	G478	<i>Lycopersicon esculentum</i>	BI933324		3.00E-45
104	G478	<i>Zea mays</i>	ZMA011617		7.00E-44
104	G478	<i>Hedyotis terminalis</i>	CB078220		3.00E-37
104	G478	<i>Antirrhinum majus</i>	gi25458128		7.40E-64
104	G478	<i>Zea mays</i>	gi5931784		2.30E-44
104	G478	<i>Oryza sativa</i> (japonica cultivar-group)	gi32488855		3.80E-37
104	G478	<i>Betula pendula</i>	gi30577628		3.00E-28
104	G478	<i>Oryza sativa</i>	gi8468036		4.00E-24
104	G478	<i>Mitochondrion Beta vulgaris</i> var. <i>altissima</i>	gi9087308		8.10E-13
104	G478	<i>Lycopersicon esculentum</i>	gi7489001		0.00037
104	G478	<i>Solanum tuberosum</i>	gi13161908		0.12
104	G478	<i>Glycine max</i>	gi5524682		0.15
104	G478	<i>Triticum aestivum</i>	gi4101568		0.67
105	G485	<i>Oryza sativa</i>	G3394	2135	2.00E-50
105	G485	<i>Oryza sativa</i>	G3395	2137	3.00E-46
105	G485	<i>Oryza sativa</i>	G3396	2139	2.00E-42
105	G485	<i>Oryza sativa</i>	G3397	2141	1.00E-55
105	G485	<i>Oryza sativa</i>	G3398	2143	3.00E-60
105	G485	<i>Oryza sativa</i>	G3429	2145	3.00E-18
105	G485	<i>Zea mays</i>	G3434	2149	1.00E-49
105	G485	<i>Zea mays</i>	G3435	2151	1.00E-57
105	G485	<i>Zea mays</i>	G3436	2153	9.00E-60
105	G485	<i>Zea mays</i>	G3437	2155	3.00E-53
105	G485	<i>Glycine max</i>	G3470	2171	7.00E-46
105	G485	<i>Glycine max</i>	G3471	2173	1.00E-46
105	G485	<i>Glycine max</i>	G3472	2175	3.00E-57
105	G485	<i>Glycine max</i>	G3473	2177	2.00E-53
105	G485	<i>Glycine max</i>	G3474	2179	5.00E-58
105	G485	<i>Glycine max</i>	G3475	2181	5.00E-56
105	G485	<i>Glycine max</i>	G3476	2183	9.00E-57
105	G485	<i>Glycine max</i>	G3477	2185	7.00E-46
105	G485	<i>Glycine max</i>	G3478	2187	3.00E-56
105	G485	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER24839 1	798	
105	G485	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER31103 1	799	
105	G485	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER33504 1	800	
105	G485	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER33504 3	801	
105	G485	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER33504 4	802	
105	G485	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER33504 5	803	
105	G485	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER33504 6	804	
105	G485	<i>Glycine max</i>	GLYMA-28NOV01-	805	

			CLUSTER4778_1		
105	G485	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER4778_3	806	
105	G485	<i>Oryza sativa</i>	OSC12630.C1.p5.fg	807	
105	G485	<i>Oryza sativa</i>	OSC1404.C1.p3.fg	808	
105	G485	<i>Oryza sativa</i>	OSC30077.C1.p6.fg	809	
105	G485	<i>Oryza sativa</i>	OSC512.C1.p2.fg	810	
105	G485	<i>Oryza sativa</i>	OSC5489.C1.p2.fg	811	
105	G485	<i>Oryza sativa</i>	sicef_0681.z1.abd	812	
105	G485	<i>Zea mays</i>	LIB3732-044-Q6-K6-C4	813	
105	G485	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER719_1	814	
105	G485	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER719_10	815	
105	G485	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER719_2	816	
105	G485	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER719_3	817	
105	G485	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER719_4	818	
105	G485	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER719_5	819	
105	G485	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER90408_1	820	
105	G485	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER90408_2	821	
105	G485	<i>Glycine max</i>	Gma_S4904793	1641	
105	G485	<i>Hordeum vulgare</i>	Hv_S138973	1725	
105	G485	<i>Hordeum vulgare</i>	Hv_S17617	1726	
105	G485	<i>Zea mays</i>	Zm_S11418173	1776	
105	G485	<i>Zea mays</i>	Zm_S11434692	1777	
105	G485	<i>Zea mays</i>	Zm_S11509886	1778	
105	G485	<i>Triticum aestivum</i>	Ta_S198814	1846	
105	G485	<i>Triticum aestivum</i>	Ta_S45374	1847	
105	G485	<i>Triticum aestivum</i>	Ta_S50443	1848	
105	G485	<i>Triticum aestivum</i>	Ta_S93629	1849	
105	G485	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-46859	1980	
105	G485	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-47447	1981	
106	G485	<i>Poncirus trifoliata</i>	CD574709		9.00E-62
106	G485	<i>Solanum tuberosum</i>	BQ505706		4.00E-60
106	G485	<i>Lactuca sativa</i>	BQ996905		2.00E-58
106	G485	<i>Oryza sativa (indica cultivar-group)</i>	AAAAA01003638		3.00E-57
106	G485	<i>Oryza sativa (japonica cultivar- group)</i>	AP005193		3.00E-57
106	G485	<i>Beta vulgaris</i>	BQ592365		9.00E-57
106	G485	<i>Zea mays</i>	CD438068		9.00E-57
106	G485	<i>Physcomitrella patens</i>	AX288144		3.00E-56
106	G485	<i>Populus balsamifera subsp. trichocarpa</i>	BU880488		1.00E-55
106	G485	<i>Glycine max</i>	AX584277		6.00E-55

106	G485	<i>Oryza sativa</i> (japonica cultivar-group)	gi30409461		4.60E-48
106	G485	<i>Zea mays</i>	gi115840		9.50E-48
106	G485	<i>Oryza sativa</i> (indica cultivar-group)	gi30349365		1.10E-39
106	G485	<i>Oryza sativa</i>	gi15408794		1.60E-38
106	G485	<i>Phaseolus coccineus</i>	gi22536010		2.90E-37
106	G485	<i>Gossypium barbadense</i>	gi28274147		6.30E-35
106	G485	<i>Vernonia galamensis</i>	gi16902054		2.70E-34
106	G485	<i>Glycine max</i>	gi16902050		1.20E-33
106	G485	<i>Argemone mexicana</i>	gi16902056		1.10E-32
106	G485	<i>Triticum aestivum</i>	gi16902058		2.90E-30
108	G521	<i>Brassica oleracea</i>	BH662589		2.00E-78
108	G521	<i>Prunus persica</i>	BU044475		3.00E-71
108	G521	<i>Petunia x hybrida</i>	AF509865		2.00E-67
108	G521	<i>Brassica napus</i>	CD828428		3.00E-67
108	G521	<i>Medicago truncatula</i>	AF254124		1.00E-66
108	G521	<i>Hordeum vulgare</i> subsp. <i>spontaneum</i>	BJ481205		3.00E-65
108	G521	<i>Oryza sativa</i> (japonica cultivar-group)	AK068153		5.00E-65
108	G521	<i>Hordeum vulgare</i>	BQ469035		1.00E-63
108	G521	<i>Oryza sativa</i>	AX654724		3.00E-63
108	G521	<i>Sorghum propinquum</i>	BG241938		7.00E-62
108	G521	<i>Petunia x hybrida</i>	gi21105732		7.20E-66
108	G521	<i>Medicago truncatula</i>	gi7716952		6.50E-65
108	G521	<i>Oryza sativa</i> (japonica cultivar-group)	gi27452910		1.70E-48
108	G521	<i>Oryza sativa</i>	gi6730946		4.10E-40
108	G521	<i>Glycine max</i>	gi22597158		1.10E-37
108	G521	<i>Phaseolus vulgaris</i>	gi15148914		4.80E-37
108	G521	<i>Brassica napus</i>	gi31322572		1.00E-36
108	G521	<i>Lycopersicon esculentum</i>	gi6175246		4.30E-36
108	G521	<i>Solanum tuberosum</i>	gi14485513		5.50E-36
108	G521	<i>Triticum sp.</i>	gi4218535		1.90E-33
110	G549	<i>Brassica oleracea</i>	BOBOFHA		1.0E-999
110	G549	<i>Lycopersicon esculentum</i>	AF197934		1.00E-152
110	G549	<i>Petunia x hybrida</i>	AF030171		1.00E-150
110	G549	<i>Antirrhinum majus</i> subsp. <i>majus</i>	AMAFLO		1.00E-146
110	G549	<i>Pisum sativum</i>	AF010190		1.00E-145
110	G549	<i>Eschscholzia californica</i> subsp. <i>californica</i>	AY188789		1.00E-144
110	G549	<i>Cucumis sativus</i>	AF059320		1.00E-143
110	G549	<i>Malus x domestica</i>	AB056159		1.00E-139

110	G549	<i>Salix discolor</i>	AY230817		1.00E-138
110	G549	<i>Acacia mangium</i>	AY229890		1.00E-137
110	G549	<i>Brassica oleracea</i>	gi22755		3.40E-201
110	G549	<i>Brassica oleracea</i> var. <i>botrytis</i>	gi487029		3.40E-201
110	G549	<i>Jonopsidium acaule</i>	gi6003582		1.30E-192
110	G549	<i>Nicotiana tabacum</i>	gi561688		1.30E-144
110	G549	<i>Lycopersicon</i> <i>esculentum</i>	gi7658233		2.80E-144
110	G549	<i>Petunia x hybrida</i>	gi2625050		8.40E-143
110	G549	<i>Antirrhinum majus</i>	gi100482		1.30E-137
110	G549	<i>Antirrhinum majus</i> subsp. <i>majus</i>	gi166430		1.30E-137
110	G549	<i>Eschscholzia</i> <i>californica</i> subsp. <i>californica</i>	gi30313799		1.90E-136
110	G549	<i>Platanus racemosa</i>	gi8574519		2.20E-135
112	G550	<i>Brassica oleracea</i>	BH930799		1.00E-84
112	G550	<i>Medicago</i> <i>truncatula</i>	AC140025		6.00E-82
112	G550	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AP005167		8.00E-74
112	G550	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01004298		1.00E-73
112	G550	<i>Cucurbita maxima</i>	D45066		7.00E-72
112	G550	<i>Oryza sativa</i>	AX659956		2.00E-67
112	G550	<i>Lycopersicon</i> <i>esculentum</i>	BM412713		6.00E-53
112	G550	<i>Lactuca sativa</i>	BQ860203		4.00E-52
112	G550	<i>Poncirus trifoliata</i>	CD575555		1.00E-48
112	G550	<i>Glycine max</i>	BM953958		4.00E-45
112	G550	<i>Oryza sativa</i>	gi7242908		2.80E-66
112	G550	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi19071625		1.00E-57
112	G550	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi21538791		9.10E-43
112	G550	<i>Cucurbita maxima</i>	gi1669341		8.20E-42
112	G550	<i>Dendrobium grex</i> <i>Madame Thong-In</i>	gi3929325		8.30E-33
112	G550	<i>Hordeum vulgare</i>	gi3777436		2.30E-24
112	G550	<i>Zea mays</i>	gi1346559		1.80E-23
112	G550	<i>Nicotiana tabacum</i>	gi1360078		2.40E-23
112	G550	<i>Pisum sativum</i>	gi6092016		2.40E-23
112	G550	<i>Solanum tuberosum</i>	gi7688355		1.40E-22
114	G571	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AK103174		1.00E-116
114	G571	<i>Oryza sativa</i>	AX653996		1.00E-103
114	G571	<i>Phaseolus vulgaris</i>	AF402608		1.00E-100
114	G571	<i>Triticum aestivum</i>	WHTHBP1BC1		1.00E-100
114	G571	<i>Nicotiana tabacum</i>	AF031487		3.00E-98
114	G571	<i>Zea mays</i>	ZMOCSEBFB		2.00E-96
114	G571	<i>Oryza sp.</i>	BD261827		1.00E-94
114	G571	<i>Physcomitrella</i>	AX180962		3.00E-93

		<i>patens</i>			
114	G571	<i>Vicia faba</i>	VFACREBL		7.00E-89
114	G571	<i>Glycine max</i>	BQ611848		7.00E-88
114	G571	<i>Phaseolus vulgaris</i>	gi15148924		1.50E-95
114	G571	<i>Nicotiana tabacum</i>	gi6288682		8.50E-95
114	G571	<i>Zea mays</i>	gi297018		4.80E-92
114	G571	<i>Oryza sativa</i>	gi13872972		7.90E-92
114	G571	<i>Triticum aestivum</i>	gi1076782		1.00E-91
114	G571	<i>Oryza sativa</i> (japonica cultivar-group)	gi33146487		4.30E-91
114	G571	<i>Glycine max</i>	gi7488719		9.10E-75
114	G571	<i>Vicia faba</i>	gi100099		1.90E-74
114	G571	<i>Nicotiana sp.</i>	gi19680		1.10E-71
114	G571	<i>Solanum tuberosum</i>	gi7489280		1.20E-70
116	G581	<i>Gerbera hybrida</i>	GHY7709		3.00E-73
116	G581	<i>Lotus uliginosus</i>	AF503362		1.00E-57
116	G581	<i>Brassica oleracea</i>	BZ019501		3.00E-57
116	G581	<i>Gossypium hirsutum</i>	AF336279		5.00E-54
116	G581	<i>Antirrhinum majus</i>	AMADEL		5.00E-53
116	G581	<i>Oryza sativa</i>	AB021080		7.00E-52
116	G581	<i>Perilla frutescens</i>	AB024050		2.00E-51
116	G581	<i>Petunia x hybrida</i>	AF020545		3.00E-51
116	G581	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU875274		2.00E-49
116	G581	<i>Medicago truncatula</i>	BI308638		6.00E-48
116	G581	<i>Lotus uliginosus</i>	gi20467247		6.80E-92
116	G581	<i>Gossypium hirsutum</i>	gi13346182		2.40E-81
116	G581	<i>Perilla frutescens</i>	gi4519199		6.40E-79
116	G581	<i>Antirrhinum majus</i>	gi166428		8.30E-75
116	G581	<i>Zea mays</i>	gi100897		3.50E-69
116	G581	<i>Oryza sativa</i>	gi1086540		1.20E-63
116	G581	<i>Gerbera hybrida</i>	gi3650292		5.20E-63
116	G581	<i>Lotus japonicus</i>	gi20467249		6.70E-61
116	G581	<i>Oryza sativa</i> (japonica cultivar-group)	gi32488805		8.80E-57
116	G581	<i>Petunia x hybrida</i>	gi3127045		8.00E-51
118	G600	<i>Brassica oleracea</i>	BZ035190		2.00E-41
118	G600	<i>Helianthus annuus</i>	BQ914741		2.00E-25
118	G600	<i>Medicago truncatula</i>	AW688852		3.00E-24
118	G600	<i>Glycine max</i>	AW703971		3.00E-22
118	G600	<i>Populus tremula x Populus tremuloides</i>	BU830207		1.00E-18
118	G600	<i>Vitis vinifera</i>	CB913112		2.00E-17
118	G600	<i>Gossypium arboreum</i>	BQ413633		3.00E-15
118	G600	<i>Lactuca sativa</i>	BQ859538		3.00E-11
118	G600	<i>Hedyotis centranthoides</i>	CB086932		4.00E-11
118	G600	<i>Zea mays</i>	CA830375		2.00E-09

118	G600	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi31432245		1.30E-20
118	G600	<i>Oryza sativa</i>	gi11034640		1.50E-06
118	G600	<i>Lycopersicon</i> <i>esculentum</i>	gi9858781		4.50E-06
118	G600	<i>Medicago sativa</i>	gi3334756		5.50E-06
118	G600	<i>Nicotiana</i> <i>plumbaginifolia</i>	gi3850821		2.50E-05
118	G600	<i>Cucurbita maxima</i>	gi17221648		7.00E-05
118	G600	<i>Zea mays</i>	gi11340599		9.80E-05
118	G600	<i>Chlamydomonas</i> <i>reinhardtii</i>	gi28207761		0.002
118	G600	<i>Nicotiana tabacum</i>	gi8096269		0.0023
118	G600	<i>Pisum sativum</i>	gi7440062		0.027
119	G624	<i>Glycine max</i>	Gma_S4875227	1642	
120	G624	<i>Zea mays</i>	AY103971		1.00E-56
120	G624	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK101356		7.00E-48
120	G624	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	CB620477		8.00E-42
120	G624	<i>Solanum tuberosum</i>	BQ517157		2.00E-41
120	G624	<i>Sorghum bicolor</i>	BE600697		8.00E-41
120	G624	<i>Hordeum vulgare</i>	BG367957		2.00E-39
120	G624	<i>Lactuca sativa</i>	BQ865528		3.00E-34
120	G624	<i>Lycopersicon</i> <i>esculentum</i>	AW737389		6.00E-34
120	G624	<i>Zinnia elegans</i>	AU293844		1.00E-31
120	G624	<i>Glycine max</i>	BF070672		3.00E-25
120	G624	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi23617202		4.50E-95
120	G624	<i>Oryza sativa</i>	gi391885		3.90E-13
120	G624	<i>Daucus carota</i>	gi5578746		4.30E-13
120	G624	<i>Mesembryanthemum</i> <i>crystallinum</i>	gi3219155		7.30E-13
120	G624	<i>Fagopyrum</i> <i>esculentum</i>	gi32469224		1.90E-12
120	G624	<i>Solanum tuberosum</i>	gi27528486		4.20E-12
120	G624	<i>Zea mays</i>	gi100922		5.60E-12
120	G624	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi1730475		6.30E-12
120	G624	<i>Eragrostis tef</i>	gi17906977		6.30E-12
120	G624	<i>Craterostigma</i> <i>plantagineum</i>	gi2288899		7.10E-12
121	G627	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER65192_1	822	
121	G627	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER65192_2	823	
121	G627	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER495_1	824	
121	G627	<i>Oryza sativa</i>	Os_S65371	1575	
121	G627	<i>Medicago</i> <i>truncatula</i>	Mtr_S5455444	1695	
121	G627	<i>Hordeum vulgare</i>	Hv_S12327	1727	
121	G627	<i>Triticum aestivum</i>	Ta_S329524	1850	

121	G627	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-58075	1982	
122	G627	<i>Populus tremuloides</i>	AF377868		3.00E-60
122	G627	<i>Eucalyptus globulus</i> subsp. <i>globulus</i>	AF086642		1.00E-59
122	G627	<i>Petunia x hybrida</i>	AF335239		1.00E-58
122	G627	<i>Pimpinella brachycarpa</i>	AF082531		1.00E-58
122	G627	<i>Populus tremula x Populus tremuloides</i>	BU896825		3.00E-58
122	G627	<i>Cardamine flexuosa</i>	AY257542		2.00E-57
122	G627	<i>Nicotiana tabacum</i>	NT0B		3.00E-57
122	G627	<i>Sinapis alba</i>	SAU25696		4.00E-57
122	G627	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	AY257541		7.00E-57
122	G627	<i>Oryza sativa</i>	AF141965		3.00E-55
122	G627	<i>Populus tremuloides</i>	gi31295609		1.00E-59
122	G627	<i>Eucalyptus globulus</i> subsp. <i>globulus</i>	gi4322475		2.70E-59
122	G627	<i>Pimpinella brachycarpa</i>	gi3493647		8.20E-58
122	G627	<i>Petunia x hybrida</i>	gi13384056		1.00E-57
122	G627	<i>Sinapis alba</i>	gi1049022		2.50E-56
122	G627	<i>Nicotiana tabacum</i>	gi1076646		2.50E-56
122	G627	<i>Cardamine flexuosa</i>	gi30171309		2.50E-56
122	G627	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi30171307		3.20E-56
122	G627	<i>Elaeis guineensis</i>	gi6635740		2.00E-54
122	G627	<i>Oryza sativa</i>	gi5295990		5.30E-54
124	G646	<i>Brassica oleracea</i>	BH437513		3.00E-71
124	G646	<i>Oryza sativa</i>	AB028129		2.00E-53
124	G646	<i>Brassica napus</i>	CD813699		1.00E-52
124	G646	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01002346		2.00E-51
124	G646	<i>Oryza sativa (japonica cultivar- group)</i>	AK060659		1.00E-50
124	G646	<i>Populus tremula</i>	BU821375		8.00E-49
124	G646	<i>Vitis vinifera</i>	CB910264		1.00E-48
124	G646	<i>Nicotiana tabacum</i>	NTA9594		2.00E-46
124	G646	<i>Glycine max</i>	BE611146		1.00E-44
124	G646	<i>Solanum tuberosum</i>	BG592323		9.00E-43
124	G646	<i>Oryza sativa (japonica cultivar- group)</i>	gi32482863		4.90E-51
124	G646	<i>Oryza sativa</i>	gi4996640		4.90E-51
124	G646	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20372847		9.50E-50
124	G646	<i>Nicotiana tabacum</i>	gi1360084		2.70E-42
124	G646	<i>Pisum sativum</i>	gi6092016		2.30E-35
124	G646	<i>Triticum aestivum</i>	gi3790264		4.70E-33
124	G646	<i>Solanum tuberosum</i>	gi7688355		3.20E-32
124	G646	<i>Hordeum vulgare</i>	gi3777436		8.50E-32
124	G646	<i>Zea mays</i>	gi2393775		2.00E-31
124	G646	<i>Cucurbita maxima</i>	gi1669341		2.70E-27
125	G651	<i>Glycine max</i>	GLYMA-28NOV01-	825	

			CLUSTER252329_1		
125	G651	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER28671_1	826	
125	G651	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER28671_2	827	
125	G651	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER38144_1	828	
125	G651	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER12764_1	829	
125	G651	<i>Oryza sativa</i>	OSC100181.C1.p3.fg	830	
125	G651	<i>Oryza sativa</i>	OSC100807.C1.p14.fg	831	
125	G651	<i>Oryza sativa</i>	OSC12064.C1.p26.fg	832	
125	G651	<i>Oryza sativa</i>	OSC4083.C1.p1.fg	833	
125	G651	<i>Zea mays</i>	LIB4171-012-R1-K1-B10	834	
125	G651	<i>Oryza sativa</i>	Os_S113261	1576	
125	G651	<i>Zea mays</i>	Zm_S11367031	1779	
125	G651	<i>Zea mays</i>	Zm_S11431995	1780	
125	G651	<i>Zea mays</i>	Zm_S11525554	1781	
125	G651	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-50411	1983	
125	G651	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-34777	1984	
125	G651	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-7514	1985	
126	G651	<i>Petunia x hybrida</i>	AB035133		4.00E-44
126	G651	<i>Brassica oleracea</i>	BZ474306		3.00E-40
126	G651	<i>Oryza sativa</i> (japonica cultivar-group)	AP005072		5.00E-31
126	G651	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01000406		5.00E-31
126	G651	<i>Lactuca sativa</i>	BU015249		9.00E-31
126	G651	<i>Vitis vinifera</i>	CA808162		3.00E-29
126	G651	<i>Oryza sativa</i>	AC037426		3.00E-29
126	G651	<i>Glycine max</i>	BU548087		1.00E-25
126	G651	<i>Zea mays</i>	BZ372896		1.00E-25
126	G651	<i>Solanum tuberosum</i>	BQ508073		3.00E-25
126	G651	<i>Petunia x hybrida</i>	gi2346986		5.50E-36
126	G651	<i>Oryza sativa</i> (japonica cultivar-group)	gi21740840		1.60E-32
126	G651	<i>Medicago sativa</i>	gi7228329		1.70E-16
126	G651	<i>Glycine max</i>	gi1763063		1.20E-15
126	G651	<i>Datisca glomerata</i>	gi4666360		3.20E-15
126	G651	<i>Oryza sativa</i>	gi15623826		8.80E-13
126	G651	<i>Brassica rapa</i>	gi2058504		1.20E-12
126	G651	<i>Nicotiana tabacum</i>	gi2981169		6.40E-12
126	G651	<i>Triticum aestivum</i>	gi485814		2.30E-11
126	G651	<i>Pisum sativum</i>	gi2129892		3.40E-10
127	G652	<i>Glycine max</i>	BG362937.1	835	
127	G652	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER3357_10	836	
127	G652	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER3357_14	837	
127	G652	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER3357_15	838	

127	G652	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER3357_8	839	
127	G652	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER3357_9	840	
127	G652	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER380953_1	841	
127	G652	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER4027_1	842	
127	G652	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER51249_2	843	
127	G652	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER7171_1	844	
127	G652	<i>Oryza sativa</i>	OSC100158.C1.p6.fg	845	
127	G652	<i>Oryza sativa</i>	OSC101188.C1.p2.fg	846	
127	G652	<i>Oryza sativa</i>	OSC101621.C1.p8.fg	847	
127	G652	<i>Oryza sativa</i>	OSC19412.C1.p4.fg	848	
127	G652	<i>Oryza sativa</i>	OSC20041.C1.p3.fg	849	
127	G652	<i>Oryza sativa</i>	OSC21434.C1.p27.fg	850	
127	G652	<i>Oryza sativa</i>	OSC24160.C1.p7.fg	851	
127	G652	<i>Oryza sativa</i>	OSC24791.C1.p2.fg	852	
127	G652	<i>Oryza sativa</i>	uC-osflcyp173f05b1	853	
127	G652	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER447_18	854	
127	G652	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER447_20	855	
127	G652	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER447_21	856	
127	G652	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER447_23	857	
127	G652	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER55_18	858	
127	G652	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER55_22	859	
127	G652	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER55_44	860	
127	G652	<i>Oryza sativa</i>	Os_S118507	1577	
127	G652	<i>Oryza sativa</i>	Os_S42588	1578	
127	G652	<i>Oryza sativa</i>	Os_S46064	1579	
127	G652	<i>Glycine max</i>	Gma_S4871214	1643	
127	G652	<i>Glycine max</i>	Gma_S4965905	1644	
127	G652	<i>Glycine max</i>	Gma_S5135351	1645	
127	G652	<i>Hordeum vulgare</i>	Hv_S107672	1728	
127	G652	<i>Hordeum vulgare</i>	Hv_S142991	1729	
127	G652	<i>Hordeum vulgare</i>	Hv_S147464	1730	
127	G652	<i>Zea mays</i>	Zm_S11487070	1782	
127	G652	<i>Triticum aestivum</i>	Ta_S109795	1851	
127	G652	<i>Triticum aestivum</i>	Ta_S2509	1852	
127	G652	<i>Triticum aestivum</i>	Ta_S45732	1853	
127	G652	<i>Triticum aestivum</i>	Ta_S60357	1854	
127	G652	<i>Triticum aestivum</i>	Ta_S75244	1855	
127	G652	<i>Lycopersicon esculentum</i>	Les_S5162139	1928	
127	G652	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-56979	1986	
127	G652	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-39394	1987	

128	G652	<i>Brassica oleracea</i>	BH926980	7.00E-90
128	G652	<i>Nicotiana sylvestris</i>	NSGRP2MR	2.00E-71
128	G652	<i>Zea mays</i>	AI812203	1.00E-64
128	G652	<i>Solanum tuberosum</i>	BM408211	5.00E-64
128	G652	<i>Oryza sativa</i>	AP003879	9.00E-64
128	G652	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK101577	9.00E-64
128	G652	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01000576	1.00E-62
128	G652	<i>Triticum aestivum</i>	AB066265	2.00E-62
128	G652	<i>Aegilops speltoides</i>	BQ840577	3.00E-62
128	G652	<i>Pinus pinaster</i>	BX249354	9.00E-61
128	G652	<i>Nicotiana sylvestris</i>	gi121631	1.10E-67
128	G652	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi29467522	6.00E-62
128	G652	<i>Triticum aestivum</i>	gi21322752	2.00E-61
128	G652	<i>Chlamydomonas reinhardtii</i>	gi30527347	2.40E-26
128	G652	<i>Phaseolus vulgaris</i>	gi121628	6.20E-26
128	G652	<i>Nicotiana tabacum</i>	gi395147	8.70E-25
128	G652	<i>Brassica napus</i>	gi17821	1.80E-23
128	G652	<i>Petunia x hybrida</i>	gi121627	2.20E-23
128	G652	<i>Petunia sp.</i>	gi225181	2.20E-23
128	G652	<i>Oryza sativa</i>	gi15528745	2.50E-22
130	G707	<i>Picea abies</i>	AF328842	1.0e-999
130	G707	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AB101648	1.0e-999
130	G707	<i>Oryza sativa</i>	AX658854	1.0e-999
130	G707	<i>Zea mays</i>	ZMA250985	1.0e-999
130	G707	<i>Malus domestica</i>	AF067961	1.0e-999
130	G707	<i>Phalaenopsis sp.</i> SM9108	PSU34743	1.0e-999
130	G707	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01007245	1.0e-999
130	G707	<i>Gossypium hirsutum</i>	AF530913	1.00E-172
130	G707	<i>Sorghum bicolor</i>	AF466200	1.00E-141
130	G707	<i>Helianthus annuus</i>	HNNHAHR	1.00E-138
130	G707	<i>Picea abies</i>	gi19070143	3.20E-237
130	G707	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi31339101	1.00E-231
130	G707	<i>Malus x domestica</i>	gi3925363	4.10E-230
130	G707	<i>Phalaenopsis sp.</i> SM9108	gi1173622	2.40E-200
130	G707	<i>Phalaenopsis sp.</i>	gi2147484	2.40E-200
130	G707	<i>Oryza sativa</i>	gi19072102	2.90E-197
130	G707	<i>Zea mays</i>	gi8920421	1.10E-195
130	G707	<i>Sorghum bicolor</i>	gi18481701	5.90E-190
130	G707	<i>Gossypium hirsutum</i>	gi22475195	4.80E-168
130	G707	<i>Helianthus annuus</i>	gi1208940	3.70E-127
132	G728	<i>Brassica oleracea</i>	BH471284	4.00E-41

132	G728	<i>Oryza sativa</i> (japonica cultivar-group)	AK105625		1.00E-40
132	G728	<i>Lycopersicon</i> <i>esculentum</i>	AW032021		3.00E-30
132	G728	<i>Prunus persica</i>	BU040714		4.00E-28
132	G728	<i>Prunus armeniaca</i>	CB820349		1.00E-27
132	G728	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU886442		2.00E-27
132	G728	<i>Triticum aestivum</i>	BU100819		2.00E-27
132	G728	<i>Populus</i> <i>balsamifera</i> subsp. <i>trichocarpa</i> x <i>Populus deltoides</i>	CB239440		2.00E-26
132	G728	<i>Vitis vinifera</i>	CB979887		2.00E-25
132	G728	<i>Triticum</i> <i>monococcum</i>	BQ803556		6.00E-25
132	G728	<i>Oryza sativa</i> (japonica cultivar-group)	gi33146555		2.40E-41
132	G728	<i>Oryza sativa</i>	gi11034542		5.70E-35
132	G728	<i>Nicotiana tabacum</i>	gi4519671		1.00E-11
132	G728	<i>Chlamydomonas</i> <i>reinhardtii</i>	gi5916207		2.80E-11
132	G728	<i>Zea mays</i>	gi15667625		5.40E-11
132	G728	<i>Mesembryanthemu</i> <i>m crystallinum</i>	gi6942190		1.30E-10
132	G728	<i>Solanum</i> <i>bulbocastanum</i>	gi32470629		1.70E-09
132	G728	<i>Oryza glaberrima</i>	gi31338862		2.70E-08
132	G728	<i>Oryza sativa</i> (indica cultivar-group)	gi31338860		4.50E-08
132	G728	<i>Glycine max</i>	gi23821873		0.064
134	G730	<i>Brassica oleracea</i>	BH976893		2.00E-73
134	G730	<i>Medicago</i> <i>truncatula</i>	CA922031		1.00E-41
134	G730	<i>Vitis vinifera</i>	CB005926		4.00E-36
134	G730	<i>Lactuca sativa</i>	BU004983		5.00E-34
134	G730	<i>Glycine max</i>	BG363182		2.00E-31
134	G730	<i>Triticum aestivum</i>	CA498340		4.00E-30
134	G730	<i>Solanum tuberosum</i>	BQ115344		1.00E-28
134	G730	<i>Brassica napus</i>	CD817870		3.00E-28
134	G730	<i>Populus tremula</i> x <i>Populus tremuloides</i>	AI163121		6.00E-27
134	G730	<i>Oryza sativa</i> (japonica cultivar-group)	AK108408		1.00E-26
134	G730	<i>Oryza sativa</i> (japonica cultivar-group)	gi29467563		6.40E-41
134	G730	<i>Nicotiana tabacum</i>	gi4519671		1.80E-15
134	G730	<i>Mesembryanthemu</i> <i>m crystallinum</i>	gi6942190		5.20E-15
134	G730	<i>Solanum</i> <i>bulbocastanum</i>	gi32470629		8.00E-13
134	G730	<i>Chlamydomonas</i> <i>reinhardtii</i>	gi5916207		1.90E-12

134	G730	<i>Oryza sativa</i>	gi11034542	1.70E-08
134	G730	<i>Oryza glaberrima</i>	gi31338862	6.40E-08
134	G730	<i>Oryza sativa (indica cultivar-group)</i>	gi31338860	4.00E-07
134	G730	<i>Zea mays</i>	gi15667625	1.00E-05
134	G730	<i>Theophrasta americana</i>	gi12004107	0.41
136	G738	<i>Medicago truncatula</i>	BF636532	5.00E-37
136	G738	<i>Brassica oleracea</i>	BH568823	7.00E-36
136	G738	<i>Glycine max</i>	BE555532	1.00E-35
136	G738	<i>Nicotiana tabacum</i>	NTA9594	2.00E-34
136	G738	<i>Lycopersicon esculentum</i>	AI894846	7.00E-33
136	G738	<i>Capsicum annuum</i>	CA847307	8.00E-32
136	G738	<i>Vitis vinifera</i>	CB910264	1.00E-31
136	G738	<i>Solanum tuberosum</i>	BM113542	6.00E-31
136	G738	<i>Zea mays</i>	CC698952	6.00E-31
136	G738	<i>Oryza sativa</i>	OSJN00155	4.00E-30
136	G738	<i>Nicotiana tabacum</i>	gi3341468	3.90E-35
136	G738	<i>Hordeum vulgare subsp. vulgare</i>	gi20372847	6.00E-33
136	G738	<i>Oryza sativa (japonica cultivar-group)</i>	gi32482863	2.50E-31
136	G738	<i>Oryza sativa</i>	gi4996640	2.50E-31
136	G738	<i>Pisum sativum</i>	gi6092016	8.30E-30
136	G738	<i>Solanum tuberosum</i>	gi7688355	2.10E-27
136	G738	<i>Zea mays</i>	gi2393775	2.70E-27
136	G738	<i>Triticum aestivum</i>	gi3790264	7.10E-27
136	G738	<i>Hordeum vulgare</i>	gi3777436	4.10E-24
136	G738	<i>Cucurbita maxima</i>	gi1669341	2.00E-22
138	G744	<i>Oryza sativa (japonica cultivar-group)</i>	AK070302	2.00E-63
138	G744	<i>Lactuca sativa</i>	BQ856329	5.00E-59
138	G744	<i>Vitis vinifera</i>	CA817874	2.00E-57
138	G744	<i>Oryza sativa (indica cultivar-group)</i>	CA767518	5.00E-55
138	G744	<i>Brassica oleracea</i>	BH430310	6.00E-54
138	G744	<i>Triticum aestivum</i>	BJ258750	1.00E-51
138	G744	<i>Zea mays</i>	AW257837	1.00E-50
138	G744	<i>Hordeum vulgare subsp. vulgare</i>	BF628902	2.00E-47
138	G744	<i>Pinus pinaster</i>	BX252059	1.00E-44
138	G744	<i>Brassica napus</i>	AI352966	6.00E-42
138	G744	<i>Oryza sativa</i>	gi18855037	2.40E-35
138	G744	<i>Oryza sativa (japonica cultivar-group)</i>	gi31433346	8.10E-35
138	G744	<i>Zea mays</i>	gi18092342	1.20E-13
138	G744	<i>Nicotiana tabacum</i>	gi12003386	5.40E-13
138	G744	<i>Cucumis melo</i>	gi17016985	1.40E-12
138	G744	<i>Hordeum vulgare subsp. vulgare</i>	gi20152976	8.20E-11
138	G744	<i>Hordeum vulgare</i>	gi2894379	2.00E-09

138	G744	<i>Medicago sativa</i>	gi23451086		5.60E-08
138	G744	<i>Glycine max</i>	gi1076498		1.00E-06
138	G744	<i>Pisum sativum</i>	gi4240031		1.40E-06
140	G752	<i>Brassica oleracea</i>	BZ499460		1.00E-70
140	G752	<i>Medicago truncatula</i>	CA920567		2.00E-58
140	G752	<i>Poncirus trifoliata</i>	CD573735		7.00E-55
140	G752	<i>Zea mays</i>	CD436549		1.00E-54
140	G752	<i>Oryza sativa</i> (japonica cultivar-group)	AK066069		6.00E-54
140	G752	<i>Oryza sativa</i>	AX653661		6.00E-54
140	G752	<i>Lycopersicon esculentum</i>	BI923342		2.00E-52
140	G752	<i>Hordeum vulgare</i> subsp. <i>spontaneum</i>	AV946923		1.00E-49
140	G752	<i>Oryza sativa</i> (indica cultivar-group)	CB627816		2.00E-49
140	G752	<i>Glycine max</i>	AI438025		5.00E-48
140	G752	<i>Oryza sativa</i> (japonica cultivar-group)	gi21740878		4.30E-29
140	G752	<i>Pisum sativum</i>	gi4240031		1.50E-27
140	G752	<i>Glycine max</i>	gi1076498		3.30E-27
140	G752	<i>Lotus japonicus</i>	gi1086225		8.40E-26
140	G752	<i>Oryza sativa</i>	gi8570055		8.70E-23
140	G752	<i>Cicer arietinum</i>	gi10334499		1.10E-13
140	G752	<i>Oryza sativa</i> (indica cultivar-group)	gi29164825		2.60E-07
140	G752	<i>Triticum aestivum</i>	gi32400766		1.00E-05
140	G752	<i>Zea mays</i>	gi18092342		1.60E-05
140	G752	<i>Tulipa gesneriana</i>	gi23386073		0.00011
141	G807	<i>Oryza sativa</i>	G3491	2201	1E-114
141	G807	<i>Glycine max</i>	G3494	2203	1E-116
141	G807	<i>Glycine max</i>	G3495	2205	1E-117
141	G807	<i>Glycine max</i>	G3512	2207	1E-118
141	G807	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER700_1	861	
141	G807	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER700_2	862	
141	G807	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER700_3	863	
141	G807	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER7494_1	864	
141	G807	<i>Oryza sativa</i>	OSC19953.C1.p7.fg	865	
141	G807	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER20750_1	866	
141	G807	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER8272_1	867	
141	G807	<i>Oryza sativa</i>	Os_S33091	1580	
141	G807	<i>Hordeum vulgare</i>	Hv_S99692	1731	
141	G807	<i>Zea mays</i>	Zm_S11426353	1783	
141	G807	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-57622	1988	
141	G807	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-334447	1989	

142	G807	<i>Lycopersicon peruvianum</i>	LPHSF8		1.00E-112
142	G807	<i>Oryza sativa</i> (japonica cultivar-group)	AK106118		1.00E-111
142	G807	<i>Brassica napus</i>	CD814788		6.00E-96
142	G807	<i>Medicago truncatula</i>	AC087771		4.00E-82
142	G807	<i>Solanum tuberosum</i>	BG890899		1.00E-80
142	G807	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01005302		6.00E-80
142	G807	<i>Oryza sativa</i>	AC120506		5.00E-79
142	G807	<i>Lycopersicon esculentum</i>	LEHSF8		4.00E-78
142	G807	<i>Glycine max</i>	AW569256		2.00E-76
142	G807	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU834690		1.00E-73
142	G807	<i>Oryza sativa</i> (japonica cultivar-group)	gi29126355		4.80E-101
142	G807	<i>Lycopersicon peruvianum</i>	gi100264		1.30E-100
142	G807	<i>Lycopersicon esculentum</i>	gi100225		1.60E-100
142	G807	<i>Nicotiana tabacum</i>	gi5821138		2.90E-56
142	G807	<i>Phaseolus acutifolius</i>	gi16118447		1.10E-52
142	G807	<i>Medicago sativa</i>	gi20162459		2.80E-50
142	G807	<i>Glycine max</i>	gi662924		1.90E-49
142	G807	<i>Zea mays</i>	gi2130134		1.40E-48
142	G807	<i>Oryza sativa</i>	gi14209551		1.70E-48
142	G807	<i>Helianthus annuus</i>	gi25052685		1.80E-46
144	G811	<i>Solanum tuberosum</i>	BG889138		8.00E-70
144	G811	<i>Lycopersicon esculentum</i>	AW738534		1.00E-64
144	G811	<i>Lactuca sativa</i>	BQ854304		3.00E-64
144	G811	<i>Glycine max</i>	BE347442		2.00E-52
144	G811	<i>Euphorbia esula</i>	AW874988		2.00E-50
144	G811	<i>Capsicum annuum</i>	CA514873		4.00E-50
144	G811	<i>Vitis vinifera</i>	CB920522		4.00E-48
144	G811	<i>Oryza sativa</i> (japonica cultivar-group)	AK106488		1.00E-47
144	G811	<i>Triticum aestivum</i>	CD909725		7.00E-47
144	G811	<i>Oryza sativa</i>	AX652911		2.00E-46
144	G811	<i>Oryza sativa</i>	gi15624016		1.60E-47
144	G811	<i>Oryza sativa</i> (japonica cultivar-group)	gi20161000		1.60E-47
144	G811	<i>Lycopersicon peruvianum</i>	gi100264		3.60E-39
144	G811	<i>Lycopersicon esculentum</i>	gi100225		4.70E-39
144	G811	<i>Glycine max</i>	gi2129831		5.40E-39
144	G811	<i>Nicotiana tabacum</i>	gi5821138		4.30E-36
144	G811	<i>Medicago sativa</i>	gi20162459		8.80E-36
144	G811	<i>Zea mays</i>	gi2130134		3.90E-35

144	G811	<i>Phaseolus acutifolius</i>	gi16118447		1.70E-32
144	G811	<i>Helianthus annuus</i>	gi25052685		2.80E-32
145	G839	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER16158 1	868	
145	G839	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER66623 1	869	
145	G839	<i>Glycine max</i>	LIB4164-057-R1-N1-A5	870	
145	G839	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER117082 1	871	
145	G839	<i>Oryza sativa</i>	OSC2170.C1.p5.fg	872	
145	G839	<i>Oryza sativa</i>	OSC28351.C1.p1.fg	873	
145	G839	<i>Oryza sativa</i>	rsicek_9913.y1.abd	874	
145	G839	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER1121 63	875	
145	G839	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER7249 1	876	
145	G839	<i>Glycine max</i>	Gma_S4891477	1646	
145	G839	<i>Glycine max</i>	Gma_S6669519	1647	
145	G839	<i>Zea mays</i>	Zm_S11525703	1784	
145	G839	<i>Triticum aestivum</i>	Ta_S276434	1856	
145	G839	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-53309	1990	
145	G839	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-58458	1991	
145	G839	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-453084	1992	
146	G839	<i>Nicotiana tabacum</i>	BD260600		1.00E-176
146	G839	<i>Helianthus annuus</i>	BD260596		1.00E-171
146	G839	<i>Zea mays</i>	AX041006		1.00E-158
146	G839	<i>Triticum aestivum</i>	BD263897		1.00E-154
146	G839	<i>Oryza sativa</i> (japonica cultivar-group)	AK067198		1.00E-149
146	G839	<i>Oryza sativa</i>	AX653720		1.00E-137
146	G839	<i>Beta vulgaris</i>	BD260595		1.00E-110
146	G839	<i>Lycopersicon esculentum</i>	BD260557		1.00E-110
146	G839	<i>Brassica napus</i>	AF527176		7.00E-97
146	G839	<i>Brassica oleracea</i>	BH483537		3.00E-90
146	G839	<i>Zea mays</i>	gi11340603		2.00E-153
146	G839	<i>Triticum aestivum</i>	gi18616497		5.20E-145
146	G839	<i>Oryza sativa</i> (japonica cultivar-group)	gi22535593		2.30E-144
146	G839	<i>Oryza sativa</i>	gi18616493		2.80E-131
146	G839	<i>Nicotiana tabacum</i>	gi21552981		2.00E-111
146	G839	<i>Brassica napus</i>	gi22003730		1.80E-94
146	G839	<i>Chlamydomonas reinhardtii</i>	gi30025990		0.14
146	G839	<i>Nicotiana glauca</i>	gi26418416		0.22
146	G839	<i>Pennisetum ciliare</i>	gi549986		0.64
146	G839	<i>Gossypium herbaceum</i>	gi29837373		0.9
148	G846	<i>Oryza sativa</i> (japonica cultivar-group)	AK100130		1.0e-999

148	G846	<i>Oryza sativa</i>	AX652964		1.0e-999
148	G846	<i>Medicago truncatula</i>	CB893601		1.00E-102
148	G846	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01003006		5.00E-98
148	G846	<i>Triticum aestivum</i>	BQ842184		1.00E-92
148	G846	<i>Helianthus annuus</i>	BU028886		5.00E-89
148	G846	<i>Lactuca sativa</i>	BQ869409		8.00E-87
148	G846	<i>Brassica oleracea</i>	BZ039976		6.00E-83
148	G846	<i>Lycopersicon esculentum</i>	BE433450		1.00E-74
148	G846	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU894371		1.00E-70
148	G846	<i>Oryza sativa</i>	gi15289872		3.50E-215
148	G846	<i>Oryza sativa</i> (japonica cultivar-group)	gi32489674		3.50E-176
148	G846	<i>Zea mays</i>	gi18463957		1.10E-33
148	G846	<i>Triticum monococcum</i>	gi23193487		1.80E-28
148	G846	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi23193479		2.90E-28
148	G846	<i>Hordeum vulgare</i>	gi23193481		3.70E-28
148	G846	<i>Rosa hybrid cultivar</i>	gi15029364		0.0017
148	G846	<i>Populus x canescens</i>	gi22795037		0.013
148	G846	<i>Glycine max</i>	gi25172766		0.018
148	G846	<i>Arabis gemmifera</i>	gi22775495		0.022
150	G852	<i>Oryza sativa</i> (japonica cultivar-group)	AK060833		1.00E-155
150	G852	<i>Brassica oleracea</i>	BZ426102		1.00E-121
150	G852	<i>Oryza sativa</i> (indica cultivar-group)	CB628520		1.00E-115
150	G852	<i>Oryza sativa</i>	AP003747		1.00E-112
150	G852	<i>Medicago truncatula</i>	AC137079		1.00E-107
150	G852	<i>Zea mays</i>	AY109543		1.00E-105
150	G852	<i>Glycine max</i>	BQ629578		4.00E-89
150	G852	<i>Triticum aestivum</i>	BQ744552		2.00E-88
150	G852	<i>Vitis vinifera</i>	CB980495		2.00E-86
150	G852	<i>Solanum tuberosum</i>	BQ510154		5.00E-86
150	G852	<i>Oryza sativa</i> (japonica cultivar-group)	gi20161431		5.00E-149
150	G852	<i>Lilium longiflorum</i>	gi32813435		1.20E-55
150	G852	<i>Oryza sativa</i>	gi14719333		2.20E-54
150	G852	<i>Vitis vinifera</i>	gi20334379		5.20E-53
150	G852	<i>Zea mays</i>	gi10178637		1.10E-52
150	G852	<i>Pisum sativum</i>	gi13365610		7.20E-50
150	G852	<i>Lycopersicon esculentum</i>	gi31322802		1.50E-49
150	G852	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi28143934		5.80E-48
150	G852	<i>Gossypium hirsutum</i>	gi29122893		2.00E-47
150	G852	<i>Carlquistia muiirii</i>	gi20257447		2.50E-47

152	G905	<i>Brassica oleracea</i>	BZ481426		7.00E-97
152	G905	<i>Medicago truncatula</i>	AC136503		2.00E-52
152	G905	<i>Cucumis melo</i>	AF499727		3.00E-48
152	G905	<i>Citrus sinensis</i>	CB290516		9.00E-41
152	G905	<i>Poncirus trifoliata</i>	CD576402		4.00E-39
152	G905	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU878367		2.00E-38
152	G905	<i>Capsicum annuum</i>	BM063816		2.00E-37
152	G905	<i>Gossypium hirsutum</i>	AI730749		5.00E-37
152	G905	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01018235		2.00E-36
152	G905	<i>Oryza sativa</i> (japonica cultivar-group)	AP004164		2.00E-36
152	G905	<i>Cucumis melo</i>	gi28558782		6.50E-49
152	G905	<i>Oryza sativa</i>	gi21740711		4.70E-30
152	G905	<i>Oryza sativa</i> (japonica cultivar-group)	gi24756877		4.30E-29
152	G905	<i>Medicago sativa</i>	gi23451086		6.90E-19
152	G905	<i>Nicotiana tabacum</i>	gi12003386		1.20E-18
152	G905	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152976		5.80E-15
152	G905	<i>Zea mays</i>	gi21645888		1.00E-14
152	G905	<i>Hordeum vulgare</i>	gi2894379		2.00E-12
152	G905	<i>Solanum tuberosum</i>	gi24745601		8.70E-11
152	G905	<i>Thellungiella halophila</i>	gi20340241		1.10E-09
153	G916	<i>Glycine max</i>	BE021411.1	877	
153	G916	<i>Glycine max</i>	BG652320.1	878	
153	G916	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER191657_1	879	
153	G916	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER3354_1	880	
153	G916	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER3354_2	881	
153	G916	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER3354_3	882	
153	G916	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER3354_4	883	
153	G916	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER47179_1	884	
153	G916	<i>Oryza sativa</i>	OSC101573.C1.p8.fg	885	
153	G916	<i>Oryza sativa</i>	OSC1429.C1.p2.fg	886	
153	G916	<i>Oryza sativa</i>	OSC18885.C1.p17.fg	887	
153	G916	<i>Oryza sativa</i>	rsicee_8920.y1.abd	888	
153	G916	<i>Glycine max</i>	Gma_S4878547	1648	
153	G916	<i>Glycine max</i>	Gma_S6668474	1649	
153	G916	<i>Hordeum vulgare</i>	Hv_S119532	1732	
153	G916	<i>Zea mays</i>	Zm_S11388469	1785	
153	G916	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-47034	1993	
153	G916	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-47543	1994	

153	G916	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-52279	1995	
153	G916	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-18500	1996	
153	G916	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-1941	1997	
153	G916	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-20683	1998	
154	G916	<i>Oryza sativa</i>	AX653053		7.00E-97
154	G916	<i>Citrus sinensis</i>	BQ625082		2.00E-81
154	G916	<i>Medicago truncatula</i>	CB893379		3.00E-80
154	G916	<i>Glycine max</i>	BU926713		5.00E-77
154	G916	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01004053		4.00E-76
154	G916	<i>Oryza sativa (japonica cultivar- group)</i>	AC120986		1.00E-75
154	G916	<i>Lycopersicon esculentum</i>	AI895084		5.00E-71
154	G916	<i>Prunus persica</i>	BU047549		1.00E-69
154	G916	<i>Glycine clandestina</i>	BG838724		7.00E-66
154	G916	<i>Brassica oleracea</i>	BH710263		1.00E-58
154	G916	<i>Oryza sativa</i>	gi11320830		1.50E-98
154	G916	<i>Nicotiana tabacum</i>	gi30013667		3.90E-42
154	G916	<i>Oryza sativa (japonica cultivar- group)</i>	gi20160973		1.50E-33
154	G916	<i>Avena fatua</i>	gi1159879		2.80E-30
154	G916	<i>Petroselinum crispum</i>	gi11493822		5.30E-27
154	G916	<i>Pimpinella brachycarpa</i>	gi3420906		2.30E-23
154	G916	<i>Capsella rubella</i>	gi32454266		1.00E-22
154	G916	<i>Lycopersicon esculentum</i>	gi13620227		2.00E-21
154	G916	<i>Ipomoea batatas</i>	gi1076685		4.50E-21
154	G916	<i>Avena sativa</i>	gi4894965		9.60E-21
155	G926	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER3291_14	889	
155	G926	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER3291_6	890	
155	G926	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER2283_3	891	
155	G926	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER56491_1	892	
155	G926	<i>Oryza sativa</i>	uC-osrocyp029g09a1	893	
155	G926	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER15892_1	894	
155	G926	<i>Triticum aestivum</i>	Ta_S91478	1857	
155	G926	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-52928	1999	
155	G926	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-57779	2000	
155	G926	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-15562	2001	
156	G926	<i>Prunus dulcis</i>	BU573158		1.00E-56

156	G926	<i>Medicago truncatula</i>	BI310587		3.00E-55
156	G926	<i>Citrus sinensis</i>	BQ624240		1.00E-47
156	G926	<i>Brassica oleracea</i>	BH443554		4.00E-44
156	G926	<i>Helianthus paradoxus</i>	CF082573		5.00E-40
156	G926	<i>Brassica napus</i>	BNU33885		2.00E-39
156	G926	<i>Lycopersicon esculentum</i>	BF113081		1.00E-37
156	G926	<i>Solanum tuberosum</i>	BG886494		3.00E-36
156	G926	<i>Glycine max</i>	AW472517		4.00E-36
156	G926	<i>Gossypium arboreum</i>	BQ407583		7.00E-36
156	G926	<i>Brassica napus</i>	gi1173616		1.20E-40
156	G926	<i>Oryza sativa</i> (japonica cultivar-group)	gi27552556		2.60E-36
156	G926	<i>Oryza sativa</i>	gi2826786		1.30E-27
156	G926	<i>Vitis riparia</i>	gi7141243		7.10E-27
156	G926	<i>Nicotiana tabacum</i>	gi4731314		5.00E-19
156	G926	<i>Vicia faba</i>	gi2104675		0.0075
156	G926	<i>Hordeum vulgare</i>	gi21667471		0.71
156	G926	<i>Phaseolus vulgaris</i>	gi13775107		0.74
156	G926	<i>Solanum tuberosum</i>	gi1096930		0.76
156	G926	<i>Zea mays</i>	gi1839593		0.84
158	G957	<i>Brassica oleracea</i>	BH998192		1.00E-86
158	G957	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU879250		6.00E-82
158	G957	<i>Oryza sativa</i> (japonica cultivar-group)	AK109860		2.00E-74
158	G957	<i>Hordeum vulgare</i>	BE060921		1.00E-68
158	G957	<i>Medicago truncatula</i>	BF645745		3.00E-68
158	G957	<i>Lycopersicon esculentum</i>	BF098091		3.00E-67
158	G957	<i>Oryza sativa</i>	AB028186		4.00E-66
158	G957	<i>Oryza sativa</i> (indica cultivar-group)	AAAAA01001925		1.00E-63
158	G957	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i> x <i>Populus deltoides</i>	CA826386		2.00E-63
158	G957	<i>Triticum aestivum</i>	BQ483881		1.00E-60
158	G957	<i>Oryza sativa</i>	gi11875152		5.40E-78
158	G957	<i>Oryza sativa</i> (japonica cultivar-group)	gi28190666		5.40E-78
158	G957	<i>Phaseolus vulgaris</i>	gi15148914		8.80E-45
158	G957	<i>Glycine max</i>	gi22597158		7.90E-44
158	G957	<i>Petunia x hybrida</i>	gi1279640		4.40E-43
158	G957	<i>Brassica napus</i>	gi31322568		6.40E-42
158	G957	<i>Lycopersicon esculentum</i>	gi6175246		7.40E-41
158	G957	<i>Solanum tuberosum</i>	gi14485513		3.50E-40
158	G957	<i>Triticum sp.</i>	gi4218537		8.40E-40

158	G957	<i>Triticum monococcum</i>	gi6732160		8.40E-40
159	G961	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER264630 1	895	
159	G961	<i>Glycine max</i>	jC-gmXLIB3563P021ad08d 2	896	
159	G961	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER6410 1	897	
159	G961	<i>Oryza sativa</i>	OSC21400.C1.p3.fg	898	
159	G961	<i>Zea mays</i>	LIB4743-075-R1-K1-G11	899	
159	G961	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER13382 1	900	
159	G961	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER13382 2	901	
159	G961	<i>Glycine max</i>	Gma_S5137324	1650	
159	G961	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-366637	2002	
160	G961	<i>Oryza sativa</i> (japonica cultivar-group)	AK109860		1.00E-88
160	G961	<i>Brassica oleracea</i>	BZ522709		6.00E-84
160	G961	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU879250		3.00E-81
160	G961	<i>Hordeum vulgare</i>	BE060921		3.00E-72
160	G961	<i>Lycopersicon esculentum</i>	BF098091		3.00E-70
160	G961	<i>Glycine max</i>	BU547985		4.00E-69
160	G961	<i>Medicago truncatula</i>	BF645892		3.00E-67
160	G961	<i>Oryza sativa</i>	AP002542		3.00E-66
160	G961	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01001925		3.00E-66
160	G961	<i>Triticum aestivum</i>	CD878476		2.00E-63
160	G961	<i>Oryza sativa</i>	gi11875152		5.00E-83
160	G961	<i>Oryza sativa</i> (japonica cultivar-group)	gi28190666		5.00E-83
160	G961	<i>Glycine max</i>	gi22597158		1.10E-46
160	G961	<i>Phaseolus vulgaris</i>	gi15148914		1.30E-45
160	G961	<i>Petunia x hybrida</i>	gi1279640		2.00E-45
160	G961	<i>Triticum sp.</i>	gi4218537		3.00E-44
160	G961	<i>Triticum monococcum</i>	gi6732160		3.00E-44
160	G961	<i>Brassica napus</i>	gi31322582		7.90E-44
160	G961	<i>Zea mays</i>	gi32527660		7.10E-43
160	G961	<i>Lycopersicon esculentum</i>	gi6175246		2.80E-41
161	G975	<i>Glycine max</i>	AW705973.1	902	
161	G975	<i>Glycine max</i>	BE610471.1	903	
161	G975	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER232634 1	904	
161	G975	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER8245 1	905	
161	G975	<i>Glycine max</i>	GLYMA-28NOV01-	906	

			CLUSTER84865_1		
161	G975	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER256875_1	907	
161	G975	<i>Oryza sativa</i>	OSC33871.C1.p4.fg	908	
161	G975	<i>Oryza sativa</i>	rsicek_16488.y1.abd	909	
161	G975	<i>Zea mays</i>	BG874224.1	910	
161	G975	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER277338_1	911	
161	G975	<i>Hordeum vulgare</i>	Hv_S31912	1733	
161	G975	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-52816	2003	
161	G975	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-14957	2004	
161	G975	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-330976	2005	
161	G975	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-335836	2006	
162	G975	<i>Brassica napus</i>	CD838135		2.00E-91
162	G975	<i>Brassica oleracea</i>	BH477624		2.00E-69
162	G975	<i>Triticum aestivum</i>	CA486875		4.00E-64
162	G975	<i>Oryza sativa</i> (japonica cultivar-group)	AK061163		3.00E-62
162	G975	<i>Oryza sativa</i>	AX699685		2.00E-61
162	G975	<i>Rosa chinensis</i>	BI978981		3.00E-60
162	G975	<i>Amborella trichopoda</i>	CD484088		3.00E-59
162	G975	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BU978490		2.00E-58
162	G975	<i>Vitis aestivalis</i>	CB289393		7.00E-58
162	G975	<i>Lycopersicon esculentum</i>	BG642554		1.00E-56
162	G975	<i>Oryza sativa</i> (japonica cultivar-group)	gi32479658		2.20E-30
162	G975	<i>Lycopersicon esculentum</i>	gi18650662		2.20E-25
162	G975	<i>Lupinus polyphyllus</i>	gi131754		2.60E-22
162	G975	<i>Nicotiana tabacum</i>	gi3065895		1.10E-19
162	G975	<i>Atriplex hortensis</i>	gi8571476		1.10E-19
162	G975	<i>Zea mays</i>	gi21908036		1.00E-18
162	G975	<i>Stylosanthes hamata</i>	gi4099914		1.30E-18
162	G975	<i>Hordeum vulgare</i>	gi27960757		1.70E-18
162	G975	<i>Oryza sativa</i>	gi10567106		2.00E-18
162	G975	<i>Nicotiana glauca</i>	gi8809573		1.20E-17
163	G1011	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER36089_1	912	
163	G1011	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER36089_2	913	
163	G1011	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER36089_3	914	
163	G1011	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER36089_4	915	
163	G1011	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER36089_6	916	
163	G1011	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER475715_2	917	

163	G1011	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER475_3	918	
163	G1011	<i>Oryza sativa</i>	OSC101782.C1.p2.fg	919	
163	G1011	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER48_1	920	
163	G1011	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER48_2	921	
163	G1011	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER48_4	922	
163	G1011	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER48_5	923	
163	G1011	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER8143_1	924	
163	G1011	<i>Oryza sativa</i>	Os_S60918	1581	
163	G1011	<i>Glycine max</i>	Gma_S5094568	1651	
163	G1011	<i>Medicago truncatula</i>	Mtr_S5357829	1696	
163	G1011	<i>Zea mays</i>	Zm_S11418746	1786	
163	G1011	<i>Zea mays</i>	Zm_S11527819	1787	
163	G1011	<i>Triticum aestivum</i>	Ta_S203038	1858	
163	G1011	<i>Triticum aestivum</i>	Ta_S304256	1859	
163	G1011	<i>Triticum aestivum</i>	Ta_S424724	1860	
163	G1011	<i>Lycopersicon esculentum</i>	Les_S5295933	1929	
163	G1011	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-50586	2007	
163	G1011	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-52410	2008	
163	G1011	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-366830	2009	
163	G1011	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-394847	2010	
164	G1011	<i>Petunia x hybrida</i>	AF335240		1.00E-58
164	G1011	<i>Sinapis alba</i>	SAU25696		5.00E-58
164	G1011	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	AY257541		1.00E-57
164	G1011	<i>Lycopersicon esculentum</i>	AI486684		1.00E-57
164	G1011	<i>Cardamine flexuosa</i>	AY257542		2.00E-57
164	G1011	<i>Vitis vinifera</i>	CA808988		3.00E-57
164	G1011	<i>Populus tremuloides</i>	AF377868		9.00E-57
164	G1011	<i>Pimpinella brachycarpa</i>	AF082531		8.00E-56
164	G1011	<i>Eucalyptus grandis</i>	AY263808		2.00E-55
164	G1011	<i>Draba nemorosa</i> var. <i>hebecarpa</i>	AY257543		8.00E-55
164	G1011	<i>Petunia x hybrida</i>	gi13384058		3.90E-58
164	G1011	<i>Sinapis alba</i>	gi1049022		4.50E-57
164	G1011	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi30171307		5.70E-57
164	G1011	<i>Cardamine flexuosa</i>	gi30171309		1.90E-56
164	G1011	<i>Populus tremuloides</i>	gi31295609		1.40E-55
164	G1011	<i>Pimpinella brachycarpa</i>	gi3493647		7.60E-55
164	G1011	<i>Nicotiana tabacum</i>	gi1076646		1.60E-54
164	G1011	<i>Eucalyptus grandis</i>	gi30575600		1.60E-54
164	G1011	<i>Draba nemorosa</i>	gi30171311		1.10E-53

		var. <i>hebecarpa</i>			
164	G1011	<i>Eucalyptus occidentalis</i>	gi30983946		1.10E-53
165	G1013	<i>Oryza sativa</i>	OSC102289.C1.p7.fg	925	
166	G1013	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK110625		6.00E-36
166	G1013	<i>Lotus japonicus</i>	AV419754		5.00E-21
166	G1013	<i>Glycine max</i>	BU082967		3.00E-17
166	G1013	<i>Oryza sativa</i>	BI799118		4.00E-17
166	G1013	<i>Amborella trichopoda</i>	CD483414		6.00E-17
166	G1013	<i>Zea mays</i>	BM269291		1.00E-16
166	G1013	<i>Triticum aestivum</i>	BE445081		1.00E-16
166	G1013	<i>Beta vulgaris</i>	BQ490186		1.00E-16
166	G1013	<i>Prunus persica</i>	BU044499		1.00E-16
166	G1013	<i>Hordeum vulgare</i>	CB868568		1.00E-16
166	G1013	<i>Oryza sativa</i>	gi15289994		2.40E-39
166	G1013	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi20160927		2.40E-39
166	G1013	<i>Nicotiana tabacum</i>	gi14530683		1.30E-18
166	G1013	<i>Solanum tuberosum</i>	gi24745606		1.30E-18
166	G1013	<i>Cucumis sativus</i>	gi7484759		2.90E-17
166	G1013	<i>Capsella rubella</i>	gi13620168		3.00E-17
166	G1013	<i>Ipomoea batatas</i>	gi1076685		7.30E-17
166	G1013	<i>Petroselinum crispum</i>	gi1432058		3.70E-16
166	G1013	<i>Retama raetam</i>	gi18158619		5.30E-16
166	G1013	<i>Lycopersicon esculentum</i>	gi13620227		5.50E-16
168	G1017	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK100322		1.0e-999
168	G1017	<i>Oryza sativa</i>	AB071299		1.0e-999
168	G1017	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01008877		1.00E-170
168	G1017	<i>Lotus japonicus</i>	AP004505		1.00E-139
168	G1017	<i>Physcomitrella patens</i>	AX288142		1.00E-130
168	G1017	<i>Zea mays</i>	CC657791		1.00E-104
168	G1017	<i>Brassica oleracea</i>	BH736206		1.00E-101
168	G1017	<i>Medicago truncatula</i>	BG646821		3.00E-98
168	G1017	<i>Vitis vinifera</i>	CB979491		2.00E-87
168	G1017	<i>Triticum aestivum</i>	BJ258796		5.00E-70
168	G1017	<i>Oryza sativa</i>	gi19352051		1.40E-194
168	G1017	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi13384374		7.90E-179
168	G1017	<i>Mangifera indica</i>	gi30027167		5.50E-73
168	G1017	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	gi26251300		3.10E-72
168	G1017	<i>Prunus persica</i>	gi27450533		5.00E-70
168	G1017	<i>Marchantia polymorpha</i>	gi25272004		2.60E-11

168	G1017	<i>Mirabilis jalapa</i>	gi23343944		0.00011
168	G1017	<i>Zea mays</i>	gi18697008		0.00015
168	G1017	<i>Pisum sativum</i>	gi1352057		0.01
168	G1017	<i>Populus tremula x Populus tremuloides</i>	gi20269063		0.1
170	G1033	<i>Brassica napus</i>	CD822227		6.00E-72
170	G1033	<i>Medicago truncatula</i>	BI264539		8.00E-60
170	G1033	<i>Glycine max</i>	BI967499		3.00E-59
170	G1033	<i>Hedyotis centranthoides</i>	CB087944		7.00E-58
170	G1033	<i>Phaseolus coccineus</i>	CA902244		7.00E-56
170	G1033	<i>Pisum sativum</i>	CD860485		5.00E-54
170	G1033	<i>Helianthus annuus</i>	CD856695		5.00E-54
170	G1033	<i>Capsicum annuum</i>	BM063385		9.00E-53
170	G1033	<i>Vitis vinifera</i>	CA818147		2.00E-52
170	G1033	<i>Lycopersicon esculentum</i>	AI776807		2.00E-52
170	G1033	<i>Ipomoea nil</i>	gi1052956		6.10E-37
170	G1033	<i>Nicotiana tabacum</i>	gi2196548		7.80E-37
170	G1033	<i>Solanum tuberosum</i>	gi2894109		7.00E-36
170	G1033	<i>Pisum sativum</i>	gi436424		1.10E-35
170	G1033	<i>Glycine max</i>	gi123379		3.90E-35
170	G1033	<i>Oryza sativa (indica cultivar-group)</i>	gi23345287		4.50E-34
170	G1033	<i>Oryza sativa</i>	gi3885888		4.50E-34
170	G1033	<i>Zea mays</i>	gi2196672		1.50E-33
170	G1033	<i>Vicia faba</i>	gi541981		2.50E-33
170	G1033	<i>Triticum aestivum</i>	gi100791		3.10E-33
171	G1037	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER33215_1	926	
171	G1037	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER35769_1	927	
171	G1037	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER35769_2	928	
171	G1037	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER78853_1	929	
171	G1037	<i>Oryza sativa</i>	LIB4309-004-Q1-K1-F10	930	
171	G1037	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER7899_1	931	
171	G1037	<i>Oryza sativa</i>	OSC101221.C1.p7.fg	932	
171	G1037	<i>Oryza sativa</i>	OSC101630.C1.p9.fg	933	
171	G1037	<i>Oryza sativa</i>	OSC101746.C1.p5.fg	934	
171	G1037	<i>Oryza sativa</i>	OSC101754.C1.p6.fg	935	
171	G1037	<i>Oryza sativa</i>	OSC15521.C1.p1.fg	936	
171	G1037	<i>Oryza sativa</i>	OSC22451.C1.p8.fg	937	
171	G1037	<i>Oryza sativa</i>	rsicek_16168.y1.abd	938	
171	G1037	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER1091_1	939	
171	G1037	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER586757_1	940	
171	G1037	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER724_633	941	
171	G1037	<i>Glycine max</i>	Gma_S4903453	1652	
171	G1037	<i>Zea mays</i>	Zm_S11418484	1788	

171	G1037	<i>Zea mays</i>	Zm_S11440157	1789	
171	G1037	<i>Triticum aestivum</i>	Ta_S103284	1861	
171	G1037	<i>Triticum aestivum</i>	Ta_S349182	1862	
171	G1037	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-68090	2011	
172	G1037	<i>Oryza sativa</i> (japonica cultivar-group)	AK101165		1.00E-100
172	G1037	<i>Zea mays</i>	AB062095		4.00E-94
172	G1037	<i>Oryza sativa</i> (indica cultivar-group)	CB630542		6.00E-90
172	G1037	<i>Brassica oleracea</i>	BH007675		6.00E-87
172	G1037	<i>Solanum tuberosum</i>	BM407041		6.00E-77
172	G1037	<i>Medicago truncatula</i>	BG450692		7.00E-71
172	G1037	<i>Lactuca sativa</i>	BQ858556		4.00E-62
172	G1037	<i>Stevia rebaudiana</i>	BG523436		1.00E-60
172	G1037	<i>Vitis vinifera</i>	CD800109		2.00E-58
172	G1037	<i>Oryza sativa</i>	AP004552		1.00E-56
172	G1037	<i>Zea mays</i>	gi14189890		1.80E-92
172	G1037	<i>Oryza sativa</i> (japonica cultivar-group)	gi24308616		3.80E-76
172	G1037	<i>Oryza glaberrima</i>	gi31338862		5.40E-45
172	G1037	<i>Oryza sativa</i> (indica cultivar-group)	gi31338860		1.80E-44
172	G1037	<i>Oryza sativa</i>	gi15289981		1.30E-20
172	G1037	<i>Dianthus caryophyllus</i>	gi13173408		1.00E-10
172	G1037	<i>Nicotiana tabacum</i>	gi4519671		6.80E-09
172	G1037	<i>Mesembryanthemum crystallinum</i>	gi6942190		2.20E-07
172	G1037	<i>Chlamydomonas reinhardtii</i>	gi5916207		3.30E-07
172	G1037	<i>Solanum bulbocastanum</i>	gi32470629		2.60E-06
174	G1082	<i>Oryza sativa</i> (japonica cultivar-group)	AK100643		1.00E-144
174	G1082	<i>Brassica oleracea</i>	BH666792		1.00E-90
174	G1082	<i>Solanum tuberosum</i>	BI179090		7.00E-77
174	G1082	<i>Glycine max</i>	CA785487		3.00E-75
174	G1082	<i>Helianthus annuus</i>	BU026443		4.00E-67
174	G1082	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU883184		2.00E-63
174	G1082	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	CA030236		3.00E-60
174	G1082	<i>Triticum aestivum</i>	BJ288629		2.00E-55
174	G1082	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01001043		5.00E-54
174	G1082	<i>Lactuca sativa</i>	BQ860209		6.00E-54
174	G1082	<i>Oryza sativa</i> (japonica cultivar-group)	gi32483081		4.10E-79
174	G1082	<i>Gossypium hirsutum</i>	gi22858664		2.10E-46

174	G1082	<i>Oryza sativa</i>	gi13124871		1.10E-43
174	G1082	<i>Marsilea quadrifolia</i>	gi22550110		1.10E-15
174	G1082	<i>Catharanthus roseus</i>	gi1486263		2.70E-07
174	G1082	<i>Lupinus angustifolius</i>	gi28912428		2.50E-05
174	G1082	<i>Glycine max</i>	gi347455		3.10E-05
174	G1082	<i>Vigna unguiculata</i>	gi1076556		3.80E-05
174	G1082	<i>Lycopersicon esculentum</i>	gi100210		6.10E-05
174	G1082	<i>Nicotiana tabacum</i>	gi296617		7.70E-05
176	G1100	<i>Brassica oleracea</i>	BZ515453		8.00E-61
176	G1100	<i>Medicago truncatula</i>	CB892846		1.00E-41
176	G1100	<i>Cucumis melo</i>	AF499727		2.00E-41
176	G1100	<i>Solanum tuberosum</i>	BG590574		3.00E-31
176	G1100	<i>Citrus sinensis</i>	CB290516		1.00E-30
176	G1100	<i>Zea mays</i>	CC605834		3.00E-30
176	G1100	<i>Poncirus trifoliata</i>	CD576402		3.00E-30
176	G1100	<i>Gossypium hirsutum</i>	AI730749		2.00E-29
176	G1100	<i>Oryza sativa</i> (japonica cultivar-group)	AP005399		1.00E-28
176	G1100	<i>Glycine max</i>	BQ094213		1.00E-28
176	G1100	<i>Cucumis melo</i>	gi28558782		6.50E-45
176	G1100	<i>Oryza sativa</i> (japonica cultivar-group)	gi24756877		2.10E-27
176	G1100	<i>Oryza sativa</i>	gi21740711		3.80E-25
176	G1100	<i>Medicago sativa</i>	gi23451086		7.00E-20
176	G1100	<i>Nicotiana tabacum</i>	gi12003386		3.50E-15
176	G1100	<i>Zea mays</i>	gi21645888		1.80E-12
176	G1100	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152976		2.70E-12
176	G1100	<i>Hordeum vulgare</i>	gi2894379		4.90E-12
176	G1100	<i>Solanum tuberosum</i>	gi24745601		4.80E-10
176	G1100	<i>Cicer arietinum</i>	gi4651204		2.90E-08
178	G1108	<i>Oryza sativa</i> (japonica cultivar-group)	AK066424		1.00E-113
178	G1108	<i>Zea mays</i>	BG837939		1.00E-91
178	G1108	<i>Brassica oleracea</i>	BZ486328		1.00E-89
178	G1108	<i>Lactuca sativa</i>	BQ852089		3.00E-80
178	G1108	<i>Triticum aestivum</i>	BJ319065		2.00E-78
178	G1108	<i>Oryza sativa</i> (indica cultivar-group)	CB634885		5.00E-78
178	G1108	<i>Lycopersicon esculentum</i>	BI921710		1.00E-75
178	G1108	<i>Oryza sativa</i>	AX699700		1.00E-73
178	G1108	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	AL505242		8.00E-71
178	G1108	<i>Solanum tuberosum</i>	BQ512426		6.00E-69
178	G1108	<i>Oryza sativa</i> (japonica cultivar-	gi15289774		6.00E-78

		group)			
178	G1108	<i>Phacelia tanacetifolia</i>	gi5002214		1.40E-28
178	G1108	<i>Medicago sativa</i>	gi23451086		5.10E-12
178	G1108	<i>Oryza sativa</i>	gi14164470		1.10E-11
178	G1108	<i>Cicer arietinum</i>	gi4651204		2.60E-10
178	G1108	<i>Nicotiana tabacum</i>	gi12003386		1.40E-09
178	G1108	<i>Thellungiella halophila</i>	gi20340241		1.50E-09
178	G1108	<i>Hordeum vulgare</i>	gi2894379		2.80E-09
178	G1108	<i>Cucumis melo</i>	gi17016985		2.30E-08
178	G1108	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152976		3.10E-08
180	G1113	<i>Brassica napus</i>	AI352907		7.00E-49
180	G1113	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BG543052		1.00E-26
180	G1113	<i>Ipomoea nil</i>	BJ574282		2.00E-25
180	G1113	<i>Populus tremula</i>	BU893088		3.00E-25
180	G1113	<i>Lactuca sativa</i>	BQ849490		3.00E-25
180	G1113	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU885427		4.00E-25
180	G1113	<i>Gossypium hirsutum</i>	AI729600		8.00E-24
180	G1113	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i> x <i>Populus deltoides</i>	CA825344		8.00E-24
180	G1113	<i>Lycopersicon esculentum</i>	AW034559		1.00E-23
180	G1113	<i>Capsicum annuum</i>	CA847343		3.00E-23
180	G1113	<i>Oryza sativa</i> (japonica cultivar-group)	gi32488512		6.10E-19
180	G1113	<i>Oryza sativa</i>	gi14164467		2.40E-12
180	G1113	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152976		4.90E-12
180	G1113	<i>Thellungiella halophila</i>	gi20340241		1.30E-11
180	G1113	<i>Medicago sativa</i>	gi23451086		2.60E-11
180	G1113	<i>Cucumis melo</i>	gi28558782		1.80E-10
180	G1113	<i>Glycine max</i>	gi22597166		6.50E-10
180	G1113	<i>Nicotiana tabacum</i>	gi12003386		2.90E-09
180	G1113	<i>Zea mays</i>	gi18092342		1.30E-08
180	G1113	<i>Pisum sativum</i>	gi4240031		2.40E-08
181	G1128	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER83680_3	942	
181	G1128	<i>Oryza sativa</i>	OSC795.C1.p2.fg	943	
181	G1128	<i>Glycine max</i>	Gma_S4918384	1653	
181	G1128	<i>Triticum aestivum</i>	Ta_S190134	1863	
182	G1128	<i>Brassica oleracea</i>	BH586480		1.00E-82
182	G1128	<i>Glycine max</i>	BU926769		7.00E-60
182	G1128	<i>Oryza sativa</i> (japonica cultivar-group)	AK068379		3.00E-58
182	G1128	<i>Gossypium arboreum</i>	BG441060		5.00E-53

182	G1128	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU814921		1.00E-50
182	G1128	<i>Solanum tuberosum</i>	BQ508721		4.00E-48
182	G1128	<i>Hordeum vulgare</i>	BQ765321		3.00E-47
182	G1128	<i>Populus</i> <i>balsamifera</i> subsp. <i>trichocarpa</i>	BI139442		6.00E-47
182	G1128	<i>Medicago</i> <i>truncatula</i>	BG589060		1.00E-46
182	G1128	<i>Zinnia elegans</i>	AU289368		4.00E-45
182	G1128	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi12643044		5.20E-51
182	G1128	<i>Pisum sativum</i>	gi2213534		2.50E-45
182	G1128	<i>Antirrhinum majus</i>	gi4165183		3.40E-38
182	G1128	<i>Vitis vinifera</i>	gi30421132		0.0005
182	G1128	<i>Zea mays</i>	gi9837562		0.0019
182	G1128	<i>Oryza sativa</i>	gi21740825		0.0026
182	G1128	<i>Spinacia oleracea</i>	gi6492266		0.0033
182	G1128	<i>Nicotiana tabacum</i>	gi6492262		0.068
182	G1128	<i>Volvox carteri</i> f. <i>nagariensis</i>	gi4324621		0.078
182	G1128	<i>Lycopersicon</i> <i>esculentum</i>	gi15144504		0.11
184	G1136	<i>Phaseolus vulgaris</i>	PVU18348		1.00E-156
184	G1136	<i>Gossypium</i> <i>raimondii</i>	CA994239		1.00E-138
184	G1136	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AE017122		1.00E-100
184	G1136	<i>Oryza sativa</i>	AC060755		1.00E-100
184	G1136	<i>Brassica oleracea</i>	BZ466433		7.00E-86
184	G1136	<i>Zea mays</i>	AF061107		1.00E-80
184	G1136	<i>Lycopersicon</i> <i>esculentum</i>	AF011557		2.00E-73
184	G1136	<i>Solanum tuberosum</i>	BI434651		2.00E-72
184	G1136	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01004195		6.00E-69
184	G1136	<i>Medicago</i> <i>truncatula</i>	CB893334		1.00E-68
184	G1136	<i>Phaseolus vulgaris</i>	gi1142619		2.00E-155
184	G1136	<i>Oryza sativa</i>	gi12643064		6.80E-128
184	G1136	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi31433653		6.80E-128
184	G1136	<i>Zea mays</i>	gi4321762		2.30E-127
184	G1136	<i>Lycopersicon</i> <i>esculentum</i>	gi6175252		6.40E-58
184	G1136	<i>Petunia</i> x <i>hybrida</i>	gi10998404		7.40E-36
184	G1136	<i>Perilla frutescens</i>	gi28375728		2.90E-34
184	G1136	<i>Antirrhinum majus</i>	gi166428		6.30E-26
184	G1136	<i>Gossypium</i> <i>hirsutum</i>	gi13346182		4.60E-25
184	G1136	<i>Gerbera hybrida</i>	gi3650292		6.00E-19
185	G1142	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER228631_1	944	
185	G1142	<i>Glycine max</i>	GLYMA-28NOV01-	945	

			CLUSTER228631_2		
185	G1142	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER251531_1	946	
185	G1142	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER137582_1	947	
185	G1142	<i>Zea mays</i>	Zm_S11428899	1790	
185	G1142	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-12268	2012	
186	G1142	<i>Brassica oleracea</i>	BZ072414		6.00E-71
186	G1142	<i>Brassica napus</i>	CD829735		4.00E-67
186	G1142	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU813371		3.00E-63
186	G1142	<i>Glycine max</i>	BQ094663		2.00E-62
186	G1142	<i>Medicago truncatula</i>	BF647687		2.00E-60
186	G1142	<i>Populus tremula</i>	BU891490		4.00E-55
186	G1142	<i>Lycopersicon esculentum</i>	AW622727		4.00E-43
186	G1142	<i>Oryza sativa</i> (japonica cultivar-group)	AK106649		1.00E-38
186	G1142	<i>Populus tremuloides</i>	CA931085		2.00E-33
186	G1142	<i>Oryza sativa</i> subsp. japonica	AU093196		2.00E-30
186	G1142	<i>Oryza sativa</i> (japonica cultivar-group)	gi32129332		1.40E-39
186	G1142	<i>Oryza sativa</i>	gi8570062		2.70E-27
186	G1142	<i>Pennisetum glaucum</i>	gi527657		5.20E-07
186	G1142	<i>Phyllostachys acuta</i>	gi527661		1.40E-06
186	G1142	<i>Lycopersicon esculentum</i>	gi6175252		2.10E-06
186	G1142	<i>Sorghum bicolor</i>	gi527665		2.00E-05
186	G1142	<i>Oryza australiensis</i>	gi1086526		2.40E-05
186	G1142	<i>Oryza eichingeri</i>	gi1086528		4.00E-05
186	G1142	<i>Gossypium hirsutum</i>	gi13346180		6.60E-05
186	G1142	<i>Oryza rufipogon</i>	gi1086536		6.70E-05
188	G1150	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01007141		1.00E-174
188	G1150	<i>Oryza sativa</i> (japonica cultivar-group)	AC135597		1.00E-174
188	G1150	<i>Zea mays</i>	AY109385		1.00E-157
188	G1150	<i>Brassica oleracea</i>	BH475694		1.00E-112
188	G1150	<i>Triticum aestivum</i>	BT008960		1.00E-103
188	G1150	<i>Medicago truncatula</i>	BI309506		4.00E-99
188	G1150	<i>Oryza sativa</i>	BI118817		2.00E-81
188	G1150	<i>Glycine max</i>	BU761598		2.00E-80
188	G1150	<i>Lycopersicon esculentum</i>	BG125123		6.00E-69
188	G1150	<i>Solanum tuberosum</i>	BG351593		9.00E-68
188	G1150	<i>Oryza sativa</i> (japonica cultivar-group)	gi31712081		5.60E-170

188	G1150	<i>Oryza sativa</i>	gi6539559		2.20E-97
188	G1150	<i>Zea mays</i>	gi18542175		8.40E-36
188	G1150	<i>Pisum sativum</i>	gi15021750		1.90E-05
188	G1150	<i>Vicia faba</i>	gi425682		6.60E-05
188	G1150	<i>Phaseolus vulgaris</i>	gi169349		0.0015
188	G1150	<i>Adiantum capillus-veneris</i>	gi4033606		0.0019
188	G1150	<i>Medicago truncatula</i>	gi2598593		0.007
188	G1150	<i>Lycopersicon esculentum</i>	gi170454		0.0072
188	G1150	<i>Solanum tuberosum</i>	gi688080		0.011
189	G1206	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER11328_1	948	
189	G1206	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER11328_2	949	
189	G1206	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER11328_4	950	
189	G1206	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER240450_1	951	
189	G1206	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER48180_5	952	
189	G1206	<i>Oryza sativa</i>	15855173	953	
189	G1206	<i>Oryza sativa</i>	AU172577.1	954	
189	G1206	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER100143_1	955	
189	G1206	<i>Oryza sativa</i>	OSC101221.C1.p21.fg	956	
189	G1206	<i>Oryza sativa</i>	OSC17045.C1.p1.fg	957	
189	G1206	<i>Oryza sativa</i>	OSC24705.C1.p12.fg	958	
189	G1206	<i>Oryza sativa</i>	OSC773.C1.p2.fg	959	
189	G1206	<i>Oryza sativa</i>	rsicem_13769.y1.abd	960	
189	G1206	<i>Zea mays</i>	LIB3912-033-Q6-K6-A12	961	
189	G1206	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER231432_1	962	
189	G1206	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER30971_1	963	
189	G1206	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER30971_3	964	
189	G1206	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER73342_1	965	
189	G1206	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER73342_2	966	
189	G1206	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER998548_1	967	
189	G1206	<i>Glycine max</i>	Gma_S4861534	1654	
189	G1206	<i>Glycine max</i>	Gma_S4881720	1655	
189	G1206	<i>Glycine max</i>	Gma_S5117867	1656	
189	G1206	<i>Medicago truncatula</i>	Mtr_S5329905	1697	
189	G1206	<i>Medicago truncatula</i>	Mtr_S5408746	1698	
189	G1206	<i>Zea mays</i>	Zm_S11526858	1791	
189	G1206	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-48203	2013	
189	G1206	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-385084	2014	

189	G1206	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-463300	2015	
189	G1206	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-471325	2016	
190	G1206	<i>Oryza sativa</i> (japonica cultivar- group)	AK059445		1.00E-133
190	G1206	<i>Vicia sativa</i>	VSENBPIGN		1.00E-123
190	G1206	<i>Pisum sativum</i>	PSPD3BIPR		1.00E-122
190	G1206	<i>Brassica napus</i>	CD815167		1.00E-109
190	G1206	<i>Brassica oleracea</i>	BH582293		1.00E-107
190	G1206	<i>Mesembryanthemu m crystallinum</i>	CA838861		2.00E-84
190	G1206	<i>Solanum tuberosum</i>	BQ507789		1.00E-74
190	G1206	<i>Zea mays</i>	AY106688		5.00E-74
190	G1206	<i>Zinnia elegans</i>	AU290850		5.00E-71
190	G1206	<i>Medicago truncatula</i>	AW775140		5.00E-70
190	G1206	<i>Vicia sativa</i>	gi1360637		1.20E-172
190	G1206	<i>Medicago truncatula</i>	gi11358945		2.40E-169
190	G1206	<i>Pisum sativum</i>	gi2213540		1.50E-166
190	G1206	<i>Oryza sativa</i> (japonica cultivar- group)	gi21104742		0.083
190	G1206	<i>Medicago sativa</i>	gi1279563		0.088
190	G1206	<i>Nicotiana tabacum</i>	gi8096269		0.29
190	G1206	<i>Ananas comosus</i>	gi31323668		0.38
190	G1206	<i>Gossypium hirsutum</i>	gi11291753		0.83
190	G1206	<i>Populus tremuloides</i>	gi9651406		0.83
190	G1206	<i>Cicer arietinum</i>	gi3860319		0.94
192	G1247	<i>Brassica oleracea</i>	BZ440977		3.00E-31
192	G1247	<i>Petunia x hybrida</i>	PHMYBPH33		5.00E-28
192	G1247	<i>Lactuca sativa</i>	BQ996568		6.00E-28
192	G1247	<i>Oryza sativa</i> (japonica cultivar- group)	AK063951		1.00E-27
192	G1247	<i>Oryza sativa</i>	OSGAMYB		1.00E-27
192	G1247	<i>Vitis vinifera</i>	CB004589		1.00E-27
192	G1247	<i>Lolium temulentum</i>	AF114162		2.00E-27
192	G1247	<i>Hordeum vulgare</i>	HVRNAGAM1		2.00E-27
192	G1247	<i>Triticum aestivum</i>	AB044084		2.00E-27
192	G1247	<i>Hordeum vulgare</i> subsp. vulgare	CA013607		2.00E-27
192	G1247	<i>Triticum aestivum</i>	gi8247759		9.60E-31
192	G1247	<i>Oryza sativa</i> (japonica cultivar- group)	gi32489825		4.40E-29
192	G1247	<i>Zea mays</i>	gi19072736		2.90E-28
192	G1247	<i>Oryza sativa</i>	gi1707640		1.80E-27
192	G1247	<i>Sorghum bicolor</i>	gi19073322		4.00E-27
192	G1247	<i>Hordeum vulgare</i>	gi1200239		5.50E-27
192	G1247	<i>Petunia x hybrida</i>	gi20565		8.30E-27
192	G1247	<i>Lolium temulentum</i>	gi4877649		1.30E-26
192	G1247	<i>Lycopersicon</i>	gi1430846		2.20E-26

		<i>esculentum</i>			
192	G1247	<i>Nicotiana tabacum</i>	gi11066263		3.70E-26
193	G1274	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER16030 1	968	
193	G1274	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER305171 1	969	
193	G1274	<i>Oryza sativa</i>	OSC100386.C1.p11.fg	970	
193	G1274	<i>Oryza sativa</i>	OSC100526.C1.p1.fg	971	
193	G1274	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER139642 1	972	
193	G1274	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER139642 2	973	
193	G1274	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER2967 14	974	
193	G1274	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER452657 1	975	
193	G1274	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-51404	2017	
193	G1274	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-57064	2018	
194	G1274	<i>Glycine max</i>	BQ742659		1.00E-33
194	G1274	<i>Solanum tuberosum</i>	BQ516647		2.00E-32
194	G1274	<i>Lycopersicon esculentum</i>	BI209002		2.00E-32
194	G1274	<i>Hordeum vulgare</i>	BE216050		4.00E-31
194	G1274	<i>Capsicum annuum</i>	CA524920		2.00E-30
194	G1274	<i>Stevia rebaudiana</i>	BG525040		3.00E-30
194	G1274	<i>Sorghum bicolor</i>	CD233113		3.00E-29
194	G1274	<i>Zea mays</i>	BM334368		2.00E-28
194	G1274	<i>Hordeum vulgare</i> subsp. <i>spontaneum</i>	BJ478103		3.00E-28
194	G1274	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BJ456908		3.00E-28
194	G1274	<i>Oryza sativa</i>	gi9558431		1.10E-28
194	G1274	<i>Oryza sativa</i> (japonica cultivar-group)	gi21104763		4.90E-28
194	G1274	<i>Nicotiana tabacum</i>	gi29536791		6.00E-23
194	G1274	<i>Capsella rubella</i>	gi32454266		1.70E-22
194	G1274	<i>Solanum tuberosum</i>	gi24745606		8.70E-22
194	G1274	<i>Oryza sativa</i> (indica cultivar-group)	gi23305051		1.40E-21
194	G1274	<i>Pimpinella brachycarpa</i>	gi3420906		1.70E-21
194	G1274	<i>Lycopersicon esculentum</i>	gi13620227		3.90E-21
194	G1274	<i>Cucumis sativus</i>	gi7484759		5.70E-21
194	G1274	<i>Ipomoea batatas</i>	gi1076685		7.00E-21
195	G1276	<i>Medicago truncatula</i>	Mtr_S7094215	1699	
195	G1276	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-449521	2019	
196	G1276	<i>Hyacinthus orientalis</i>	AF134116		5.00E-68
196	G1276	<i>Pisum sativum</i>	AF325506		2.00E-63
196	G1276	<i>Brassica oleracea</i>	BH541466		4.00E-62
196	G1276	<i>Antirrhinum majus</i>	AY223518		9.00E-62

196	G1276	<i>Petunia x hybrida</i>	AF132002		9.00E-62
196	G1276	<i>Zea mays</i>	AF048900		5.00E-61
196	G1276	<i>Malus x domestica</i>	AF332215		2.00E-60
196	G1276	<i>Hordeum vulgare</i>	AY069953		9.00E-60
196	G1276	<i>Glycine max</i>	CA783794		3.00E-59
196	G1276	<i>Lycopersicon esculentum</i>	BI933811		3.00E-59
196	G1276	<i>Hyacinthus orientalis</i>	gi5360996		1.00E-66
196	G1276	<i>Pisum sativum</i>	gi13173164		6.60E-65
196	G1276	<i>Antirrhinum majus</i>	gi28894443		2.20E-62
196	G1276	<i>Zea mays</i>	gi2944040		3.60E-62
196	G1276	<i>Hordeum vulgare</i>	gi18476518		1.60E-61
196	G1276	<i>Petunia x hybrida</i>	gi5081557		5.40E-61
196	G1276	<i>Oryza sativa (japonica cultivar- group)</i>	gi24059986		2.30E-60
196	G1276	<i>Malus x domestica</i>	gi21717332		7.30E-57
196	G1276	<i>Picea abies</i>	gi11181610		4.00E-56
196	G1276	<i>Fragaria x ananassa</i>	gi30314933		1.30E-36
198	G1289	<i>Oryza sativa (japonica cultivar- group)</i>	AK069906		1.0e-999
198	G1289	<i>Zea mays</i>	AY104480		1.00E-177
198	G1289	<i>Brassica napus</i>	CD842929		1.00E-124
198	G1289	<i>Oryza sativa</i>	CNS08C8Z		1.00E-123
198	G1289	<i>Oryza sativa (indica cultivar-group)</i>	AAAAA01003696		1.00E-123
198	G1289	<i>Malus domestica</i>	AF220204		1.00E-106
198	G1289	<i>Descurainia sophia</i>	BU238049		1.00E-104
198	G1289	<i>Vitis vinifera</i>	CB974203		1.00E-100
198	G1289	<i>Lactuca sativa</i>	BQ861345		2.00E-95
198	G1289	<i>Glycine max</i>	BI786110		1.00E-90
198	G1289	<i>Oryza sativa (japonica cultivar- group)</i>	gi15624052		1.60E-176
198	G1289	<i>Oryza sativa</i>	gi15408875		6.30E-122
198	G1289	<i>Malus x domestica</i>	gi6752888		5.90E-103
198	G1289	<i>Narcissus pseudonarcissus</i>	gi18419598		3.60E-24
198	G1289	<i>Pinus pinaster</i>	gi20218829		4.70E-09
198	G1289	<i>Lycopersicon esculentum</i>	gi15144514		0.0032
198	G1289	<i>Prunus persica</i>	gi27450532		0.0035
198	G1289	<i>Ricinus communis</i>	gi2246458		0.0043
198	G1289	<i>Nicotiana tabacum</i>	gi17044043		0.0055
198	G1289	<i>Glycine max</i>	gi1399380		0.013
199	G1313	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER110578 1	976	
199	G1313	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER1200 1	977	
199	G1313	<i>Oryza sativa</i>	OSC101811.C1.pl.fg	978	
199	G1313	<i>Oryza sativa</i>	OSC102408.C1.p25.fg	979	
199	G1313	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER163873 1	980	

199	G1313	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER163873_4	981	
199	G1313	<i>Oryza sativa</i>	Os_S60589	1582	
199	G1313	<i>Oryza sativa</i>	Os_S60753	1583	
199	G1313	<i>Hordeum vulgare</i>	Hv_S73931	1734	
200	G1313	<i>Hordeum vulgare</i>	HVRNAGAM1		4.00E-72
200	G1313	<i>Lolium temulentum</i>	AF114162		7.00E-72
200	G1313	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK063951		4.00E-71
200	G1313	<i>Oryza sativa</i>	AX699725		4.00E-71
200	G1313	<i>Avena sativa</i>	ASA133638		4.00E-71
200	G1313	<i>Vitis vinifera</i>	CB005976		3.00E-66
200	G1313	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	CA014662		2.00E-58
200	G1313	<i>Triticum aestivum</i>	BQ245589		8.00E-58
200	G1313	<i>Zea mays</i>	CD439889		3.00E-55
200	G1313	<i>Petunia x hybrida</i>	PHMYBPH33		7.00E-54
200	G1313	<i>Hordeum vulgare</i>	gi13236696		4.00E-72
200	G1313	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi18844771		8.40E-72
200	G1313	<i>Oryza sativa</i>	gi1707640		1.40E-71
200	G1313	<i>Lolium temulentum</i>	gi4877649		2.20E-71
200	G1313	<i>Avena sativa</i>	gi4581969		1.60E-70
200	G1313	<i>Triticum aestivum</i>	gi8247759		1.40E-55
200	G1313	<i>Petunia x hybrida</i>	gi20565		3.80E-53
200	G1313	<i>Nicotiana tabacum</i>	gi11066265		2.60E-52
200	G1313	<i>Lotus corniculatus</i> var. <i>japonicus</i>	gi30024602		2.40E-41
200	G1313	<i>Glycine max</i>	gi30024604		1.50E-40
202	G1327	<i>Oryza sativa</i>	AX652823		1.00E-52
202	G1327	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	CB619057		3.00E-52
202	G1327	<i>Petunia x hybrida</i>	PHMYBPH22		4.00E-52
202	G1327	<i>Brassica napus</i>	CD834677		1.00E-50
202	G1327	<i>Glycine max</i>	AB029160		6.00E-50
202	G1327	<i>Sorghum bicolor</i>	CD214131		8.00E-50
202	G1327	<i>Triticum aestivum</i>	BJ312394		8.00E-50
202	G1327	<i>Hordeum vulgare</i>	BG343209		8.00E-50
202	G1327	<i>Nicotiana tabacum</i>	AB028650		8.00E-50
202	G1327	<i>Solanum tuberosum</i>	BQ514539		1.00E-49
202	G1327	<i>Petunia x hybrida</i>	gi20561		1.10E-51
202	G1327	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi33087073		2.40E-51
202	G1327	<i>Zea mays</i>	gi127580		6.30E-51
202	G1327	<i>Oryza sativa</i>	gi1946265		1.00E-50
202	G1327	<i>Nicotiana tabacum</i>	gi6552361		1.30E-50
202	G1327	<i>Glycine max</i>	gi5139802		1.20E-49
202	G1327	<i>Vitis labrusca x Vitis vinifera</i>	gi22266675		3.10E-49
202	G1327	<i>Lycopersicon esculentum</i>	gi1370140		4.00E-49
202	G1327	<i>Sorghum bicolor</i>	gi19548405		5.10E-49

202	G1327	<i>Populus x canescens</i>	gi22795039		3.60E-48
204	G1340	<i>Brassica oleracea</i>	BZ504572		5.00E-64
204	G1340	<i>Populus tremula x Populus tremuloides</i>	BU832210		7.00E-56
204	G1340	<i>Gossypium arboreum</i>	BQ407507		1.00E-53
204	G1340	<i>Oryza sativa (japonica cultivar-group)</i>	AC135792		1.00E-51
204	G1340	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01006150		3.00E-47
204	G1340	<i>Lotus corniculatus var. japonicus</i>	AP006423		2.00E-41
204	G1340	<i>Oryza sativa</i>	OSIG00051		1.00E-40
204	G1340	<i>Solanum tuberosum</i>	BQ510169		3.00E-37
204	G1340	<i>Zea mays</i>	CC658096		1.00E-34
204	G1340	<i>Sorghum bicolor</i>	BZ346856		7.00E-29
204	G1340	<i>Oryza sativa (japonica cultivar-group)</i>	gi32488407		3.20E-56
204	G1340	<i>Lycopersicon esculentum</i>	gi1345538		0.00087
204	G1340	<i>Oryza sativa</i>	gi13786451		0.0023
204	G1340	<i>Glycine max</i>	gi18182309		0.0075
204	G1340	<i>Triticum aestivum</i>	gi5292165		0.0099
204	G1340	<i>Nicotiana tabacum</i>	gi6691123		0.011
204	G1340	<i>Solanum tuberosum</i>	gi688080		0.013
204	G1340	<i>Volvox carteri</i>	gi21992		0.023
204	G1340	<i>Vicia faba</i>	gi425682		0.03
204	G1340	<i>Bromheadia finlaysoniana</i>	gi2108258		0.046
206	G1341	<i>Gossypium hirsutum</i>	AY125487		1.0e-999
206	G1341	<i>Oryza sativa</i>	AF268596		1.00E-103
206	G1341	<i>Oryza sativa (japonica cultivar-group)</i>	AK064970		1.00E-101
206	G1341	<i>Poncirus trifoliata</i>	CD575941		5.00E-95
206	G1341	<i>Medicago truncatula</i>	CF068570		5.00E-90
206	G1341	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01000469		1.00E-88
206	G1341	<i>Helianthus annuus</i>	CD852109		1.00E-85
206	G1341	<i>Zea mays</i>	BZ968534		2.00E-72
206	G1341	<i>Triticum aestivum</i>	BJ301302		2.00E-69
206	G1341	<i>Brassica napus</i>	CD825286		2.00E-61
206	G1341	<i>Gossypium hirsutum</i>	gi22858664		3.10E-191
206	G1341	<i>Oryza sativa</i>	gi13124871		1.80E-95
206	G1341	<i>Oryza sativa (japonica cultivar-group)</i>	gi31433523		1.80E-95
206	G1341	<i>Marsilea quadrifolia</i>	gi22550110		4.50E-24
206	G1341	<i>Volvox carteri</i>	gi226743		1.20E-12
206	G1341	<i>Volvox carteri f.</i>	gi6523547		2.10E-12

		<i>nagariensis</i>			
206	G1341	<i>Lupinus angustifolius</i>	gi28912428		1.10E-11
206	G1341	<i>Lycopersicon esculentum</i>	gi7488999		1.30E-10
206	G1341	<i>Adiantum capillus-veneris</i>	gi4033606		2.80E-10
206	G1341	<i>Cicer arietinum</i>	gi3204132		3.50E-10
207	G1357	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER80398_1	982	
207	G1357	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-52387	2020	
208	G1357	<i>Brassica oleracea</i>	BH590226		3.00E-94
208	G1357	<i>Medicago truncatula</i>	BF645605		5.00E-59
208	G1357	<i>Sorghum bicolor</i>	BI140703		8.00E-44
208	G1357	<i>Hordeum vulgare</i> subsp. <i>spontaneum</i>	BJ481205		8.00E-44
208	G1357	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BU967516		8.00E-44
208	G1357	<i>Hordeum vulgare</i>	BQ469035		8.00E-44
208	G1357	<i>Petunia x hybrida</i>	AF509874		9.00E-42
208	G1357	<i>Triticum aestivum</i>	BJ257015		9.00E-42
208	G1357	<i>Oryza sativa</i>	AX654515		3.00E-41
208	G1357	<i>Oryza sativa</i> (japonica cultivar-group)	AK099540		5.00E-41
208	G1357	<i>Oryza sativa</i> (japonica cultivar-group)	gi19225018		1.50E-42
208	G1357	<i>Petunia x hybrida</i>	gi21105751		2.40E-42
208	G1357	<i>Medicago truncatula</i>	gi7716952		7.20E-42
208	G1357	<i>Oryza sativa</i>	gi6730946		3.50E-41
208	G1357	<i>Glycine max</i>	gi22597158		1.10E-37
208	G1357	<i>Brassica napus</i>	gi31322582		4.30E-36
208	G1357	<i>Phaseolus vulgaris</i>	gi15148914		7.00E-36
208	G1357	<i>Lycopersicon esculentum</i>	gi6175246		2.20E-32
208	G1357	<i>Triticum sp.</i>	gi4218537		2.80E-32
208	G1357	<i>Triticum monococcum</i>	gi6732160		2.80E-32
210	G1361	<i>Oryza sativa</i> (japonica cultivar-group)	AK102794		1.00E-103
210	G1361	<i>Brassica oleracea</i>	BH541034		7.00E-97
210	G1361	<i>Brassica napus</i>	AF319771		1.00E-96
210	G1361	<i>Hordeum vulgare</i>	BI960052		5.00E-90
210	G1361	<i>Populus tremula x Populus tremuloides</i>	BI129724		2.00E-88
210	G1361	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01011028		4.00E-86
210	G1361	<i>Glycine max</i>	BM527360		4.00E-86
210	G1361	<i>Zea mays</i>	CC340048		3.00E-84
210	G1361	<i>Medicago truncatula</i>	BG646679		2.00E-83
210	G1361	<i>Sorghum bicolor</i>	CD235886		2.00E-72

210	G1361	<i>Oryza sativa</i> (japonica cultivar-group)	gi18461166		3.10E-97
210	G1361	<i>Brassica napus</i>	gi12751304		1.30E-91
210	G1361	<i>Oryza sativa</i>	gi9049470		2.20E-70
210	G1361	<i>Triticum monococcum</i>	gi6732156		6.10E-12
210	G1361	<i>Lycopersicon esculentum</i>	gi6175246		3.40E-11
210	G1361	<i>Glycine max</i>	gi22597158		2.90E-10
210	G1361	<i>Triticum sp.</i>	gi4218537		8.10E-10
210	G1361	<i>Phaseolus vulgaris</i>	gi15148914		7.40E-09
210	G1361	<i>Petunia x hybrida</i>	gi1279640		1.00E-08
210	G1361	<i>Medicago truncatula</i>	gi7716952		2.20E-08
212	G1384	<i>Solanum tuberosum</i>	BQ115095		7.00E-49
212	G1384	<i>Lycopersicon esculentum</i>	AF506825		7.00E-49
212	G1384	<i>Brassica oleracea</i>	BH517407		1.00E-46
212	G1384	<i>Brassica napus</i>	CD829462		9.00E-46
212	G1384	<i>Prunus persica</i>	BU046010		2.00E-45
212	G1384	<i>Hedyotis centranthoides</i>	CB083964		2.00E-44
212	G1384	<i>Atriplex hortensis</i>	AF274033		5.00E-44
212	G1384	<i>Oryza sativa</i> (japonica cultivar-group)	AK105877		6.00E-44
212	G1384	<i>Oryza sativa</i>	AP004119		6.00E-44
212	G1384	<i>Glycine max</i>	BE807772		1.00E-43
212	G1384	<i>Lycopersicon esculentum</i>	gi27436378		1.50E-49
212	G1384	<i>Oryza sativa</i> (japonica cultivar-group)	gi32140997		1.90E-43
212	G1384	<i>Zea mays</i>	gi21908036		4.50E-41
212	G1384	<i>Atriplex hortensis</i>	gi8571476		4.20E-38
212	G1384	<i>Oryza sativa</i>	gi5091503		3.60E-22
212	G1384	<i>Nicotiana tabacum</i>	gi1208498		1.00E-20
212	G1384	<i>Prunus armeniaca</i>	gi3264767		1.70E-20
212	G1384	<i>Mesembryanthemum crystallinum</i>	gi32401273		1.50E-19
212	G1384	<i>Solanum tuberosum</i>	gi28268684		5.00E-19
212	G1384	<i>Glycine max</i>	gi31324058		1.00E-18
214	G1389	<i>Brassica oleracea</i>	BH720211		2.00E-96
214	G1389	<i>Medicago truncatula</i>	AC144893		8.00E-47
214	G1389	<i>Lotus japonicus</i>	AP006146		3.00E-46
214	G1389	<i>Lactuca sativa</i>	BQ996587		3.00E-39
214	G1389	<i>Lupinus albus</i>	LAL426419		8.00E-39
214	G1389	<i>Glycine max</i>	AW760150		2.00E-38
214	G1389	<i>Oryza sativa</i> (japonica cultivar-group)	AB071805		3.00E-38
214	G1389	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01005156		3.00E-38
214	G1389	<i>Oryza sativa</i>	AP003104		3.00E-38

214	G1389	<i>Gossypium arboreum</i>	BG440212		5.00E-38
214	G1389	<i>Oryza sativa</i> (japonica cultivar-group)	gi20975253		3.00E-45
214	G1389	<i>Lupinus albus</i>	gi20269127		2.80E-44
214	G1389	<i>Oryza sativa</i>	gi14164473		1.20E-43
214	G1389	<i>Lycopersicon esculentum</i>	gi12002867		1.90E-39
214	G1389	<i>Pueraria montana</i> var. <i>lobata</i>	gi21624281		6.10E-21
214	G1389	<i>Digitalis purpurea</i>	gi6358561		8.30E-21
214	G1389	<i>Misopates orontium</i>	gi6358605		1.50E-20
214	G1389	<i>Antirrhinum majus</i> subsp. <i>linkianum</i>	gi6358551		2.80E-20
214	G1389	<i>Antirrhinum microphyllum</i>	gi32481583		3.40E-20
214	G1389	<i>Antirrhinum graniticum</i>	gi6358548		3.40E-20
215	G1412	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER16227_1	983	
215	G1412	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER16227_2	984	
215	G1412	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER16227_3	985	
215	G1412	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER16227_5	986	
215	G1412	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER444_125	987	
215	G1412	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER444_267	988	
215	G1412	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER444_320	989	
215	G1412	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER444_337	990	
215	G1412	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER721_119	991	
215	G1412	<i>Glycine max</i>	Gma_S5050636	1657	
215	G1412	<i>Lycopersicon esculentum</i>	Les_S5295623	1930	
215	G1412	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-45948	2021	
215	G1412	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-48215	2022	
216	G1412	<i>Brassica napus</i>	AY245887		1.00E-149
216	G1412	<i>Citrus sinensis</i>	CB290927		1.00E-106
216	G1412	<i>Lycopersicon esculentum</i>	AF011555		1.00E-103
216	G1412	<i>Mesembryanthemum crystallinum</i>	BE034140		1.00E-100
216	G1412	<i>Beta vulgaris</i>	BQ586991		5.00E-98
216	G1412	<i>Solanum tuberosum</i>	BQ516602		1.00E-96
216	G1412	<i>Lactuca sativa</i>	BQ854150		2.00E-95
216	G1412	<i>Medicago truncatula</i>	AJ498717		4.00E-94
216	G1412	<i>Vitis vinifera</i>	CB915147		2.00E-93
216	G1412	<i>Glycine max</i>	BG510868		7.00E-84
216	G1412	<i>Brassica napus</i>	gi31322582		2.00E-141

216	G1412	<i>Lycopersicon esculentum</i>	gi6175246		2.70E-98
216	G1412	<i>Oryza sativa</i>	gi15528779		1.80E-62
216	G1412	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi20161457		8.80E-61
216	G1412	<i>Petunia x hybrida</i>	gi21105748		2.30E-60
216	G1412	<i>Solanum tuberosum</i>	gi14485513		9.10E-59
216	G1412	<i>Triticum sp.</i>	gi4218535		1.30E-57
216	G1412	<i>Triticum monococcum</i>	gi6732158		1.30E-57
216	G1412	<i>Phaseolus vulgaris</i>	gi15148914		4.60E-55
216	G1412	<i>Glycine max</i>	gi22597158		1.70E-50
217	G1420	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER227245 1	992	
217	G1420	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER90086 1	993	
217	G1420	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER22982 1	994	
217	G1420	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER453197 1	995	
218	G1420	<i>Brassica rapa</i>	L35779		1.00E-62
218	G1420	<i>Vitis vinifera</i>	BQ799236		2.00E-55
218	G1420	<i>Glycine max</i>	BF425463		1.00E-50
218	G1420	<i>Brassica oleracea</i>	BH451149		2.00E-47
218	G1420	<i>Populus tremula x Populus tremuloides</i>	BU884581		1.00E-44
218	G1420	<i>Lycopersicon esculentum</i>	AW034229		3.00E-44
218	G1420	<i>Amborella trichopoda</i>	CD483414		2.00E-42
218	G1420	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AK108745		8.00E-40
218	G1420	<i>Medicago truncatula</i>	BF645445		2.00E-39
218	G1420	<i>Oryza sativa</i>	AX654272		6.00E-39
218	G1420	<i>Oryza sativa</i>	gi11761085		7.40E-41
218	G1420	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi22830985		3.90E-35
218	G1420	<i>Lycopersicon esculentum</i>	gi13620227		1.40E-33
218	G1420	<i>Nicotiana tabacum</i>	gi14530681		4.40E-32
218	G1420	<i>Capsella rubella</i>	gi32454266		5.70E-32
218	G1420	<i>Pimpinella brachycarpa</i>	gi3420906		5.80E-30
218	G1420	<i>Petroselinum crispum</i>	gi5917653		2.90E-28
218	G1420	<i>Avena fatua</i>	gi1159877		5.60E-27
218	G1420	<i>Solanum tuberosum</i>	gi24745606		5.60E-27
218	G1420	<i>Retama rietam</i>	gi18158619		3.10E-24
220	G1423	<i>Brassica oleracea</i>	BH449565		1.00E-53
220	G1423	<i>Lycopersicon esculentum</i>	BI929334		2.00E-10
220	G1423	<i>Medicago truncatula</i>	AC139746		1.00E-08

220	G1423	<i>Lotus corniculatus</i> var. <i>japonicus</i>	CB827123		1.00E-08
220	G1423	<i>Lotus japonicus</i>	AP006142		1.00E-08
220	G1423	<i>Oryza sativa</i>	CNS07YPB		1.00E-07
220	G1423	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01005416		3.00E-07
220	G1423	<i>Brassica napus</i>	CD815249		3.00E-07
220	G1423	<i>Sorghum bicolor</i>	BZ627051		7.00E-07
220	G1423	<i>Gossypium</i> <i>arboreum</i>	BQ412101		7.00E-07
220	G1423	<i>Oryza sativa</i>	gi15290141		3.80E-06
220	G1423	<i>Oryza sativa</i> (japonica cultivar- group)	gi30313673		4.30E-06
220	G1423	<i>Brassica oleracea</i> var. <i>capitata</i>	gi30523252		4.50E-05
220	G1423	<i>Zea mays</i>	gi29372756		4.90E-05
220	G1423	<i>Raphanus sativus</i>	gi30523250		5.10E-05
220	G1423	<i>Ceratopteris</i> <i>richardii</i>	gi1944532		5.90E-05
220	G1423	<i>Brassica napus</i>	gi17933454		6.00E-05
220	G1423	<i>Brassica rapa</i>	gi30523360		6.00E-05
220	G1423	<i>Petunia x hybrida</i>	gi13384062		6.20E-05
220	G1423	<i>Hordeum vulgare</i>	gi9367234		8.70E-05
222	G1446	<i>Brassica rapa</i>	AC137926		1.00E-113
222	G1446	<i>Brassica oleracea</i>	BH602216		3.00E-66
222	G1446	<i>Lotus japonicus</i>	AP004983		8.00E-37
222	G1446	<i>Medicago</i> <i>truncatula</i>	BI309565		2.00E-25
222	G1446	<i>Lactuca sativa</i>	BU005471		2.00E-19
222	G1446	<i>Glycine max</i>	BM525749		2.00E-18
222	G1446	<i>Lycopersicon</i> <i>esculentum</i>	BI934904		2.00E-18
222	G1446	<i>Oryza sativa</i> (japonica cultivar- group)	AC137991		3.00E-17
222	G1446	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01014243		4.00E-17
222	G1446	<i>Solanum tuberosum</i>	BG594881		2.00E-16
222	G1446	<i>Oryza sativa</i> (japonica cultivar- group)	gi21104742		0.00012
222	G1446	<i>Nicotiana tabacum</i>	gi8096269		0.0003
222	G1446	<i>Raphanus sativus</i>	gi9049359		0.0012
222	G1446	<i>Oryza sativa</i> (indica cultivar-group)	gi23345287		0.0016
222	G1446	<i>Oryza sativa</i>	gi3885888		0.0016
222	G1446	<i>Boea crassifolia</i>	gi13992713		0.0023
222	G1446	<i>Phaseolus vulgaris</i>	gi1326161		0.0037
222	G1446	<i>Zea mays</i>	gi123378		0.017
222	G1446	<i>Cucurbita maxima</i>	gi17221648		0.023
222	G1446	<i>Lycopersicon</i> <i>esculentum</i>	gi135171		0.051
223	G1451	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER34672 1	996	
223	G1451	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER34672 2	997	

223	G1451	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER11409 1	998	
223	G1451	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER2788 1	999	
223	G1451	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER294601 1	1000	
223	G1451	<i>Oryza sativa</i>	OSC100137.C1.p3.fg	1001	
223	G1451	<i>Oryza sativa</i>	OSC100815.C1.p16.fg	1002	
223	G1451	<i>Oryza sativa</i>	OSC17225.C1.p4.fg	1003	
223	G1451	<i>Oryza sativa</i>	OSC21362.C1.p3.fg	1004	
223	G1451	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER16365 1	1005	
223	G1451	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER16500 1	1006	
223	G1451	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER36166 1	1007	
223	G1451	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER9201 1	1008	
223	G1451	<i>Oryza sativa</i>	Os_S113016	1584	
223	G1451	<i>Oryza sativa</i>	Os_S113019	1585	
223	G1451	<i>Oryza sativa</i>	Os_S113021	1586	
223	G1451	<i>Glycine max</i>	Gma_S4864163	1658	
223	G1451	<i>Glycine max</i>	Gma_S4867879	1659	
223	G1451	<i>Medicago truncatula</i>	Mtr_S5443860	1700	
223	G1451	<i>Hordeum vulgare</i>	Hv_S73176	1735	
223	G1451	<i>Zea mays</i>	Zm_S11325188	1792	
223	G1451	<i>Zea mays</i>	Zm_S11325542	1793	
223	G1451	<i>Zea mays</i>	Zm_S11486245	1794	
223	G1451	<i>Zea mays</i>	Zm_S11521797	1795	
223	G1451	<i>Zea mays</i>	Zm_S11523792	1796	
223	G1451	<i>Zea mays</i>	Zm_S11526178	1797	
223	G1451	<i>Triticum aestivum</i>	Ta_S132434	1864	
223	G1451	<i>Triticum aestivum</i>	Ta_S133054	1865	
223	G1451	<i>Triticum aestivum</i>	Ta_S142068	1866	
223	G1451	<i>Lycopersicon esculentum</i>	Les_S5190833	1931	
223	G1451	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-47770	2023	
223	G1451	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-49633	2024	
223	G1451	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-52521	2025	
223	G1451	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-56226	2026	
223	G1451	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-58048	2027	
223	G1451	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-339069	2028	
223	G1451	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-360353	2029	
223	G1451	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-62180	2030	
224	G1451	<i>Oryza sativa</i>	AB071298		1.0e-999
224	G1451	<i>Oryza sativa</i> (japonica cultivar-group)	AK071455		1.0e-999

224	G1451	<i>Zea mays</i>	AY105215		1.00E-157
224	G1451	<i>Medicago truncatula</i>	CB894037		1.00E-110
224	G1451	<i>Poncirus trifoliata</i>	CD576399		1.00E-109
224	G1451	<i>Lactuca sativa</i>	BQ862285		1.00E-107
224	G1451	<i>Solanum tuberosum</i>	BG597435		1.00E-107
224	G1451	<i>Triticum aestivum</i>	BJ303602		1.00E-103
224	G1451	<i>Mangifera indica</i>	AY255705		5.00E-99
224	G1451	<i>Populus tremuloides</i>	CA930279		2.00E-92
224	G1451	<i>Oryza sativa</i> (japonica cultivar-group)	gi32488726		2.20E-247
224	G1451	<i>Oryza sativa</i>	gi19352049		4.50E-247
224	G1451	<i>Prunus persica</i>	gi27450533		2.20E-159
224	G1451	<i>Oryza sativa</i> (indica cultivar-group)	gi26251300		2.20E-116
224	G1451	<i>Mangifera indica</i>	gi30027167		4.10E-115
224	G1451	<i>Mirabilis jalapa</i>	gi23343944		2.90E-28
224	G1451	<i>Marchantia polymorpha</i>	gi25272004		2.30E-12
224	G1451	<i>Populus tremula</i> x <i>Populus tremuloides</i>	gi20269053		8.60E-10
224	G1451	<i>Vigna radiata</i>	gi287566		3.80E-06
224	G1451	<i>Glycine max</i>	gi114733		1.40E-05
225	G1452	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER80398_1	982	
225	G1452	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-52387	2020	
226	G1452	<i>Medicago truncatula</i>	BF645605		5.00E-65
226	G1452	<i>Sorghum bicolor</i>	BI140703		7.00E-43
226	G1452	<i>Hordeum vulgare</i>	BQ469035		1.00E-42
226	G1452	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BU967516		1.00E-42
226	G1452	<i>Hordeum vulgare</i> subsp. <i>spontaneum</i>	BJ481205		1.00E-42
226	G1452	<i>Triticum aestivum</i>	BQ620568		3.00E-42
226	G1452	<i>Oryza sativa</i> (indica cultivar-group)	CB630990		3.00E-42
226	G1452	<i>Oryza sativa</i>	AX654172		8.00E-42
226	G1452	<i>Oryza sativa</i> (japonica cultivar-group)	CB657109		1.00E-41
226	G1452	<i>Lactuca sativa</i>	BQ997138		4.00E-41
226	G1452	<i>Oryza sativa</i>	gi6730946		1.30E-44
226	G1452	<i>Petunia x hybrida</i>	gi21105746		1.20E-41
226	G1452	<i>Oryza sativa</i> (japonica cultivar-group)	gi27452910		5.10E-41
226	G1452	<i>Medicago truncatula</i>	gi7716952		5.80E-41
226	G1452	<i>Glycine max</i>	gi22597158		5.30E-38
226	G1452	<i>Phaseolus vulgaris</i>	gi15148914		7.00E-36
226	G1452	<i>Brassica napus</i>	gi31322578		2.30E-35
226	G1452	<i>Triticum sp.</i>	gi4218537		3.90E-35
226	G1452	<i>Triticum monococcum</i>	gi6732160		3.90E-35

226	G1452	<i>Lycopersicon esculentum</i>	gi6175246		7.20E-34
227	G1468	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER310714 1	1009	
227	G1468	<i>Oryza sativa</i>	OSC100112.C1.p1.fg	1010	
227	G1468	<i>Oryza sativa</i>	OSC100807.C1.p13.fg	1011	
227	G1468	<i>Oryza sativa</i>	OSC101260.C1.p1.fg	1012	
227	G1468	<i>Oryza sativa</i>	Os_S109216	1587	
227	G1468	<i>Oryza sativa</i>	Os_S114084	1588	
227	G1468	<i>Oryza sativa</i>	Os_S16324	1589	
227	G1468	<i>Oryza sativa</i>	Os_S76625	1590	
227	G1468	<i>Oryza sativa</i>	Os_S79274	1591	
227	G1468	<i>Glycine max</i>	Gma_S5105862	1660	
227	G1468	<i>Glycine max</i>	Gma_S5112587	1661	
227	G1468	<i>Medicago truncatula</i>	Mtr_S5310408	1701	
227	G1468	<i>Medicago truncatula</i>	Mtr_S5369405	1702	
227	G1468	<i>Hordeum vulgare</i>	Hv_S19455	1736	
227	G1468	<i>Hordeum vulgare</i>	Hv_S206003	1737	
227	G1468	<i>Hordeum vulgare</i>	Hv_S30762	1738	
227	G1468	<i>Zea mays</i>	Zm_S11376904	1798	
227	G1468	<i>Zea mays</i>	Zm_S11394555	1799	
227	G1468	<i>Zea mays</i>	Zm_S11433720	1800	
227	G1468	<i>Zea mays</i>	Zm_S11525354	1801	
227	G1468	<i>Triticum aestivum</i>	Ta_S124759	1867	
227	G1468	<i>Triticum aestivum</i>	Ta_S126524	1868	
227	G1468	<i>Triticum aestivum</i>	Ta_S170737	1869	
227	G1468	<i>Triticum aestivum</i>	Ta_S306243	1870	
227	G1468	<i>Triticum aestivum</i>	Ta_S318815	1871	
227	G1468	<i>Triticum aestivum</i>	Ta_S318948	1872	
227	G1468	<i>Triticum aestivum</i>	Ta_S324081	1873	
227	G1468	<i>Triticum aestivum</i>	Ta_S327698	1874	
227	G1468	<i>Triticum aestivum</i>	Ta_S331818	1875	
227	G1468	<i>Triticum aestivum</i>	Ta_S347368	1876	
227	G1468	<i>Triticum aestivum</i>	Ta_S51995	1877	
227	G1468	<i>Triticum aestivum</i>	Ta_S62789	1878	
227	G1468	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-58660	2031	
228	G1468	<i>Brassica oleracea</i>	BH517020		2.00E-98
228	G1468	<i>Petunia x hybrida</i>	AB000453		1.00E-37
228	G1468	<i>Oryza sativa (japonica cultivar- group)</i>	AK069623		2.00E-27
228	G1468	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01005957		5.00E-27
228	G1468	<i>Oryza sativa</i>	OSJN00060		1.00E-26
228	G1468	<i>Zea mays</i>	CC671589		4.00E-23
228	G1468	<i>Datisca glomerata</i>	AF119050		5.00E-19
228	G1468	<i>Vitis aestivalis</i>	CB289561		1.00E-18
228	G1468	<i>Vitis vinifera</i>	BM437679		2.00E-18
228	G1468	<i>Medicago truncatula</i>	AC126007		2.00E-18
228	G1468	<i>Petunia x hybrida</i>	gi1786138		1.00E-36
228	G1468	<i>Oryza sativa</i>	gi32482980		2.30E-30

		(japonica cultivar-group)			
228	G1468	<i>Datisca glomerata</i>	gi4666360		3.50E-21
228	G1468	<i>Glycine max</i>	gi1763063		6.70E-20
228	G1468	<i>Pisum sativum</i>	gi2129892		6.50E-17
228	G1468	<i>Nicotiana tabacum</i>	gi2981169		1.10E-16
228	G1468	<i>Oryza sativa</i>	gi15623826		5.70E-12
228	G1468	<i>Brassica rapa</i>	gi2058504		8.30E-11
228	G1468	<i>Triticum aestivum</i>	gi485814		2.10E-10
228	G1468	<i>Medicago sativa</i>	gi7228329		3.00E-08
230	G1474	<i>Brassica oleracea</i>	BZ030450		1.00E-78
230	G1474	<i>Medicago truncatula</i>	AC135233		1.00E-25
230	G1474	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01001411		2.00E-22
230	G1474	<i>Oryza sativa</i> (japonica cultivar-group)	AP005869		6.00E-22
230	G1474	<i>Hordeum vulgare</i>	BG308988		1.00E-20
230	G1474	<i>Zea mays</i>	CC652748		7.00E-20
230	G1474	<i>Glycine max</i>	BG363109		3.00E-19
230	G1474	<i>Oryza sativa</i>	AC133008		3.00E-19
230	G1474	<i>Helianthus annuus</i>	BQ977193		8.00E-18
230	G1474	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BZ614339		2.00E-14
230	G1474	<i>Oryza sativa</i> (japonica cultivar-group)	gi32489630		5.50E-20
230	G1474	<i>Zea ramosa</i>	gi18674684		3.40E-12
230	G1474	<i>Petunia x hybrida</i>	gi14275902		2.40E-10
230	G1474	<i>Oryza sativa</i>	gi15528588		3.90E-05
230	G1474	<i>Sorghum bicolor</i>	gi18390109		0.00065
230	G1474	<i>Medicago sativa</i>	gi7228329		0.022
230	G1474	<i>Nicotiana tabacum</i>	gi2981169		0.081
230	G1474	<i>Glycine max</i>	gi1763063		0.11
230	G1474	<i>Brassica rapa</i>	gi2058506		0.17
230	G1474	<i>Pisum sativum</i>	gi2129892		0.21
231	G1476	<i>Oryza sativa</i>	OSC101556.C1.p17.fg	1013	
232	G1476	<i>Brassica oleracea</i>	BZ450400		2.00E-51
232	G1476	<i>Lotus japonicus</i>	AP006103		2.00E-11
232	G1476	<i>Lotus corniculatus</i> var. <i>japonicus</i>	CB826842		9.00E-11
232	G1476	<i>Medicago truncatula</i>	AC145202		9.00E-11
232	G1476	<i>Oryza sativa</i> (japonica cultivar-group)	AP004336		2.00E-10
232	G1476	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01025258		2.00E-10
232	G1476	<i>Zea mays</i>	BH871177		4.00E-09
232	G1476	<i>Oryza sativa</i>	AP004020		1.00E-08
232	G1476	<i>Petunia x hybrida</i>	AB035093		1.00E-08
232	G1476	<i>Glycine max</i>	AI973860		9.00E-08
232	G1476	<i>Oryza sativa</i> (japonica cultivar-group)	gi27261062		2.30E-14

232	G1476	<i>Petunia x hybrida</i>	gi14275902		2.90E-14
232	G1476	<i>Zea mays</i>	gi18674684		1.70E-09
232	G1476	<i>Oryza sativa</i>	gi9558464		1.60E-07
232	G1476	<i>Sorghum bicolor</i>	gi18390109		5.30E-06
232	G1476	<i>Datisca glomerata</i>	gi4666360		0.0047
232	G1476	<i>Pisum sativum</i>	gi2129892		0.0057
232	G1476	<i>Medicago sativa</i>	gi7228329		0.011
232	G1476	<i>Brassica rapa</i>	gi2058504		0.011
232	G1476	<i>Nicotiana tabacum</i>	gi2981169		0.02
233	G1482	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER228559_1	1014	
233	G1482	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER228559_2	1015	
233	G1482	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER38097_1	1016	
233	G1482	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER39971_1	1017	
233	G1482	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER39971_2	1018	
233	G1482	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER17570_1	1019	
233	G1482	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER17570_2	1020	
233	G1482	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER687_1	1021	
233	G1482	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER99743_1	1022	
233	G1482	<i>Oryza sativa</i>	OSC101266.C1.p1.fg	1023	
233	G1482	<i>Oryza sativa</i>	OSC15654.C1.p3.fg	1024	
233	G1482	<i>Zea mays</i>	15631093	1025	
233	G1482	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER35072_1	1026	
233	G1482	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER35072_2	1027	
233	G1482	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER366705_1	1028	
233	G1482	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER439033_1	1029	
233	G1482	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER439033_2	1030	
233	G1482	<i>Oryza sativa</i>	Os_S60490	1592	
233	G1482	<i>Medicago truncatula</i>	Mtr_S10820905	1703	
233	G1482	<i>Zea mays</i>	Zm_S11432778	1802	
233	G1482	<i>Triticum aestivum</i>	Ta_S288030	1879	
233	G1482	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-47593	2032	
234	G1482	<i>Solanum tuberosum</i>	BM406201		1.00E-60
234	G1482	<i>Medicago truncatula</i>	CB894280		2.00E-57
234	G1482	<i>Robinia pseudoacacia</i>	BI678186		1.00E-52
234	G1482	<i>Glycine max</i>	BM954087		6.00E-52
234	G1482	<i>Lotus japonicus</i>	BI420251		1.00E-48
234	G1482	<i>Zinnia elegans</i>	AU288043		2.00E-45
234	G1482	<i>Populus tremula</i>	BU892726		2.00E-45
234	G1482	<i>Lycopersicon</i>	BM409788		2.00E-44

		<i>esculentum</i>			
234	G1482	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK071507		1.00E-43
234	G1482	<i>Oryza sativa</i>	AB001884		5.00E-43
234	G1482	<i>Oryza sativa</i>	gi3618312		1.90E-45
234	G1482	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi32488104		2.00E-38
234	G1482	<i>Brassica nigra</i>	gi11037311		4.90E-18
234	G1482	<i>Raphanus sativus</i>	gi3341723		8.00E-17
234	G1482	<i>Brassica napus</i>	gi30984027		2.70E-15
234	G1482	<i>Malus x domestica</i>	gi4091806		7.40E-15
234	G1482	<i>Ipomoea nil</i>	gi10946337		2.00E-14
234	G1482	<i>Hordeum vulgare</i>	gi21667485		2.90E-13
234	G1482	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi21655154		1.50E-11
234	G1482	<i>Pinus radiata</i>	gi4557093		3.10E-10
236	G1483	<i>Brassica oleracea</i>	BZ463417		3.00E-57
236	G1483	<i>Sorghum bicolor</i>	CD212257		6.00E-34
236	G1483	<i>Glycine max</i>	CA802403		1.00E-33
236	G1483	<i>Zinnia elegans</i>	AU293301		3.00E-33
236	G1483	<i>Oryza sativa</i>	AB001886		4.00E-33
236	G1483	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	CB658637		4.00E-33
236	G1483	<i>Lycopersicon</i> <i>esculentum</i>	BI935213		4.00E-32
236	G1483	<i>Populus tremula x</i> <i>Populus tremuloides</i>	BU864618		6.00E-32
236	G1483	<i>Beta vulgaris</i>	BQ589815		7.00E-32
236	G1483	<i>Ipomoea nil</i>	BJ559082		2.00E-31
236	G1483	<i>Oryza sativa</i>	gi3618316		7.20E-34
236	G1483	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi32488104		6.00E-30
236	G1483	<i>Brassica nigra</i>	gi22854916		1.20E-12
236	G1483	<i>Malus x domestica</i>	gi4091806		4.70E-12
236	G1483	<i>Brassica napus</i>	gi2303681		7.90E-12
236	G1483	<i>Raphanus sativus</i>	gi3341723		1.40E-11
236	G1483	<i>Hordeum vulgare</i>	gi21667475		2.90E-11
236	G1483	<i>Ipomoea nil</i>	gi10946337		3.50E-09
236	G1483	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi21655160		1.90E-08
236	G1483	<i>Pinus radiata</i>	gi4557093		4.30E-07
238	G1493	<i>Medicago</i> <i>truncatula</i>	CB891281		9.00E-98
238	G1493	<i>Zea mays</i>	AB060130		5.00E-95
238	G1493	<i>Brassica napus</i>	CD825309		7.00E-84
238	G1493	<i>Vitis vinifera</i>	CD800109		9.00E-84
238	G1493	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK100530		7.00E-81
238	G1493	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	CB630542		3.00E-77
238	G1493	<i>Brassica oleracea</i>	BH687265		2.00E-74

238	G1493	<i>Glycine max</i>	AW596288		4.00E-70
238	G1493	<i>Poncirus trifoliata</i>	CD574729		6.00E-69
238	G1493	<i>Lactuca sativa</i>	BQ858556		1.00E-66
238	G1493	<i>Zea mays</i>	gi13661174		1.00E-84
238	G1493	<i>Oryza sativa</i> (japonica cultivar-group)	gi24308616		9.20E-82
238	G1493	<i>Oryza sativa</i> (indica cultivar-group)	gi31338860		2.20E-42
238	G1493	<i>Oryza glaberrima</i>	gi31338862		2.20E-42
238	G1493	<i>Oryza sativa</i>	gi15289981		9.60E-19
238	G1493	<i>Solanum bulbocastanum</i>	gi32470629		1.00E-10
238	G1493	<i>Chlamydomonas reinhardtii</i>	gi5916207		1.20E-09
238	G1493	<i>Mesembryanthemum crystallinum</i>	gi6942190		8.00E-09
238	G1493	<i>Nicotiana tabacum</i>	gi4519671		2.50E-08
238	G1493	<i>Dianthus caryophyllus</i>	gi13173408		1.40E-07
240	G1507	<i>Glycine max</i>	BE440901		3.00E-61
240	G1507	<i>Triticum aestivum</i>	BQ295376		6.00E-56
240	G1507	<i>Triticum monococcum</i>	BF199732		1.00E-54
240	G1507	<i>Ipomoea nil</i>	BJ569796		4.00E-54
240	G1507	<i>Oryza sativa</i> (japonica cultivar-group)	AK068931		3.00E-53
240	G1507	<i>Zea mays</i>	AY103800		6.00E-53
240	G1507	<i>Lactuca sativa</i>	BQ987329		2.00E-51
240	G1507	<i>Beta vulgaris</i>	BQ591642		4.00E-51
240	G1507	<i>Hordeum vulgare</i>	BU993000		1.00E-49
240	G1507	<i>Medicago truncatula</i>	CA991109		7.00E-49
240	G1507	<i>Oryza sativa</i>	gi13174240		6.30E-51
240	G1507	<i>Oryza sativa</i> (japonica cultivar-group)	gi24960749		3.50E-07
240	G1507	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi21655156		7.50E-07
240	G1507	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi28193631		1.20E-06
240	G1507	<i>Raphanus sativus</i>	gi3341723		2.10E-06
240	G1507	<i>Brassica nigra</i>	gi11037313		7.30E-06
240	G1507	<i>Brassica napus</i>	gi30984027		9.90E-06
240	G1507	<i>Hordeum vulgare</i>	gi21667485		9.60E-05
240	G1507	<i>Malus x domestica</i>	gi4091806		0.00013
240	G1507	<i>Ipomoea nil</i>	gi10946337		0.00068
241	G1510	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER159728_1	1031	
241	G1510	<i>Oryza sativa</i>	OSC101036.C1.p2.fg	1032	
241	G1510	<i>Glycine max</i>	Gma_S5061040	1662	
241	G1510	<i>Triticum aestivum</i>	Ta_S206702	1880	
241	G1510	<i>Lycopersicon esculentum</i>	Les_S5271097	1932	
241	G1510	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-56179	2033	

242	G1510	<i>Brassica oleracea</i>	BZ493938		8.00E-58
242	G1510	<i>Brassica napus</i>	CB686317		3.00E-31
242	G1510	<i>Vitis vinifera</i>	BM437179		5.00E-23
242	G1510	<i>Glycine max</i>	BF425622		5.00E-23
242	G1510	<i>Oryza sativa</i> (japonica cultivar-group)	AK099607		7.00E-23
242	G1510	<i>Sorghum bicolor</i>	CD213245		9.00E-20
242	G1510	<i>Medicago truncatula</i>	BQ165696		2.00E-18
242	G1510	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU863159		5.00E-18
242	G1510	<i>Triticum aestivum</i>	AL816777		4.00E-17
242	G1510	<i>Oryza sativa</i>	AC087597		3.00E-15
242	G1510	<i>Oryza sativa</i> (japonica cultivar-group)	gi28372691		7.00E-19
242	G1510	<i>Oryza sativa</i>	gi14165317		5.10E-10
242	G1510	<i>Nicotiana tabacum</i>	gi12711287		3.70E-07
242	G1510	<i>Nicotiana plumbaginifolia</i>	gi1076609		4.20E-05
242	G1510	<i>Fagopyrum</i> sp. C97107	gi31088153		0.013
242	G1510	<i>Fagopyrum rubifolium</i>	gi31088139		0.016
242	G1510	<i>Fagopyrum gracilipes</i>	gi31088119		0.032
242	G1510	<i>Fagopyrum</i> sp. C97106	gi31088151		0.032
242	G1510	<i>Fagopyrum capillatum</i>	gi31088129		0.032
242	G1510	<i>Fagopyrum callianthum</i>	gi31088131		0.04
244	G1535	<i>Gossypium hirsutum</i>	AF530914		1.0e-999
244	G1535	<i>Oryza sativa</i> (japonica cultivar-group)	AB101646		1.0e-999
244	G1535	<i>Oryza sativa</i>	AX699728		1.0e-999
244	G1535	<i>Zea mays</i>	ZMA250986		1.0e-999
244	G1535	<i>Picea abies</i>	AF172931		1.00E-147
244	G1535	<i>Phalaenopsis</i> sp. SM9108	PSU34743		1.00E-147
244	G1535	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01007245		1.00E-123
244	G1535	<i>Malus domestica</i>	AF067961		1.00E-110
244	G1535	<i>Sorghum bicolor</i>	AF466200		1.00E-106
244	G1535	<i>Helianthus annuus</i>	HNNHAHR		2.00E-97
244	G1535	<i>Gossypium hirsutum</i>	gi22475197		1.50E-186
244	G1535	<i>Oryza sativa</i>	gi18266646		9.30E-174
244	G1535	<i>Oryza sativa</i> (japonica cultivar-group)	gi31339099		9.30E-174
244	G1535	<i>Phalaenopsis</i> sp. SM9108	gi1173622		1.10E-146
244	G1535	<i>Phalaenopsis</i> sp.	gi2147484		1.10E-146

244	G1535	<i>Picea abies</i>	gi12002853		9.90E-146
244	G1535	<i>Sorghum bicolor</i>	gi18481701		1.60E-141
244	G1535	<i>Zea mays</i>	gi5531484		6.50E-134
244	G1535	<i>Malus x domestica</i>	gi3925363		3.10E-104
244	G1535	<i>Helianthus annuus</i>	gi1208940		1.40E-97
246	G1538	<i>Brassica oleracea</i>	BH555867		3.00E-57
246	G1538	<i>Lycopersicon esculentum</i>	AI897201		1.00E-37
246	G1538	<i>Solanum tuberosum</i>	BQ506359		3.00E-36
246	G1538	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BI138094		3.00E-36
246	G1538	<i>Glycine max</i>	BE660082		8.00E-36
246	G1538	<i>Brassica napus</i>	CD818428		2.00E-35
246	G1538	<i>Medicago truncatula</i>	BE204081		1.00E-34
246	G1538	<i>Helianthus argophyllus</i>	CF087358		1.00E-33
246	G1538	<i>Gossypium arboreum</i>	BG447432		3.00E-31
246	G1538	<i>Beta vulgaris</i>	BQ584396		4.00E-30
246	G1538	<i>Oryza sativa (japonica cultivar- group)</i>	gi33146844		2.10E-27
246	G1538	<i>Lycopersicon esculentum</i>	gi1161575		1.10E-21
246	G1538	<i>Craterostigma plantagineum</i>	gi18034441		2.10E-20
246	G1538	<i>Ceratopteris richardii</i>	gi3868841		2.70E-20
246	G1538	<i>Oryza sativa</i>	gi5006853		3.40E-20
246	G1538	<i>Daucus carota</i>	gi4433048		2.40E-19
246	G1538	<i>Nicotiana tabacum</i>	gi22651698		3.00E-19
246	G1538	<i>Brassica rapa subsp. pekinensis</i>	gi8133126		3.90E-19
246	G1538	<i>Phaseolus vulgaris</i>	gi15148916		5.00E-19
246	G1538	<i>Physcomitrella patens</i>	gi21623495		1.30E-18
247	G1539	<i>Glycine max</i>	BE800562.1	1033	
247	G1539	<i>Glycine max</i>	uC-gmflminsoy098c11b1	1034	
248	G1539	<i>Brassica oleracea</i>	BH725803		3.00E-46
248	G1539	<i>Lactuca sativa</i>	BU006325		1.00E-38
248	G1539	<i>Ipomoea nil</i>	BJ555660		4.00E-35
248	G1539	<i>Medicago truncatula</i>	AC137078		9.00E-32
248	G1539	<i>Glycine max</i>	BE800562		1.00E-25
248	G1539	<i>Vigna radiata</i>	AF322401		2.00E-25
248	G1539	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01009392		3.00E-24
248	G1539	<i>Populus tremula x Populus tremuloides</i>	BI128104		5.00E-24
248	G1539	<i>Lycopersicon esculentum</i>	BG134747		5.00E-24
248	G1539	<i>Zea mays</i>	CC337134		2.00E-23
248	G1539	<i>Lycopersicon esculentum</i>	gi28070968		3.30E-31
248	G1539	<i>Petunia x hybrida</i>	gi22087128		7.10E-27

248	G1539	<i>Oryza sativa</i> (japonica cultivar-group)	gi21740884		1.30E-25
248	G1539	<i>Oryza sativa</i>	gi10241438		4.20E-25
248	G1539	<i>Populus tremula</i> x <i>Populus tremuloides</i>	gi3955021		4.50E-12
248	G1539	<i>Narcissus</i> <i>pseudonarcissus</i>	gi18419580		0.00089
248	G1539	<i>Zinnia elegans</i>	gi18076738		0.0053
248	G1539	<i>Ceratopteris</i> <i>richardii</i>	gi3868829		0.074
248	G1539	<i>Juniperus rigida</i>	gi9280017		0.49
248	G1539	<i>Physcomitrella</i> <i>patens</i>	gi7209912		0.53
250	G1549	<i>Brassica napus</i>	CD842307		2.00E-30
250	G1549	<i>Medicago</i> <i>truncatula</i>	AC139525		2.00E-29
250	G1549	<i>Brassica oleracea</i>	BZ482689		5.00E-28
250	G1549	<i>Glycine max</i>	BI787228		1.00E-21
250	G1549	<i>Physcomitrella</i> <i>patens</i>	AB028079		2.00E-21
250	G1549	<i>Ipomoea batatas</i>	BM878740		5.00E-21
250	G1549	<i>Populus</i> <i>balsamifera</i> subsp. <i>trichocarpa</i>	BU881786		7.00E-21
250	G1549	<i>Lycopersicon</i> <i>esculentum</i>	AI488741		9.00E-21
250	G1549	<i>Oryza sativa</i>	AX654801		9.00E-21
250	G1549	<i>Oryza sativa</i> (japonica cultivar-group)	AK105484		1.00E-20
250	G1549	<i>Physcomitrella</i> <i>patens</i>	gi7415628		7.60E-23
250	G1549	<i>Lycopersicon</i> <i>esculentum</i>	gi1161575		8.70E-22
250	G1549	<i>Daucus carota</i>	gi1435021		8.70E-22
250	G1549	<i>Oryza sativa</i>	gi5006853		8.70E-22
250	G1549	<i>Ceratopteris</i> <i>richardii</i>	gi3868839		2.30E-21
250	G1549	<i>Glycine max</i>	gi6091551		6.10E-21
250	G1549	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi8133126		1.00E-20
250	G1549	<i>Nicotiana tabacum</i>	gi22651698		1.30E-20
250	G1549	<i>Phaseolus vulgaris</i>	gi15148916		1.60E-20
250	G1549	<i>Helianthus annuus</i>	gi349379		4.30E-20
252	G1554	<i>Brassica oleracea</i>	BZ436074		1.00E-70
252	G1554	<i>Oryza sativa</i> (japonica cultivar-group)	AK109808		5.00E-68
252	G1554	<i>Lycopersicon</i> <i>pennellii</i>	AW398166		4.00E-38
252	G1554	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01012151		5.00E-34
252	G1554	<i>Lycopersicon</i> <i>esculentum</i>	BE450553		1.00E-33
252	G1554	<i>Solanum tuberosum</i>	BM111266		2.00E-33
252	G1554	<i>Oryza sativa</i>	AP002523		6.00E-33

252	G1554	<i>Populus tremuloides</i>	CA926221		1.00E-31
252	G1554	<i>Medicago truncatula</i>	CF068634		2.00E-31
252	G1554	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BU988945		8.00E-31
252	G1554	<i>Oryza sativa</i>	gi11034542		4.00E-72
252	G1554	<i>Oryza sativa</i> (japonica cultivar-group)	gi33146555		5.70E-44
252	G1554	<i>Nicotiana tabacum</i>	gi4519671		6.20E-13
252	G1554	<i>Zea mays</i>	gi14189890		3.00E-12
252	G1554	<i>Mesembryanthemum crystallinum</i>	gi6942190		7.70E-11
252	G1554	<i>Chlamydomonas reinhardtii</i>	gi5916207		7.80E-11
252	G1554	<i>Oryza glaberrima</i>	gi31338862		6.80E-09
252	G1554	<i>Solanum bulbocastanum</i>	gi32470629		8.30E-09
252	G1554	<i>Oryza sativa</i> (indica cultivar-group)	gi31338860		4.20E-08
252	G1554	<i>Nicotiana glauca</i>	gi1087017		0.0056
254	G1556	<i>Oryza sativa</i>	AU172823		3.00E-18
254	G1556	<i>Medicago truncatula</i>	BE319599		3.00E-18
254	G1556	<i>Gossypium hirsutum</i>	AI730937		4.00E-18
254	G1556	<i>Oryza sativa</i> (japonica cultivar-group)	AK107297		4.00E-18
254	G1556	<i>Solanum tuberosum</i>	BG597254		1.00E-17
254	G1556	<i>Lycopersicon esculentum</i>	AW219675		1.00E-17
254	G1556	<i>Beta vulgaris</i>	BQ585483		4.00E-17
254	G1556	<i>Sorghum bicolor</i>	BG240038		8.00E-17
254	G1556	<i>Hordeum vulgare</i>	BQ465062		1.00E-16
254	G1556	<i>Triticum aestivum</i>	CD913537		1.00E-16
254	G1556	<i>Oryza sativa</i> (japonica cultivar-group)	gi21741799		2.70E-18
254	G1556	<i>Solanum bulbocastanum</i>	gi32470629		2.30E-17
254	G1556	<i>Mesembryanthemum crystallinum</i>	gi6942190		2.80E-15
254	G1556	<i>Nicotiana tabacum</i>	gi4519671		4.70E-13
254	G1556	<i>Chlamydomonas reinhardtii</i>	gi5916207		2.50E-12
254	G1556	<i>Zea mays</i>	gi13940496		1.20E-09
254	G1556	<i>Oryza sativa</i>	gi13940500		2.20E-09
254	G1556	<i>Oryza sativa</i> (indica cultivar-group)	gi31338860		1.10E-06
254	G1556	<i>Oryza glaberrima</i>	gi31338862		1.10E-06
254	G1556	<i>Lycopersicon esculentum</i>	gi22900937		0.96
255	G1557	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER70177 1	1035	
256	G1557	<i>Gossypium hirsutum</i>	AI730937		2.00E-24

256	G1557	<i>Beta vulgaris</i>	BQ585483		2.00E-24
256	G1557	<i>Solanum tuberosum</i>	BG597254		3.00E-24
256	G1557	<i>Mesembryanthemu m crystallinum</i>	BE036811		1.00E-23
256	G1557	<i>Medicago truncatula</i>	BG646240		1.00E-23
256	G1557	<i>Lycopersicon esculentum</i>	BG643313		3.00E-23
256	G1557	<i>Oryza sativa (japonica cultivar- group)</i>	AK107297		4.00E-22
256	G1557	<i>Populus balsamifera subsp. trichocarpa</i>	BU872452		8.00E-22
256	G1557	<i>Oryza sativa</i>	AU172823		1.00E-21
256	G1557	<i>Hordeum vulgare</i>	BQ465062		7.00E-21
256	G1557	<i>Oryza sativa (japonica cultivar- group)</i>	gi21741799		2.90E-23
256	G1557	<i>Nicotiana tabacum</i>	gi4519671		3.60E-16
256	G1557	<i>Solanum bulbocastanum</i>	gi32470629		1.20E-15
256	G1557	<i>Mesembryanthemu m crystallinum</i>	gi6942190		3.60E-15
256	G1557	<i>Chlamydomonas reinhardtii</i>	gi5916207		3.50E-13
256	G1557	<i>Oryza sativa</i>	gi11034542		3.20E-09
256	G1557	<i>Oryza sativa (indica cultivar-group)</i>	gi31338860		1.80E-07
256	G1557	<i>Oryza glaberrima</i>	gi31338862		1.80E-07
256	G1557	<i>Zea mays</i>	gi13661174		1.80E-07
256	G1557	<i>Triticum aestivum</i>	gi100791		0.99
258	G1585	<i>Brassica oleracea</i>	BZ441174		6.00E-57
258	G1585	<i>Ipomoea nil</i>	BJ559013		3.00E-37
258	G1585	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01009903		2.00E-29
258	G1585	<i>Oryza sativa</i>	AP003760		2.00E-29
258	G1585	<i>Zea mays</i>	AQ844430		5.00E-29
258	G1585	<i>Oryza sativa (japonica cultivar- group)</i>	AC121360		9.00E-29
258	G1585	<i>Pinus taeda</i>	AW981538		2.00E-24
258	G1585	<i>Hordeum vulgare subsp. vulgare</i>	BQ467157		3.00E-18
258	G1585	<i>Brassica napus</i>	CD827898		4.00E-18
258	G1585	<i>Triticum aestivum</i>	CD923002		5.00E-18
258	G1585	<i>Oryza sativa (japonica cultivar- group)</i>	gi20161583		1.50E-47
258	G1585	<i>Petunia x hybrida</i>	gi22087128		1.50E-13
258	G1585	<i>Populus tremula x Populus tremuloides</i>	gi3955019		2.70E-12
258	G1585	<i>Lycopersicon esculentum</i>	gi28070968		3.90E-12
258	G1585	<i>Oryza sativa</i>	gi10241438		3.10E-11
258	G1585	<i>Narcissus pseudonarcissus</i>	gi18419580		3.00E-05

258	G1585	<i>Prunus armeniaca</i>	gi5031277		0.027
258	G1585	<i>Daucus carota</i>	gi1076569		0.53
258	G1585	<i>Picea abies</i>	gi19070143		0.63
258	G1585	<i>Zea mays</i>	gi8920423		0.71
260	G1591	<i>Brassica oleracea</i>	BZ084919		2.00E-35
260	G1591	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	CNS09S4R		3.00E-35
260	G1591	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01009392		3.00E-35
260	G1591	<i>Zea mays</i>	CC337119		1.00E-33
260	G1591	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BU998450		2.00E-31
260	G1591	<i>Oryza sativa</i>	AC078977		1.00E-29
260	G1591	<i>Ipomoea nil</i>	BJ553325		1.00E-21
260	G1591	<i>Medicago truncatula</i>	AC137078		1.00E-21
260	G1591	<i>Lactuca sativa</i>	BU006325		2.00E-21
260	G1591	<i>Lycopersicon esculentum</i>	BI204369		3.00E-20
260	G1591	<i>Oryza sativa</i>	gi8099120		7.50E-31
260	G1591	<i>Petunia x hybrida</i>	gi22087128		4.10E-23
260	G1591	<i>Lycopersicon esculentum</i>	gi28070968		8.40E-23
260	G1591	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi18461215		2.80E-22
260	G1591	<i>Populus tremula</i> x <i>Populus tremuloides</i>	gi3955019		3.00E-12
260	G1591	<i>Chlamydomonas reinhardtii</i>	gi16209575		0.00053
260	G1591	<i>Gossypium hirsutum</i>	gi5731257		0.0021
260	G1591	<i>Narcissus pseudonarcissus</i>	gi18419580		0.0022
260	G1591	<i>Dicentra eximia</i>	gi3170468		0.0027
260	G1591	<i>Zinnia elegans</i>	gi18076738		0.012
262	G1593	<i>Solanum tuberosum</i>	AF406697		4.00E-67
262	G1593	<i>Lycopersicon esculentum</i>	AF375966		4.00E-67
262	G1593	<i>Medicago truncatula</i>	AW688195		1.00E-57
262	G1593	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK070465		4.00E-57
262	G1593	<i>Citrus sinensis</i>	CB292855		1.00E-56
262	G1593	<i>Glycine max</i>	BQ629874		1.00E-56
262	G1593	<i>Prunus persica</i>	BU043836		6.00E-55
262	G1593	<i>Vitis vinifera</i>	CB343619		3.00E-54
262	G1593	<i>Mesembryanthemum crystallinum</i>	CA839352		6.00E-54
262	G1593	<i>Malus x domestica</i>	AF053769		1.00E-49
262	G1593	<i>Solanum tuberosum</i>	gi22652115		9.50E-68
262	G1593	<i>Lycopersicon esculentum</i>	gi31323447		2.20E-64
262	G1593	<i>Malus x domestica</i>	gi7239157		3.00E-52
262	G1593	<i>Gnetum gnemon</i>	gi31746344		5.40E-52

262	G1593	<i>Oryza sativa</i> (japonica cultivar-group)	gi20219036		6.80E-51
262	G1593	<i>Hordeum vulgare</i>	gi13752407		1.80E-48
262	G1593	<i>Oryza sativa</i>	gi15408891		3.20E-47
262	G1593	<i>Oryza sativa</i> (indica cultivar-group)	gi19352101		3.20E-47
262	G1593	<i>Zea mays</i>	gi19743685		4.90E-37
262	G1593	<i>Dendrobium grex</i> <i>Madame Thong-In</i>	gi3929314		4.30E-12
263	G1660	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER30666_1	1036	
263	G1660	<i>Glycine max</i>	uC- gmflIB3275P059b07b1	1037	
263	G1660	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER6548_1	1038	
263	G1660	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER93242_1	1039	
263	G1660	<i>Oryza sativa</i>	OSC100113.C1.p9.fg	1040	
263	G1660	<i>Oryza sativa</i>	OSC101572.C1.p8.fg	1041	
263	G1660	<i>Oryza sativa</i>	OSC34319.C1.p4.fg	1042	
263	G1660	<i>Zea mays</i>	700167489_FLI	1043	
263	G1660	<i>Zea mays</i>	LIB3279-010-H4_FLI	1044	
263	G1660	<i>Zea mays</i>	LIB4767-001-R1-M1-D1	1045	
263	G1660	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER43109_1	1046	
263	G1660	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER64649_1	1047	
263	G1660	<i>Oryza sativa</i>	Os_S94670	1593	
263	G1660	<i>Zea mays</i>	Zm_S11454293	1803	
263	G1660	<i>Zea mays</i>	Zm_S11520265	1804	
263	G1660	<i>Triticum aestivum</i>	Ta_S142271	1881	
263	G1660	<i>Lycopersicon</i> <i>esculentum</i>	SGN-UNIGENE- SINGLET-35095	2034	
263	G1660	<i>Lycopersicon</i> <i>esculentum</i>	SGN-UNIGENE- SINGLET-53090	2035	
264	G1660	<i>Oryza sativa</i> (japonica cultivar-group)	AK102604		1.00E-109
264	G1660	<i>Brassica oleracea</i>	BZ431607		1.00E-108
264	G1660	<i>Brassica napus</i>	CD818917		2.00E-95
264	G1660	<i>Oryza sativa</i>	BE040229		2.00E-62
264	G1660	<i>Ipomoea nil</i>	BJ576287		1.00E-54
264	G1660	<i>Lycopersicon</i> <i>esculentum</i>	AW443990		7.00E-54
264	G1660	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01001098		2.00E-52
264	G1660	<i>Zea mays</i>	CB886289		3.00E-50
264	G1660	<i>Hordeum vulgare</i>	BM377843		3.00E-50
264	G1660	<i>Triticum aestivum</i>	BJ238027		6.00E-47
264	G1660	<i>Oryza sativa</i> (japonica cultivar-group)	gi27452912		7.70E-62
264	G1660	<i>Zea mays</i>	gi23928441		3.30E-22
264	G1660	<i>Solanum tuberosum</i>	gi1881585		1.60E-17
264	G1660	<i>Lycopersicon</i> <i>esculentum</i>	gi4731573		1.20E-16

264	G1660	<i>Nicotiana tabacum</i>	gi8096269		0.0017
264	G1660	<i>Cucurbita maxima</i>	gi17221648		0.002
264	G1660	<i>Cicer arietinum</i>	gi7208779		0.0026
264	G1660	<i>Oryza sativa</i>	gi11875196		0.006
264	G1660	<i>Plastid Oenothera elata</i> subsp. <i>hookeri</i>	gi13276714		0.0063
264	G1660	<i>Oenothera elata</i> subsp. <i>hookeri</i>	gi23822375		0.0063
266	G1718	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BG543482		2.00E-77
266	G1718	<i>Brassica oleracea</i>	BH533325		2.00E-65
266	G1718	<i>Citrus sinensis</i>	CB292402		2.00E-47
266	G1718	<i>Vitis vinifera</i>	CA812994		3.00E-47
266	G1718	<i>Populus tremula</i>	BU889204		4.00E-47
266	G1718	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU835838		3.00E-46
266	G1718	<i>Populus tremuloides</i>	CA925038		8.00E-46
266	G1718	<i>Euphorbia esula</i>	BE056347		1.00E-44
266	G1718	<i>Medicago truncatula</i>	BG452491		4.00E-44
266	G1718	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU869861		7.00E-44
266	G1718	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi32129334		1.60E-21
266	G1718	<i>Oryza sativa</i>	gi6539567		4.30E-20
266	G1718	<i>Cicer arietinum</i>	gi4651204		6.50E-17
266	G1718	<i>Tulipa gesneriana</i>	gi23386073		3.30E-14
266	G1718	<i>Cucumis melo</i>	gi17016985		3.40E-11
266	G1718	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152976		1.40E-08
266	G1718	<i>Thellungiella halophila</i>	gi20340241		1.60E-08
266	G1718	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	gi29164825		2.40E-08
266	G1718	<i>Medicago sativa</i>	gi23451086		1.30E-07
266	G1718	<i>Lotus japonicus</i>	gi1086225		2.30E-07
267	G1730	<i>Zea mays</i>	LIB5074-010-R1-XP1-A11	1048	
268	G1730	<i>Brassica oleracea</i>	BZ472679		6.00E-67
268	G1730	<i>Medicago truncatula</i>	AC126787		1.00E-27
268	G1730	<i>Brassica napus</i>	CD814199		4.00E-27
268	G1730	<i>Zea mays</i>	BZ715596		4.00E-21
268	G1730	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK108491		5.00E-21
268	G1730	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01009602		7.00E-21
268	G1730	<i>Oryza sativa</i>	AX653298		1.00E-18
268	G1730	<i>Cucumis melo</i>	AF499727		2.00E-18
268	G1730	<i>Solanum tuberosum</i>	BG593372		5.00E-18
268	G1730	<i>Lycopersicon esculentum</i>	AW032769		2.00E-17
268	G1730	<i>Cucumis melo</i>	gi28558782		6.70E-23
268	G1730	<i>Oryza sativa</i>	gi12643047		1.90E-19

268	G1730	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi31433649		1.90E-19
268	G1730	<i>Nicotiana tabacum</i>	gi12003386		5.10E-17
268	G1730	<i>Zea mays</i>	gi21645888		1.40E-16
268	G1730	<i>Medicago sativa</i>	gi23451086		1.30E-14
268	G1730	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152976		5.70E-14
268	G1730	<i>Hordeum vulgare</i>	gi2894379		1.10E-09
268	G1730	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	gi29164825		4.10E-09
268	G1730	<i>Thellungiella</i> <i>halophila</i>	gi20340241		1.10E-08
270	G1743	<i>Brassica oleracea</i>	BH985728		1.00E-89
270	G1743	<i>Populus tremula</i>	BU891914		3.00E-61
270	G1743	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU885427		3.00E-61
270	G1743	<i>Lycopersicon</i> <i>esculentum</i>	AW034559		1.00E-56
270	G1743	<i>Ipomoea nil</i>	BJ561648		1.00E-56
270	G1743	<i>Gossypium</i> <i>hirsutum</i>	CA993166		1.00E-55
270	G1743	<i>Populus</i> <i>balsamifera</i> subsp. <i>trichocarpa</i> x <i>Populus deltoides</i>	CA825344		2.00E-54
270	G1743	<i>Vitis vinifera</i>	CB918599		3.00E-53
270	G1743	<i>Lactuca sativa</i>	BQ849490		4.00E-53
270	G1743	<i>Capsicum annuum</i>	CA847343		2.00E-52
270	G1743	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi32488512		1.80E-35
270	G1743	<i>Oryza sativa</i>	gi6069662		1.30E-18
270	G1743	<i>Thellungiella</i> <i>halophila</i>	gi20340241		1.70E-16
270	G1743	<i>Zea mays</i>	gi18092342		6.30E-12
270	G1743	<i>Medicago sativa</i>	gi23451086		1.20E-10
270	G1743	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152976		1.50E-10
270	G1743	<i>Nicotiana tabacum</i>	gi12003386		2.20E-09
270	G1743	<i>Cucumis melo</i>	gi28558782		2.20E-09
270	G1743	<i>Hordeum vulgare</i>	gi2894379		2.70E-08
270	G1743	<i>Cicer arietinum</i>	gi4651204		8.50E-08
271	G1753	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER91438_1	1049	
271	G1753	<i>Oryza sativa</i>	OSC101736.C1.p16.fg	1050	
272	G1753	<i>Brassica oleracea</i>	BZ063578		4.00E-78
272	G1753	<i>Lycopersicon</i> <i>esculentum</i>	AW030833		4.00E-35
272	G1753	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01009545		9.00E-35
272	G1753	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AP005775		1.00E-34
272	G1753	<i>Poncirus trifoliata</i>	CD576150		1.00E-33
272	G1753	<i>Oryza sativa</i>	AX653721		4.00E-33
272	G1753	<i>Helianthus annuus</i>	BQ976989		5.00E-33

272	G1753	<i>Zea mays</i>	BZ737969		1.00E-32
272	G1753	<i>Nicotiana tabacum</i>	AF211531		4.00E-32
272	G1753	<i>Vitis vinifera</i>	CB035846		1.00E-31
272	G1753	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi21742362		1.00E-34
272	G1753	<i>Oryza sativa</i>	gi14140155		2.70E-34
272	G1753	<i>Nicotiana tabacum</i>	gi12003384		1.90E-33
272	G1753	<i>Brassica napus</i>	gi20303011		5.10E-33
272	G1753	<i>Lycopersicon esculentum</i>	gi18535580		1.60E-31
272	G1753	<i>Prunus avium</i>	gi23495458		1.40E-30
272	G1753	<i>Hordeum vulgare</i>	gi19071243		1.40E-28
272	G1753	<i>Zea mays</i>	gi21908034		1.70E-25
272	G1753	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152903		5.50E-20
272	G1753	<i>Gossypium hirsutum</i>	gi32481079		1.30E-18
274	G1772	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK073139		1.0e-999
274	G1772	<i>Thellungiella halophila</i>	BM985639		1.00E-134
274	G1772	<i>Lactuca sativa</i>	BQ996439		1.00E-119
274	G1772	<i>Vitis vinifera</i>	CD008605		6.00E-99
274	G1772	<i>Brassica oleracea</i>	BH998711		6.00E-93
274	G1772	<i>Glycine max</i>	BM887188		1.00E-90
274	G1772	<i>Helianthus annuus</i>	BU026535		9.00E-89
274	G1772	<i>Zea mays</i>	BM661323		1.00E-84
274	G1772	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01003274		4.00E-73
274	G1772	<i>Oryza sativa</i>	AC103891		5.00E-73
274	G1772	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi20330766		1.30E-191
274	G1772	<i>Nicotiana glauca</i>	gi1666171		2.20E-34
274	G1772	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi27804453		0.16
274	G1772	<i>Calycanthus floridus</i>	gi8163958		0.64
274	G1772	<i>Picea glauca</i>	gi1350524		0.66
274	G1772	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi23954355		0.84
274	G1772	<i>Adiantum capillus-veneris</i>	gi30266733		0.95
274	G1772	<i>Macrotyloma axillare</i>	gi124034		0.98
274	G1772	<i>Canavalia lineata</i>	gi543526		1
274	G1772	<i>Glycine max</i>	gi2306979		1
275	G1779	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER185518 1	1051	
275	G1779	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER264928 1	1052	
275	G1779	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER76652 1	1053	
275	G1779	<i>Oryza sativa</i>	OSC21832.C1.p4.fg	1054	

275	G1779	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER78309_1	1055	
275	G1779	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-56681	2036	
276	G1779	<i>Brassica oleracea</i>	BH558232		3.00E-36
276	G1779	<i>Vitis vinifera</i>	BM437179		2.00E-26
276	G1779	<i>Glycine max</i>	BF425622		1.00E-24
276	G1779	<i>Oryza sativa</i> (japonica cultivar-group)	AK099607		5.00E-21
276	G1779	<i>Sorghum bicolor</i>	CD213245		3.00E-20
276	G1779	<i>Medicago truncatula</i>	BQ165696		2.00E-19
276	G1779	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU863159		2.00E-18
276	G1779	<i>Brassica napus</i>	CB686317		9.00E-18
276	G1779	<i>Poncirus trifoliata</i>	CD576018		3.00E-17
276	G1779	<i>Triticum aestivum</i>	AL816777		2.00E-16
276	G1779	<i>Oryza sativa</i> (japonica cultivar-group)	gi28564714		1.20E-20
276	G1779	<i>Oryza sativa</i>	gi5091599		2.80E-08
276	G1779	<i>Nicotiana tabacum</i>	gi12711287		2.90E-07
276	G1779	<i>Nicotiana glauca</i>	gi1076609		3.50E-05
276	G1779	<i>Lycopersicon esculentum</i>	gi1418988		0.36
276	G1779	<i>Eutrema wasabi</i>	gi23200602		0.55
276	G1779	<i>Amicia glandulosa</i>	gi30313971		0.62
276	G1779	<i>Ipomoea batatas</i>	gi604324		0.8
276	G1779	<i>Triticum aestivum</i>	gi23451222		1
276	G1779	<i>Gnetum gnemon</i>	gi31746346		1
277	G1792	<i>Oryza sativa</i>	G3380	2124	5.00E-29
277	G1792	<i>Oryza sativa</i>	G3383	2128	3.00E-33
277	G1792	<i>Oryza sativa</i>	G3515	2209	7.00E-30
277	G1792	<i>Zea mays</i>	G3516	2211	2.00E-31
277	G1792	<i>Zea mays</i>	G3517	2213	9.00E-33
277	G1792	<i>Glycine max</i>	G3518	2215	9.00E-35
277	G1792	<i>Glycine max</i>	G3519	2217	3.00E-35
277	G1792	<i>Glycine max</i>	G3520	2219	3.00E-36
277	G1792	<i>Glycine max</i>	AW308784.1	685	
277	G1792	<i>Glycine max</i>	BG790680.1	686	
277	G1792	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER602185_1	687	
277	G1792	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER91218_1	688	
277	G1792	<i>Glycine max</i>	LIB5118-009-Q1-PF1-F2	689	
277	G1792	<i>Oryza sativa</i>	OSC20174.C1.p2.fg	690	
277	G1792	<i>Zea mays</i>	LIB4756-134-A1-K1-G10	691	
277	G1792	<i>Glycine max</i>	Gma_S5001644	1633	
277	G1792	<i>Zea mays</i>	Zm_S11513768	1754	
278	G1792	<i>Lycopersicon esculentum</i>	AI776626		7.00E-35
278	G1792	<i>Solanum tuberosum</i>	BQ045702		1.00E-32
278	G1792	<i>Glycine max</i>	BM178875		9.00E-32

278	G1792	<i>Medicago truncatula</i>	BF649790		2.00E-31
278	G1792	<i>Eucalyptus grandis</i>	CB967722		1.00E-30
278	G1792	<i>Brassica oleracea</i>	BZ020356		1.00E-30
278	G1792	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01002491		4.00E-30
278	G1792	<i>Oryza sativa</i> (japonica cultivar-group)	AE017099		4.00E-30
278	G1792	<i>Oryza sativa</i>	AC025907		4.00E-30
278	G1792	<i>Sorghum bicolor</i>	BZ337899		4.00E-30
278	G1792	<i>Oryza sativa</i> (japonica cultivar-group)	gi31432356		1.10E-30
278	G1792	<i>Lycopersicon esculentum</i>	gi23452024		4.90E-26
278	G1792	<i>Nicotiana tabacum</i>	gi1732406		2.60E-25
278	G1792	<i>Oryza sativa</i>	gi12597874		4.50E-25
278	G1792	<i>Mesembryanthemum crystallinum</i>	gi32401273		9.40E-25
278	G1792	<i>Catharanthus roseus</i>	gi8980313		2.20E-23
278	G1792	<i>Nicotiana glauca</i>	gi8809571		2.20E-23
278	G1792	<i>Matricaria chamomilla</i>	gi17385636		1.40E-21
278	G1792	<i>Glycine max</i>	gi21304712		3.80E-21
278	G1792	<i>Atriplex hortensis</i>	gi8571476		1.30E-20
279	G1796	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER50695_1	1056	
279	G1796	<i>Oryza sativa</i>	Os_S43212	1594	
279	G1796	<i>Zea mays</i>	Zm_S11435953	1805	
279	G1796	<i>Triticum aestivum</i>	Ta_S369485	1882	
280	G1796	<i>Brassica oleracea</i>	BH503101		2.00E-54
280	G1796	<i>Medicago truncatula</i>	AC119414		2.00E-35
280	G1796	<i>Oryza sativa</i>	AP004079		2.00E-25
280	G1796	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01000133		2.00E-25
280	G1796	<i>Zea mays</i>	CD437690		3.00E-24
280	G1796	<i>Lactuca sativa</i>	BQ987300		4.00E-24
280	G1796	<i>Sorghum bicolor</i>	CD228394		4.00E-24
280	G1796	<i>Lupinus albus</i>	CA411234		6.00E-24
280	G1796	<i>Glycine max</i>	CA800025		8.00E-24
280	G1796	<i>Oryza sativa</i> (japonica cultivar-group)	AP005845		2.00E-23
280	G1796	<i>Oryza sativa</i> (japonica cultivar-group)	gi32487928		6.40E-26
280	G1796	<i>Zea mays</i>	gi27802487		1.80E-24
280	G1796	<i>Nicotiana tabacum</i>	gi1208496		1.10E-23
280	G1796	<i>Oryza sativa</i>	gi10567106		2.20E-23
280	G1796	<i>Stylosanthes hamata</i>	gi4099914		3.70E-23
280	G1796	<i>Nicotiana glauca</i>	gi8809573		1.20E-22
280	G1796	<i>Lycopersicon esculentum</i>	gi30526297		2.60E-22

280	G1796	<i>Thellungiella halophila</i>	gi20340233		4.20E-22
280	G1796	<i>Mesembryanthemum crystallinum</i>	gi32401273		7.80E-21
280	G1796	<i>Solanum tuberosum</i>	gi28268684		1.30E-20
282	G1797	<i>Petunia x hybrida</i>	AF335240		5.00E-52
282	G1797	<i>Lycopersicon esculentum</i>	AI486684		7.00E-49
282	G1797	<i>Eucalyptus grandis</i>	AY263808		8.00E-47
282	G1797	<i>Eucalyptus occidentalis</i>	AY273872		7.00E-46
282	G1797	<i>Populus tremuloides</i>	CA925124		8.00E-45
282	G1797	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	AY257541		5.00E-44
282	G1797	<i>Sinapis alba</i>	SAU25696		5.00E-44
282	G1797	<i>Pimpinella brachycarpa</i>	AF082531		5.00E-44
282	G1797	<i>Cardamine flexuosa</i>	AY257542		2.00E-43
282	G1797	<i>Nicotiana tabacum</i>	NTTOB		5.00E-43
282	G1797	<i>Petunia x hybrida</i>	gi13384058		4.40E-50
282	G1797	<i>Eucalyptus grandis</i>	gi30575600		8.60E-47
282	G1797	<i>Eucalyptus occidentalis</i>	gi30983946		6.00E-46
282	G1797	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi30171307		4.90E-44
282	G1797	<i>Populus tremuloides</i>	gi31295609		4.90E-44
282	G1797	<i>Sinapis alba</i>	gi1049022		1.60E-43
282	G1797	<i>Pimpinella brachycarpa</i>	gi3493647		1.60E-43
282	G1797	<i>Cardamine flexuosa</i>	gi30171309		2.70E-43
282	G1797	<i>Nicotiana tabacum</i>	gi1076646		1.50E-42
282	G1797	<i>Draba nemorosa</i> var. <i>hebecarpa</i>	gi30171311		1.00E-41
284	G1798	<i>Petunia x hybrida</i>	AF335240		5.00E-53
284	G1798	<i>Lycopersicon esculentum</i>	AI486684		3.00E-52
284	G1798	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	AY257541		3.00E-48
284	G1798	<i>Sinapis alba</i>	SAU25696		3.00E-47
284	G1798	<i>Cardamine flexuosa</i>	AY257542		5.00E-47
284	G1798	<i>Pimpinella brachycarpa</i>	AF082531		5.00E-47
284	G1798	<i>Populus tremuloides</i>	CA925124		1.00E-44
284	G1798	<i>Eucalyptus grandis</i>	AY263807		1.00E-43
284	G1798	<i>Nicotiana tabacum</i>	NTTOB		1.00E-43
284	G1798	<i>Oryza sativa</i> (japonica cultivar-group)	AK104921		5.00E-43
284	G1798	<i>Petunia x hybrida</i>	gi13384058		1.30E-52
284	G1798	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi30171307		4.60E-48
284	G1798	<i>Sinapis alba</i>	gi1049022		2.50E-47
284	G1798	<i>Cardamine flexuosa</i>	gi30171309		1.40E-46
284	G1798	<i>Pimpinella brachycarpa</i>	gi3493647		1.40E-46
284	G1798	<i>Populus tremuloides</i>	gi31295609		2.30E-44
284	G1798	<i>Oryza sativa</i>	gi5295990		6.20E-44

284	G1798	<i>Eucalyptus grandis</i>	gi30575598		1.00E-43
284	G1798	<i>Zea mays</i>	gi12002139		1.30E-43
284	G1798	<i>Nicotiana tabacum</i>	gi1076646		5.60E-43
286	G1808	<i>Brassica oleracea</i>	BH950967		1.00E-85
286	G1808	<i>Lycopersicon esculentum</i>	BF051268		2.00E-30
286	G1808	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU870843		2.00E-29
286	G1808	<i>Glycine max</i>	BM269595		6.00E-21
286	G1808	<i>Brassica napus</i>	CD833815		3.00E-17
286	G1808	<i>Gossypium hirsutum</i>	CA992680		6.00E-14
286	G1808	<i>Zinnia elegans</i>	AU294545		4.00E-12
286	G1808	<i>Solanum tuberosum</i>	BQ519273		9.00E-12
286	G1808	<i>Medicago truncatula</i>	CA918476		1.00E-11
286	G1808	<i>Phaseolus vulgaris</i>	AF350505		2.00E-11
286	G1808	<i>Phaseolus vulgaris</i>	gi13430400		2.90E-14
286	G1808	<i>Phaseolus acutifolius</i>	gi12829956		6.10E-14
286	G1808	<i>Petroselinum crispum</i>	gi9650828		7.70E-14
286	G1808	<i>Glycine max</i>	gi22597162		1.30E-13
286	G1808	<i>Nicotiana tabacum</i>	gi16580130		1.10E-12
286	G1808	<i>Capsicum chinense</i>	gi24460973		1.80E-12
286	G1808	<i>Zea mays</i>	gi1060935		2.00E-11
286	G1808	<i>Lycopersicon esculentum</i>	gi5901747		8.10E-11
286	G1808	<i>Zea perennis</i>	gi27652122		1.30E-10
286	G1808	<i>Oryza sativa</i>	gi14289165		1.40E-10
287	G1816	<i>Oryza sativa</i>	G3392	2131	2.00E-16
287	G1816	<i>Oryza sativa</i>	G3392	2133	2.00E-15
287	G1816	<i>Zea mays</i>	G3431	2147	1.00E-13
287	G1816	<i>Zea mays</i>	G3444	2157	1.00E-13
287	G1816	<i>Glycine max</i>	G3445	2159	5.00E-12
287	G1816	<i>Glycine max</i>	G3446	2161	5.00E-12
287	G1816	<i>Glycine max</i>	G3447	2163	5.00E-12
287	G1816	<i>Glycine max</i>	G3448	2165	1.00E-13
287	G1816	<i>Glycine max</i>	G3449	2167	3.00E-14
287	G1816	<i>Glycine max</i>	G3450	2168	3.00E-22
287	G1816	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER31802 1	1057	
287	G1816	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER586 102	1058	
287	G1816	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER586 116	1059	
287	G1816	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER8724 1	1060	
287	G1816	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER8724 2	1061	
287	G1816	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER30974 2	1062	
287	G1816	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER30974 3	1063	
287	G1816	<i>Oryza sativa</i>	OSC20053.C1.p5.fg	1064	

287	G1816	<i>Oryza sativa</i>	OSC20055.C1.p5.fg	1065	
287	G1816	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER69699 1	1066	
287	G1816	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER69699 2	1067	
287	G1816	<i>Glycine max</i>	Gma_S4901946	1663	
287	G1816	<i>Triticum aestivum</i>	Ta_S45274	1883	
288	G1816	<i>Vitis vinifera</i>	BM437313		8.00E-28
288	G1816	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU872107		2.00E-27
288	G1816	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU831849		2.00E-27
288	G1816	<i>Vitis aestivalis</i>	CB289238		7.00E-27
288	G1816	<i>Glycine max</i>	AI495284		7.00E-19
288	G1816	<i>Brassica napus</i>	CD843377		6.00E-15
288	G1816	<i>Nuphar advena</i>	CD473522		1.00E-14
288	G1816	<i>Pinus pinaster</i>	AL750151		3.00E-14
288	G1816	<i>Lactuca sativa</i>	BU015255		5.00E-14
288	G1816	<i>Brassica oleracea</i>	BH961028		8.00E-14
288	G1816	<i>Gossypioideis kirkii</i>	gi23476295		4.90E-12
288	G1816	<i>Gossypium raimondii</i>	gi14269333		2.70E-11
288	G1816	<i>Gossypium herbaceum</i>	gi14269335		2.70E-11
288	G1816	<i>Gossypium hirsutum</i>	gi14269337		2.70E-11
288	G1816	<i>Solanum tuberosum</i>	gi9954118		1.50E-10
288	G1816	<i>Oryza sativa</i>	gi2605619		2.40E-10
288	G1816	<i>Cucumis sativus</i>	gi20514371		3.10E-10
288	G1816	<i>Zea mays</i> subsp. <i>parviglumis</i>	gi15042108		4.00E-10
288	G1816	<i>Zea luxurians</i>	gi15042124		4.00E-10
288	G1816	<i>Anthurium andraeanum</i>	gi29824962		5.20E-10
290	G1823	<i>Zea mays</i>	AB060130		3.00E-81
290	G1823	<i>Oryza sativa</i> (japonica cultivar-group)	AK065276		8.00E-74
290	G1823	<i>Oryza sativa</i> (indica cultivar-group)	CB630542		5.00E-68
290	G1823	<i>Lactuca sativa</i>	BQ858556		3.00E-64
290	G1823	<i>Brassica oleracea</i>	BH485050		3.00E-58
290	G1823	<i>Solanum tuberosum</i>	BM407041		3.00E-56
290	G1823	<i>Medicago truncatula</i>	CB891281		3.00E-54
290	G1823	<i>Vitis vinifera</i>	CD800109		3.00E-52
290	G1823	<i>Sorghum bicolor</i>	CD424269		1.00E-51
290	G1823	<i>Stevia rebaudiana</i>	BG523436		1.00E-47
290	G1823	<i>Zea mays</i>	gi15667625		3.10E-79
290	G1823	<i>Oryza sativa</i> (japonica cultivar-group)	gi24308616		3.70E-78
290	G1823	<i>Oryza sativa</i> (indica cultivar-group)	gi31338860		4.50E-41
290	G1823	<i>Oryza glaberrima</i>	gi31338862		4.50E-41

290	G1823	<i>Oryza sativa</i>	gi15289981		2.40E-19
290	G1823	<i>Chlamydomonas reinhardtii</i>	gi5916207		4.80E-11
290	G1823	<i>Nicotiana tabacum</i>	gi4519671		1.40E-09
290	G1823	<i>Solanum bulbocastanum</i>	gi32470629		6.40E-09
290	G1823	<i>Mesembryanthemum crystallinum</i>	gi6942190		3.80E-08
290	G1823	<i>Dianthus caryophyllus</i>	gi13173408		6.50E-07
292	G1825	<i>Lycopersicon esculentum</i>	BG643313		4.00E-28
292	G1825	<i>Medicago truncatula</i>	BG646240		3.00E-27
292	G1825	<i>Oryza sativa</i> (japonica cultivar-group)	AK073606		6.00E-27
292	G1825	<i>Oryza sativa</i>	AU172823		6.00E-27
292	G1825	<i>Gossypium hirsutum</i>	AI730937		1.00E-25
292	G1825	<i>Triticum aestivum</i>	BJ288732		3.00E-25
292	G1825	<i>Hordeum vulgare</i>	BQ465062		1.00E-24
292	G1825	<i>Lactuca sativa</i>	BQ867305		2.00E-22
292	G1825	<i>Beta vulgaris</i>	BQ585483		3.00E-22
292	G1825	<i>Solanum tuberosum</i>	BQ507198		8.00E-22
292	G1825	<i>Oryza sativa</i> (japonica cultivar-group)	gi21741799		8.70E-22
292	G1825	<i>Mesembryanthemum crystallinum</i>	gi6942190		2.50E-18
292	G1825	<i>Nicotiana tabacum</i>	gi4519671		1.10E-16
292	G1825	<i>Solanum bulbocastanum</i>	gi32470629		2.20E-16
292	G1825	<i>Chlamydomonas reinhardtii</i>	gi5916207		4.80E-14
292	G1825	<i>Oryza sativa</i>	gi15289981		1.10E-08
292	G1825	<i>Zea mays</i>	gi14189890		5.10E-08
292	G1825	<i>Oryza glaberrima</i>	gi31338862		1.00E-06
292	G1825	<i>Oryza sativa</i> (indica cultivar-group)	gi31338860		1.40E-06
292	G1825	<i>Juglans nigra</i> x <i>Juglans regia</i>	gi20068283		0.13
294	G1832	<i>Brassica oleracea</i>	BZ063396		4.00E-42
294	G1832	<i>Lotus japonicus</i>	AP004945		2.00E-29
294	G1832	<i>Zea mays</i>	BZ413336		2.00E-24
294	G1832	<i>Petunia x hybrida</i>	AB000455		1.00E-23
294	G1832	<i>Oryza sativa</i> (japonica cultivar-group)	AP003988		8.00E-22
294	G1832	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01007143		7.00E-21
294	G1832	<i>Vitis vinifera</i>	CD010326		2.00E-17
294	G1832	<i>Oryza sativa</i>	OSJN00060		2.00E-16
294	G1832	<i>Theilungiella halophila</i>	BM985806		7.00E-16
294	G1832	<i>Glycine max</i>	GMU68763		3.00E-15
294	G1832	<i>Petunia x hybrida</i>	gi1786142		1.30E-31

294	G1832	<i>Brassica rapa</i>	gi2058504		7.00E-20
294	G1832	<i>Oryza sativa</i> (japonica cultivar-group)	gi21740840		2.10E-19
294	G1832	<i>Glycine max</i>	gi1763063		7.50E-16
294	G1832	<i>Medicago sativa</i>	gi7228329		1.80E-14
294	G1832	<i>Datisca glomerata</i>	gi4666360		3.10E-13
294	G1832	<i>Nicotiana tabacum</i>	gi2981169		4.70E-12
294	G1832	<i>Triticum aestivum</i>	gi485814		7.00E-12
294	G1832	<i>Oryza sativa</i>	gi12698882		1.20E-11
294	G1832	<i>Pisum sativum</i>	gi2129892		4.00E-09
296	G1837	<i>Brassica oleracea</i>	BH675531		5.00E-59
296	G1837	<i>Oryza sativa</i> (japonica cultivar-group)	AK100643		4.00E-34
296	G1837	<i>Populus tremuloides</i>	CA925570		1.00E-30
296	G1837	<i>Oryza sativa</i>	AP003238		7.00E-30
296	G1837	<i>Gossypium hirsutum</i>	AY125487		7.00E-27
296	G1837	<i>Ipomoea batatas</i>	CB329929		1.00E-26
296	G1837	<i>Helianthus annuus</i>	BU026443		6.00E-26
296	G1837	<i>Lactuca sativa</i>	BU007581		7.00E-26
296	G1837	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	CA030236		4.00E-25
296	G1837	<i>Hordeum vulgare</i>	BQ470403		3.00E-24
296	G1837	<i>Oryza sativa</i> (japonica cultivar-group)	gi20146230		2.20E-36
296	G1837	<i>Gossypium hirsutum</i>	gi22858664		2.40E-29
296	G1837	<i>Oryza sativa</i>	gi13124871		2.60E-29
296	G1837	<i>Marsilea quadrifolia</i>	gi22550110		1.30E-11
296	G1837	<i>Lycopersicon esculentum</i>	gi15144510		0.00029
296	G1837	<i>Zea mays</i>	gi18568274		0.013
296	G1837	<i>Nicotiana tabacum</i>	gi14423763		0.016
296	G1837	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152975		0.024
296	G1837	<i>Cucurbita maxima</i>	gi17221648		0.07
296	G1837	<i>Nicotiana glauca</i>	gi7649694		0.089
297	G1840	<i>Triticum aestivum</i>	Ta_S359268	1884	
298	G1840	<i>Brassica oleracea</i>	BH560552		2.00E-47
298	G1840	<i>Medicago truncatula</i>	AW559374		2.00E-19
298	G1840	<i>Vitis vinifera</i>	CB003361		3.00E-19
298	G1840	<i>Vitis aestivalis</i>	CB289747		9.00E-19
298	G1840	<i>Glycine max</i>	AW152963		1.00E-17
298	G1840	<i>Zea mays</i>	CC729672		3.00E-15
298	G1840	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01012262		4.00E-15
298	G1840	<i>Oryza sativa</i> (japonica cultivar-group)	AP004399		4.00E-15
298	G1840	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BU998389		4.00E-14

298	G1840	<i>Hordeum vulgare</i>	BQ469024		9.00E-14
298	G1840	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi20160854		6.80E-14
298	G1840	<i>Zea mays</i>	gi21908036		3.20E-13
298	G1840	<i>Lycopersicon</i> <i>esculentum</i>	gi18535580		2.40E-12
298	G1840	<i>Nicotiana tabacum</i>	gi10798644		1.00E-11
298	G1840	<i>Oryza sativa</i>	gi14018047		1.40E-11
298	G1840	<i>Solanum tuberosum</i>	gi28268684		1.60E-11
298	G1840	<i>Thellungiella</i> <i>halophila</i>	gi20340233		2.70E-11
298	G1840	<i>Narcissus</i> <i>pseudonarcissus</i>	gi18266198		4.40E-11
298	G1840	<i>Hordeum vulgare</i>	gi27960760		8.20E-11
298	G1840	<i>Fagus sylvatica</i>	gi18496063		1.10E-10
300	G1846	<i>Brassica oleracea</i>	BH486983		1.00E-68
300	G1846	<i>Vitis vinifera</i>	CB971990		4.00E-48
300	G1846	<i>Solanum tuberosum</i>	BG593364		3.00E-45
300	G1846	<i>Medicago</i> <i>truncatula</i>	AC137546		5.00E-43
300	G1846	<i>Glycine max</i>	BM271306		6.00E-43
300	G1846	<i>Vitis aestivalis</i>	CB288995		2.00E-42
300	G1846	<i>Lycopersicon</i> <i>esculentum</i>	AF500012		2.00E-39
300	G1846	<i>Beta vulgaris</i>	BQ594833		2.00E-39
300	G1846	<i>Lactuca sativa</i>	BQ988768		3.00E-39
300	G1846	<i>Oryza sativa</i>	AX653721		3.00E-34
300	G1846	<i>Lycopersicon</i> <i>esculentum</i>	gi25992102		1.40E-39
300	G1846	<i>Oryza sativa</i>	gi14140155		3.90E-35
300	G1846	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi21742358		9.30E-34
300	G1846	<i>Zea mays</i>	gi21908034		1.60E-31
300	G1846	<i>Brassica napus</i>	gi17352283		1.70E-25
300	G1846	<i>Nicotiana tabacum</i>	gi12003382		2.80E-25
300	G1846	<i>Prunus avium</i>	gi23495460		3.70E-23
300	G1846	<i>Hordeum vulgare</i>	gi19071243		2.00E-22
300	G1846	<i>Gossypium</i> <i>hirsutum</i>	gi32481079		2.30E-21
300	G1846	<i>Fagus sylvatica</i>	gi18496063		2.70E-19
302	G1850	<i>Lotus japonicus</i>	AP006148		6.00E-81
302	G1850	<i>Medicago</i> <i>truncatula</i>	BG646618		7.00E-76
302	G1850	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK106525		2.00E-75
302	G1850	<i>Glycine max</i>	GMHSF29		7.00E-68
302	G1850	<i>Phaseolus</i> <i>coccineus</i>	CA902448		4.00E-66
302	G1850	<i>Beta vulgaris</i>	BQ583051		6.00E-66
302	G1850	<i>Brassica napus</i>	CD814489		4.00E-64
302	G1850	<i>Citrus sinensis</i>	CB292708		9.00E-62
302	G1850	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01022757		1.00E-60

302	G1850	<i>Triticum aestivum</i>	CD894087		1.00E-55
302	G1850	<i>Glycine max</i>	gi2129829		2.10E-66
302	G1850	<i>Lycopersicon peruvianum</i>	gi100267		1.50E-49
302	G1850	<i>Nicotiana tabacum</i>	gi5821136		1.10E-48
302	G1850	<i>Oryza sativa</i> (japonica cultivar-group)	gi32482876		4.60E-48
302	G1850	<i>Oryza sativa</i>	gi16580739		1.60E-42
302	G1850	<i>Lycopersicon esculentum</i>	gi100225		9.00E-38
302	G1850	<i>Helianthus annuus</i>	gi25052685		7.80E-35
302	G1850	<i>Zea mays</i>	gi2130134		1.40E-33
302	G1850	<i>Phaseolus acutifolius</i>	gi16118447		1.80E-33
302	G1850	<i>Medicago sativa</i>	gi20162459		8.50E-32
304	G1863	<i>Brassica oleracea</i>	BH582941		5.00E-61
304	G1863	<i>Oryza sativa</i>	AF201895		2.00E-34
304	G1863	<i>Solanum tuberosum</i>	BM404872		3.00E-34
304	G1863	<i>Medicago truncatula</i>	AW981431		1.00E-33
304	G1863	<i>Glycine max</i>	BI786182		1.00E-33
304	G1863	<i>Oryza sativa</i> (japonica cultivar-group)	AK103508		2.00E-33
304	G1863	<i>Lactuca sativa</i>	BQ852906		4.00E-33
304	G1863	<i>Lycopersicon esculentum</i>	AW442227		2.00E-32
304	G1863	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	CA029723		4.00E-32
304	G1863	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01004865		1.00E-31
304	G1863	<i>Oryza sativa</i> (japonica cultivar-group)	gi32492205		1.90E-43
304	G1863	<i>Oryza sativa</i>	gi6573149		2.40E-39
304	G1863	<i>Solanum bulbocastanum</i>	gi32470630		3.90E-39
304	G1863	<i>Sorghum bicolor</i>	gi18390099		1.50E-37
304	G1863	<i>Lycopersicon esculentum</i>	gi19171209		0.15
304	G1863	<i>Pisum sativum</i>	gi7008009		0.75
304	G1863	<i>Zea mays</i>	gi1061308		0.85
304	G1863	<i>Glycine max</i>	gi2129829		0.98
304	G1863	<i>Oryza sativa</i> (indica cultivar-group)	gi4680184		0.99
304	G1863	<i>Brassica rapa</i>	gi12655953		1
305	G1893	<i>Glycine max</i>	AW278047.1	1068	
305	G1893	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER111370 1	1069	
305	G1893	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER118579 1	1070	
305	G1893	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER118579 2	1071	
305	G1893	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER149196 1	1072	
305	G1893	<i>Oryza sativa</i>	LIB4309-019-R1-N1-A5	1073	

305	G1893	<i>Oryza sativa</i>	OSC101916.C1.p4.fg	1074	
305	G1893	<i>Oryza sativa</i>	OSC102096.C1.p3.fg	1075	
305	G1893	<i>Oryza sativa</i>	OSC22542.C1.p1.fg	1076	
305	G1893	<i>Oryza sativa</i>	OSC25365.C1.p1.fg	1077	
305	G1893	<i>Oryza sativa</i>	OSC33187.C1.p5.fg	1078	
305	G1893	<i>Oryza sativa</i>	OSC5704.C1.p2.fg	1079	
305	G1893	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER288538_1	1080	
305	G1893	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER344060_1	1081	
305	G1893	<i>Glycine max</i>	Gma_S5146217	1664	
305	G1893	<i>Zea mays</i>	Zm_S11445592	1806	
305	G1893	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-43508	2037	
306	G1893	<i>Oryza sativa</i> (japonica cultivar- group)	AK071104		1.00E-97
306	G1893	<i>Medicago truncatula</i>	CA921097		4.00E-90
306	G1893	<i>Helianthus annuus</i>	CD849311		8.00E-90
306	G1893	<i>Glycine max</i>	BU547066		9.00E-89
306	G1893	<i>Gossypium arboreum</i>	BQ415977		8.00E-87
306	G1893	<i>Populus tremula x Populus tremuloides</i>	BU825617		2.00E-85
306	G1893	<i>Triticum turgidum</i>	BF293596		7.00E-83
306	G1893	<i>Eschscholzia californica</i>	CD476634		7.00E-80
306	G1893	<i>Brassica oleracea</i>	BH503569		1.00E-79
306	G1893	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01004319		5.00E-71
306	G1893	<i>Oryza sativa</i>	gi15290024		2.20E-78
306	G1893	<i>Oryza sativa</i> (japonica cultivar- group)	gi20161636		2.20E-78
306	G1893	<i>Glycine max</i>	gi18376601		1.30E-76
306	G1893	<i>Lycopersicon esculentum</i>	gi15984226		2.80E-25
306	G1893	<i>Solanum tuberosum</i>	gi563623		1.90E-14
306	G1893	<i>Zea mays</i>	gi3170601		3.40E-13
306	G1893	<i>Nicotiana tabacum</i>	gi4519673		0.31
306	G1893	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi29569129		0.79
306	G1893	<i>Chloroplast Fagopyrum sp. C97106</i>	gi13366059		0.94
306	G1893	<i>Pisum sativum</i>	gi2129892		0.97
308	G1917	<i>Brassica oleracea</i>	BH700529		1.00E-76
308	G1917	<i>Gossypium arboreum</i>	BG440881		4.00E-53
308	G1917	<i>Brassica napus</i>	CD838237		6.00E-45
308	G1917	<i>Glycine max</i>	AW569177		2.00E-32
308	G1917	<i>Medicago truncatula</i>	BE240450		7.00E-28
308	G1917	<i>Oryza sativa</i> (japonica cultivar- group)	AK073464		7.00E-25

308	G1917	<i>Vitis vinifera</i>	CD009085		1.00E-20
308	G1917	<i>Oryza sativa</i> (indica cultivar-group)	AAAAA01000157		6.00E-19
308	G1917	<i>Oryza sativa</i>	10A19I		6.00E-19
308	G1917	<i>Physcomitrella patens</i>	AW497013		4.00E-12
308	G1917	<i>Oryza sativa</i> (japonica cultivar-group)	gi20521225		1.90E-26
308	G1917	<i>Oryza sativa</i>	gi5091599		1.30E-13
308	G1917	<i>Nicotiana tabacum</i>	gi12711287		3.20E-07
308	G1917	<i>Nicotiana glauca</i>	gi1076609		7.00E-05
308	G1917	<i>Pisum sativum</i>	gi7008009		0.0064
308	G1917	<i>Glycine max</i>	gi913654		0.018
308	G1917	<i>Medicago sativa</i>	gi166376		0.022
308	G1917	<i>Cicer arietinum</i>	gi3893085		0.061
308	G1917	<i>Silene latifolia</i>	gi1628463		0.075
308	G1917	<i>Lycopersicon esculentum</i>	gi19322		0.083
310	G1923	<i>Medicago truncatula</i>	BF649854		5.00E-60
310	G1923	<i>Lycopersicon esculentum</i>	BI422020		3.00E-59
310	G1923	<i>Oryza sativa</i>	AX654704		7.00E-57
310	G1923	<i>Oryza sativa</i> (japonica cultivar-group)	AK073539		7.00E-57
310	G1923	<i>Phaseolus coccineus</i>	CA897028		9.00E-49
310	G1923	<i>Sorghum bicolor</i>	CB927306		1.00E-48
310	G1923	<i>Glycine max</i>	BU926268		3.00E-48
310	G1923	<i>Vitis vinifera</i>	CA810372		1.00E-42
310	G1923	<i>Zea mays</i>	CC629895		5.00E-42
310	G1923	<i>Brassica napus</i>	CD841307		2.00E-39
310	G1923	<i>Oryza sativa</i> (japonica cultivar-group)	gi20303588		3.50E-57
310	G1923	<i>Oryza sativa</i>	gi15528779		1.80E-39
310	G1923	<i>Brassica napus</i>	gi31322568		2.90E-39
310	G1923	<i>Phaseolus vulgaris</i>	gi15148914		1.80E-37
310	G1923	<i>Petunia x hybrida</i>	gi21105748		3.80E-37
310	G1923	<i>Solanum tuberosum</i>	gi14485513		6.10E-37
310	G1923	<i>Lycopersicon esculentum</i>	gi6175246		3.40E-36
310	G1923	<i>Glycine max</i>	gi22597158		9.00E-36
310	G1923	<i>Triticum sp.</i>	gi4218537		1.00E-34
310	G1923	<i>Triticum monococcum</i>	gi6732160		1.00E-34
311	G1928	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER1575_1	1082	
311	G1928	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER1575_2	1083	
311	G1928	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER37555_1	1084	
311	G1928	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER2748_3	1085	

311	G1928	<i>Oryza sativa</i>	OSC18621.C1.p15.fg	1086	
311	G1928	<i>Oryza sativa</i>	OSC8169.C1.p1.fg	1087	
311	G1928	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER31066 1	1088	
311	G1928	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER483 4	1089	
311	G1928	<i>Glycine max</i>	Gma_S4880916	1665	
311	G1928	<i>Medicago truncatula</i>	Mtr_S5366182	1704	
311	G1928	<i>Hordeum vulgare</i>	Hv_S151736	1739	
311	G1928	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-47862	2038	
311	G1928	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-48122	2039	
311	G1928	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-54189	2040	
311	G1928	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-14800	2041	
311	G1928	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-332512	2042	
312	G1928	<i>Brassica napus</i>	BQ704702		1.00E-125
312	G1928	<i>Oryza sativa</i> (japonica cultivar-group)	AK105663		1.00E-107
312	G1928	<i>Solanum tuberosum</i>	STPCP1		1.00E-104
312	G1928	<i>Lycopersicon esculentum</i>	BI932742		1.00E-96
312	G1928	<i>Triticum aestivum</i>	BT009453		1.00E-91
312	G1928	<i>Brassica oleracea</i>	BH958905		6.00E-88
312	G1928	<i>Oryza sativa</i>	AX699673		5.00E-86
312	G1928	<i>Medicago truncatula</i>	BG645203		2.00E-85
312	G1928	<i>Prunus persica</i>	BU039744		2.00E-84
312	G1928	<i>Glycine max</i>	CA938031		6.00E-83
312	G1928	<i>Oryza sativa</i>	gi10934090		2.40E-108
312	G1928	<i>Solanum tuberosum</i>	gi563623		6.70E-95
312	G1928	<i>Oryza sativa</i> (japonica cultivar-group)	gi20160482		1.00E-84
312	G1928	<i>Lycopersicon esculentum</i>	gi9858780		1.70E-82
312	G1928	<i>Zea mays</i>	gi3170601		4.20E-78
312	G1928	<i>Glycine max</i>	gi18376601		6.60E-18
312	G1928	<i>Capsella rubella</i>	gi32454266		3.60E-06
312	G1928	<i>Chlamydomonas reinhardtii</i>	gi16209575		5.50E-06
312	G1928	<i>Petunia x hybrida</i>	gi2346972		0.0062
312	G1928	<i>Nicotiana tabacum</i>	gi100367		0.076
314	G1932	<i>Brassica oleracea</i>	BZ451301		2.00E-45
314	G1932	<i>Populus tremula x Populus tremuloides</i>	BU831322		3.00E-43
314	G1932	<i>Prunus persica</i>	BU044042		3.00E-39
314	G1932	<i>Lotus corniculatus</i> var. japonicus	AP006411		2.00E-37
314	G1932	<i>Medicago truncatula</i>	CF069961		1.00E-35
314	G1932	<i>Populus</i>	CA825154		3.00E-32

		<i>balsamifera</i> subsp. <i>trichocarpa</i> x <i>Populus deltoides</i>			
314	G1932	<i>Helianthus annuus</i>	AJ412445		5.00E-31
314	G1932	<i>Lotus japonicus</i>	AV422273		3.00E-30
314	G1932	<i>Glycine max</i>	BM732568		4.00E-30
314	G1932	<i>Lactuca sativa</i>	BQ873409		8.00E-29
314	G1932	<i>Stylosanthes hamata</i>	gi4099921		5.70E-33
314	G1932	<i>Nicotiana tabacum</i>	gi1208496		2.80E-29
314	G1932	<i>Lycopersicon esculentum</i>	gi30526297		5.70E-29
314	G1932	<i>Nicotiana sylvestris</i>	gi8809573		6.40E-28
314	G1932	<i>Oryza sativa</i>	gi10567106		2.10E-27
314	G1932	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi20160965		2.10E-27
314	G1932	<i>Thellungiella halophila</i>	gi20340233		5.60E-27
314	G1932	<i>Solanum tuberosum</i>	gi28268684		9.30E-22
314	G1932	<i>Zea mays</i>	gi27802487		1.30E-20
314	G1932	<i>Prunus armeniaca</i>	gi3264767		3.40E-20
316	G1938	<i>Brassica oleracea</i>	BH464032		1.00E-76
316	G1938	<i>Vitis vinifera</i>	CB972449		6.00E-67
316	G1938	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AP004672		3.00E-52
316	G1938	<i>Medicago truncatula</i>	BF642346		2.00E-47
316	G1938	<i>Lactuca sativa</i>	BQ874162		8.00E-45
316	G1938	<i>Solanum tuberosum</i>	BQ507674		3.00E-43
316	G1938	<i>Glycine max</i>	CA937850		1.00E-42
316	G1938	<i>Zea mays</i>	AX540653		5.00E-42
316	G1938	<i>Beta vulgaris</i>	BQ588349		4.00E-33
316	G1938	<i>Gossypium arboreum</i>	BG445379		7.00E-33
316	G1938	<i>Gossypium hirsutum</i>	gi5731257		3.20E-32
316	G1938	<i>Oryza sativa</i>	gi2580440		2.00E-29
316	G1938	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi20975251		2.60E-29
316	G1938	<i>Sophora flavescens</i>	gi21624283		2.20E-05
316	G1938	<i>Pueraria montana</i> var. <i>lobata</i>	gi21624275		0.0003
316	G1938	<i>Bothriochloa odorata</i>	gi13649873		0.00045
316	G1938	<i>Capillipedium parviflorum</i>	gi13649864		0.00058
316	G1938	<i>Linaria vulgaris</i>	gi29788713		0.00059
316	G1938	<i>Antirrhinum cornutum</i>	gi31296478		0.0013
316	G1938	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	gi12061239		0.0016
318	G1945	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BG543096		2.00E-85
318	G1945	<i>Pisum sativum</i>	CD860359		9.00E-69

318	G1945	<i>Brassica oleracea</i>	BH480897		1.00E-66
318	G1945	<i>Glycine max</i>	CD397129		4.00E-66
318	G1945	<i>Medicago truncatula</i>	BG647027		4.00E-66
318	G1945	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01000383		7.00E-56
318	G1945	<i>Oryza sativa</i> (japonica cultivar-group)	AP005755		9.00E-56
318	G1945	<i>Helianthus annuus</i>	BU023570		3.00E-52
318	G1945	<i>Zea mays</i>	BZ412041		7.00E-51
318	G1945	<i>Oryza sativa</i>	AP004020		2.00E-48
318	G1945	<i>Oryza sativa</i> (japonica cultivar-group)	gi32489626		1.60E-47
318	G1945	<i>Antirrhinum majus</i>	gi4165183		1.20E-21
318	G1945	<i>Pisum sativum</i>	gi2213534		2.20E-14
318	G1945	<i>Helianthus hirsutus</i>	gi27526446		0.091
318	G1945	<i>Helianthus tuberosus</i>	gi27526452		0.12
318	G1945	<i>Helianthus niveus</i>	gi27526450		0.12
318	G1945	<i>Helianthus ciliaris</i>	gi14588999		0.2
318	G1945	<i>Helianthus praecox</i>	gi18073228		0.25
318	G1945	<i>Helianthus debilis</i>	gi27526440		0.46
318	G1945	<i>Lycopersicon esculentum</i>	gi1345538		0.46
320	G1957	<i>Brassica oleracea</i>	BZ468915		1.00E-101
320	G1957	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01011764		1.00E-55
320	G1957	<i>Oryza sativa</i>	AX654655		2.00E-55
320	G1957	<i>Oryza sativa</i> (japonica cultivar-group)	AK106367		4.00E-55
320	G1957	<i>Lactuca sativa</i>	BU005803		1.00E-52
320	G1957	<i>Lycopersicon esculentum</i>	BI934637		4.00E-50
320	G1957	<i>Glycine max</i>	AW760132		1.00E-49
320	G1957	<i>Zea mays</i>	CC648948		4.00E-48
320	G1957	<i>Solanum tuberosum</i>	BQ119486		2.00E-45
320	G1957	<i>Prunus dulcis</i>	BU645464		3.00E-39
320	G1957	<i>Oryza sativa</i> (japonica cultivar-group)	gi21426118		1.40E-55
320	G1957	<i>Marchantia polymorpha</i>	gi25272004		1.30E-35
320	G1957	<i>Oryza sativa</i>	gi19352051		2.40E-10
320	G1957	<i>Pisum sativum</i>	gi22335711		3.90E-08
320	G1957	<i>Eragrostis tef</i>	gi17906977		1.10E-07
320	G1957	<i>Mangifera indica</i>	gi31747324		1.60E-07
320	G1957	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi1730475		3.10E-07
320	G1957	<i>Phaseolus vulgaris</i>	gi1046278		3.10E-07
320	G1957	<i>Prunus persica</i>	gi27450533		3.30E-07
320	G1957	<i>Daucus carota</i>	gi5578746		1.20E-06
321	G1968	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER38154_1	1090	

321	G1968	<i>Glycine max</i>	uC-gmflminsoy034g08b1	1091	
321	G1968	<i>Oryza sativa</i>	OSC102229.C1.p13.fg	1092	
321	G1968	<i>Oryza sativa</i>	OSC27802.C1.p1.fg	1093	
321	G1968	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-336915	2043	
322	G1968	<i>Brassica oleracea</i>	BH950957		9.00E-85
322	G1968	<i>Petunia x hybrida</i>	AB003672		2.00E-69
322	G1968	<i>Limnanthes alba</i>	BV007314		7.00E-32
322	G1968	<i>Medicago truncatula</i>	CB892199		2.00E-18
322	G1968	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01000555		7.00E-16
322	G1968	<i>Oryza sativa</i>	AP003840		1.00E-15
322	G1968	<i>Triticum aestivum</i>	CA596598		1.00E-14
322	G1968	<i>Solanum tuberosum</i>	BG096505		3.00E-14
322	G1968	<i>Sorghum bicolor</i>	BZ628830		2.00E-12
322	G1968	<i>Zea mays</i>	CC642714		2.00E-12
322	G1968	<i>Petunia x hybrida</i>	gi1786146		9.60E-58
322	G1968	<i>Oryza sativa (japonica cultivar- group)</i>	gi22775640		2.30E-19
322	G1968	<i>Pisum sativum</i>	gi2129892		3.00E-09
322	G1968	<i>Glycine max</i>	gi1763063		5.80E-09
322	G1968	<i>Medicago sativa</i>	gi7228329		1.50E-08
322	G1968	<i>Brassica rapa</i>	gi2058504		1.60E-07
322	G1968	<i>Oryza sativa</i>	gi15623826		1.40E-06
322	G1968	<i>Datisca glomerata</i>	gi4666360		2.40E-05
322	G1968	<i>Triticum aestivum</i>	gi485814		9.80E-05
322	G1968	<i>Nicotiana tabacum</i>	gi2981169		0.012
323	G1983	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER30038_1	1094	
323	G1983	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER30038_2	1095	
323	G1983	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER10519_1	1096	
323	G1983	<i>Oryza sativa</i>	Os_S120617	1595	
323	G1983	<i>Oryza sativa</i>	Os_S16654	1596	
323	G1983	<i>Oryza sativa</i>	Os_S44308	1597	
323	G1983	<i>Oryza sativa</i>	Os_S71743	1598	
323	G1983	<i>Oryza sativa</i>	Os_S75089	1599	
323	G1983	<i>Oryza sativa</i>	Os_S77891	1600	
323	G1983	<i>Zea mays</i>	Zm_S11326674	1807	
323	G1983	<i>Zea mays</i>	Zm_S11446637	1808	
323	G1983	<i>Zea mays</i>	Zm_S11525047	1809	
323	G1983	<i>Triticum aestivum</i>	Ta_S119681	1885	
323	G1983	<i>Triticum aestivum</i>	Ta_S137934	1886	
323	G1983	<i>Triticum aestivum</i>	Ta_S142014	1887	
323	G1983	<i>Triticum aestivum</i>	Ta_S142165	1888	
323	G1983	<i>Triticum aestivum</i>	Ta_S143760	1889	
323	G1983	<i>Triticum aestivum</i>	Ta_S147217	1890	
323	G1983	<i>Triticum aestivum</i>	Ta_S147350	1891	
323	G1983	<i>Triticum aestivum</i>	Ta_S383385	1892	
323	G1983	<i>Triticum aestivum</i>	Ta_S412629	1893	
323	G1983	<i>Triticum aestivum</i>	Ta_S66264	1894	
323	G1983	<i>Triticum aestivum</i>	Ta_S75983	1895	

323	G1983	<i>Triticum aestivum</i>	Ta_S78150	1896	
323	G1983	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-21519	2044	
324	G1983	<i>Brassica oleracea</i>	BZ436393		1.00E-120
324	G1983	<i>Brassica napus</i>	CD837762		1.00E-113
324	G1983	<i>Lactuca sativa</i>	BQ850782		8.00E-64
324	G1983	<i>Solanum tuberosum</i>	BG599598		5.00E-61
324	G1983	<i>Populus tremula x Populus tremuloides</i>	BU866147		2.00E-60
324	G1983	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01006041		5.00E-58
324	G1983	<i>Oryza sativa</i>	AP002746		2.00E-56
324	G1983	<i>Oryza sativa (japonica cultivar- group)</i>	AK106392		2.00E-56
324	G1983	<i>Glycine max</i>	AW568218		2.00E-56
324	G1983	<i>Medicago truncatula</i>	AC144766		3.00E-54
324	G1983	<i>Oryza sativa</i>	gi9988428		2.20E-55
324	G1983	<i>Oryza sativa (japonica cultivar- group)</i>	gi28273376		1.40E-51
324	G1983	<i>Brassica oleracea</i>	gi15054380		0.00024
324	G1983	<i>Glycine max</i>	gi18736		0.021
324	G1983	<i>Pinus pinaster</i>	gi18129298		0.49
324	G1983	<i>Atropa belladonna</i>	gi14329820		0.58
324	G1983	<i>Pisum sativum</i>	gi31580860		0.58
324	G1983	<i>Pyrus communis</i>	gi559557		0.78
324	G1983	<i>Zea mays</i>	gi4321762		0.81
324	G1983	<i>Gossypioideis kirkii</i>	gi29836513		0.84
325	G1985	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER65388_1	1097	
326	G1985	<i>Medicago truncatula</i>	BE124794		3.00E-13
326	G1985	<i>Lotus japonicus</i>	AP006103		5.00E-12
326	G1985	<i>Lotus corniculatus var. japonicus</i>	CB826842		3.00E-11
326	G1985	<i>Brassica oleracea</i>	BH732988		3.00E-11
326	G1985	<i>Brassica rapa subsp. pekinensis</i>	BZ614339		5.00E-10
326	G1985	<i>Petunia x hybrida</i>	AB035093		1.00E-09
326	G1985	<i>Glycine max</i>	AI973860		1.00E-09
326	G1985	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01001411		3.00E-09
326	G1985	<i>Oryza sativa (japonica cultivar- group)</i>	AP005869		3.00E-09
326	G1985	<i>Zea mays</i>	CC652748		4.00E-09
326	G1985	<i>Petunia x hybrida</i>	gi14275902		1.60E-15
326	G1985	<i>Oryza sativa (japonica cultivar- group)</i>	gi32489630		6.50E-13
326	G1985	<i>Zea ramosa</i>	gi18674684		2.90E-11
326	G1985	<i>Oryza sativa</i>	gi15528588		2.70E-05
326	G1985	<i>Sorghum bicolor</i>	gi18390109		0.00088
326	G1985	<i>Brassica rapa</i>	gi2058504		0.001

326	G1985	<i>Pisum sativum</i>	gi2129892		0.0076
326	G1985	<i>Datisca glomerata</i>	gi4666360		0.051
326	G1985	<i>Nicotiana tabacum</i>	gi2981169		0.053
326	G1985	<i>Medicago sativa</i>	gi7228329		0.07
327	G1988	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER75453 1	1098	
327	G1988	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER75453 2	1099	
327	G1988	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER153439 2	1100	
327	G1988	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER10890 1	1101	
327	G1988	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER10890 3	1102	
327	G1988	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER201962 1	1103	
327	G1988	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER3040 3	1104	
327	G1988	<i>Oryza sativa</i>	Os_S91481	1601	
327	G1988	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-5090	2045	
328	G1988	<i>Brassica oleracea</i>	BH478747		5.00E-23
328	G1988	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU873581		7.00E-22
328	G1988	<i>Citrus unshiu</i>	C95300		2.00E-18
328	G1988	<i>Lycopersicon esculentum</i>	AW034552		2.00E-18
328	G1988	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01000340		1.00E-17
328	G1988	<i>Beta vulgaris</i>	BQ594583		1.00E-16
328	G1988	<i>Zea mays</i>	CC655765		2.00E-15
328	G1988	<i>Glycine max</i>	BI469275		8.00E-15
328	G1988	<i>Prunus persica</i>	BU046688		7.00E-14
328	G1988	<i>Vitis vinifera</i>	CD719941		2.00E-13
328	G1988	<i>Malus x domestica</i>	gi4091806		2.60E-07
328	G1988	<i>Brassica napus</i>	gi30984027		1.10E-06
328	G1988	<i>Brassica nigra</i>	gi22854920		1.10E-06
328	G1988	<i>Raphanus sativus</i>	gi3341723		2.70E-06
328	G1988	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi32488104		4.80E-06
328	G1988	<i>Ipomoea nil</i>	gi10946337		5.10E-06
328	G1988	<i>Oryza sativa</i>	gi11094211		2.20E-05
328	G1988	<i>Hordeum vulgare</i>	gi21667475		4.50E-05
328	G1988	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi21655168		0.00018
328	G1988	<i>Pinus radiata</i>	gi4557093		0.0016
330	G1990	<i>Brassica oleracea</i>	BH009262		2.00E-99
330	G1990	<i>Petunia x hybrida</i>	AB000452		9.00E-44
330	G1990	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU879483		1.00E-42
330	G1990	<i>Lotus japonicus</i>	AP004479		4.00E-39
330	G1990	<i>Medicago truncatula</i>	AC126007		7.00E-35
330	G1990	<i>Oryza sativa</i>	AP003989		2.00E-32

330	G1990	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01004471		2.00E-32
330	G1990	<i>Ipomoea nil</i>	BJ573446		6.00E-32
330	G1990	<i>Pisum sativum</i>	PSZINCFIN		1.00E-31
330	G1990	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU887507		3.00E-31
330	G1990	<i>Pisum sativum</i>	gi2129892		3.90E-42
330	G1990	<i>Petunia x hybrida</i>	gi100396		1.30E-40
330	G1990	<i>Oryza sativa</i> (japonica cultivar-group)	gi32480087		1.40E-23
330	G1990	<i>Oryza sativa</i>	gi15623820		1.10E-18
330	G1990	<i>Triticum aestivum</i>	gi485814		2.30E-18
330	G1990	<i>Brassica rapa</i>	gi2058506		2.50E-15
330	G1990	<i>Glycine max</i>	gi1763063		3.30E-14
330	G1990	<i>Datisca glomerata</i>	gi4666360		1.80E-08
330	G1990	<i>Medicago sativa</i>	gi7228329		2.20E-06
330	G1990	<i>Nicotiana tabacum</i>	gi2981169		1.40E-05
332	G1993	<i>Lotus japonicus</i>	AP006103		7.00E-12
332	G1993	<i>Medicago truncatula</i>	CF069502		1.00E-11
332	G1993	<i>Lotus corniculatus</i> var. <i>japonicus</i>	CB826842		3.00E-11
332	G1993	<i>Petunia x hybrida</i>	AB035093		6.00E-10
332	G1993	<i>Brassica oleracea</i>	BH732988		6.00E-10
332	G1993	<i>Glycine max</i>	AI973860		1.00E-09
332	G1993	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BZ614339		7.00E-09
332	G1993	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01001411		3.00E-08
332	G1993	<i>Oryza sativa</i> (japonica cultivar-group)	AP005869		3.00E-08
332	G1993	<i>Zea mays</i>	BZ735433		5.00E-08
332	G1993	<i>Petunia x hybrida</i>	gi14275902		4.30E-15
332	G1993	<i>Oryza sativa</i> (japonica cultivar-group)	gi27261062		8.20E-13
332	G1993	<i>Zea ramosa</i>	gi18674684		6.00E-11
332	G1993	<i>Oryza sativa</i>	gi15528588		3.50E-08
332	G1993	<i>Sorghum bicolor</i>	gi18390109		8.80E-06
332	G1993	<i>Brassica rapa</i>	gi2058504		0.0056
332	G1993	<i>Medicago sativa</i>	gi7228329		0.084
332	G1993	<i>Datisca glomerata</i>	gi4666360		0.12
332	G1993	<i>Nicotiana tabacum</i>	gi2981169		0.14
332	G1993	<i>Pisum sativum</i>	gi2129892		0.38
333	G1995	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER166362_1	753	
333	G1995	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER180202_1	754	
333	G1995	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER726571_1	755	
333	G1995	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER74662_1	756	
333	G1995	<i>Glycine max</i>	uC-gmflminsoy032f06b1	757	
333	G1995	<i>Oryza sativa</i>	ORYSA-22JAN02-	759	

			CLUSTER200967_1		
333	G1995	<i>Oryza sativa</i>	OSC100895.C1.p14.fg	760	
333	G1995	<i>Oryza sativa</i>	OSC23411.C1.p1.fg	761	
333	G1995	<i>Oryza sativa</i>	OSC2409.C1.p2.fg	762	
333	G1995	<i>Oryza sativa</i>	OSC25680.C1.p1.fg	763	
333	G1995	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER436044_1	764	
333	G1995	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER518126_1	765	
333	G1995	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-54039	1959	
333	G1995	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-54252	1960	
333	G1995	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-392715	1961	
334	G1995	<i>Brassica oleracea</i>	BZ475765		1.00E-68
334	G1995	<i>Lycopersicon esculentum</i>	BG123251		3.00E-30
334	G1995	<i>Vitis vinifera</i>	CD716644		1.00E-29
334	G1995	<i>Gossypium arboreum</i>	BF272143		2.00E-27
334	G1995	<i>Oryza sativa</i> (japonica cultivar- group)	AP005538		4.00E-24
334	G1995	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01009505		9.00E-23
334	G1995	<i>Oryza sativa</i>	AC105732		1.00E-18
334	G1995	<i>Zea mays</i>	BH875187		2.00E-18
334	G1995	<i>Hordeum vulgare</i>	BF616974		3.00E-18
334	G1995	<i>Sorghum bicolor</i>	BE360413		4.00E-17
334	G1995	<i>Sorghum bicolor</i>	gi18390109		4.30E-20
334	G1995	<i>Oryza sativa</i>	gi15528588		5.80E-08
334	G1995	<i>Oryza sativa</i> (japonica cultivar- group)	gi32482926		1.90E-07
334	G1995	<i>Petunia x hybrida</i>	gi2346976		1.30E-05
334	G1995	<i>Glycine max</i>	gi1763063		0.0043
334	G1995	<i>Medicago sativa</i>	gi7228329		0.007
334	G1995	<i>Zea mays</i>	gi18674684		0.0093
334	G1995	<i>Datisca glomerata</i>	gi4666360		0.082
334	G1995	<i>Brassica rapa</i>	gi2058506		0.098
334	G1995	<i>Triticum aestivum</i>	gi485814		0.24
336	G1998	<i>Oryza sativa</i> (japonica cultivar- group)	AK071630		3.00E-53
336	G1998	<i>Oryza sativa</i>	AB001888		3.00E-53
336	G1998	<i>Triticum aestivum</i>	BJ209915		1.00E-30
336	G1998	<i>Hordeum vulgare</i>	BE558327		4.00E-30
336	G1998	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01003074		2.00E-29
336	G1998	<i>Zea mays</i>	BZ985999		4.00E-29
336	G1998	<i>Oryza minuta</i>	CB210857		1.00E-28
336	G1998	<i>Lactuca sativa</i>	BU009733		3.00E-28
336	G1998	<i>Medicago truncatula</i>	BG644908		1.00E-27
336	G1998	<i>Solanum tuberosum</i>	BQ121038		5.00E-27

336	G1998	<i>Oryza sativa</i>	gi3618320		9.60E-58
336	G1998	<i>Brassica nigra</i>	gi22854986		1.70E-25
336	G1998	<i>Raphanus sativus</i>	gi3341723		1.00E-23
336	G1998	<i>Ipomoea nil</i>	gi10946337		1.00E-23
336	G1998	<i>Malus x domestica</i>	gi4091806		1.20E-22
336	G1998	<i>Brassica napus</i>	gi2895184		2.80E-22
336	G1998	<i>Oryza sativa</i> (japonica cultivar-group)	gi23589949		1.20E-21
336	G1998	<i>Hordeum vulgare</i>	gi21667475		1.80E-21
336	G1998	<i>Pinus radiata</i>	gi4557093		2.50E-20
336	G1998	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi21655154		1.60E-18
338	G1999	<i>Medicago truncatula</i>	BE316747		3.00E-22
338	G1999	<i>Lactuca sativa</i>	BQ995915		1.00E-20
338	G1999	<i>Lycopersicon esculentum</i>	AI772841		5.00E-20
338	G1999	<i>Brassica oleracea</i>	BH927868		9.00E-20
338	G1999	<i>Mesembryanthemum crystallinum</i>	CA840421		2.00E-19
338	G1999	<i>Brassica napus</i>	A50832		2.00E-18
338	G1999	<i>Beta vulgaris</i>	BQ489587		1.00E-17
338	G1999	<i>Eschscholzia californica</i>	CD477071		2.00E-16
338	G1999	<i>Glycine max</i>	CD401749		1.00E-15
338	G1999	<i>Ipomoea nil</i>	BJ554943		3.00E-15
338	G1999	<i>Oryza sativa</i>	gi13702811		1.10E-27
338	G1999	<i>Malus x domestica</i>	gi4091806		2.10E-20
338	G1999	<i>Raphanus sativus</i>	gi3341723		4.80E-19
338	G1999	<i>Brassica nigra</i>	gi22854916		8.80E-18
338	G1999	<i>Oryza sativa</i> (japonica cultivar-group)	gi23589949		1.30E-17
338	G1999	<i>Brassica napus</i>	gi2895184		1.30E-17
338	G1999	<i>Hordeum vulgare</i>	gi21667471		2.70E-17
338	G1999	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi21655168		5.00E-17
338	G1999	<i>Pinus radiata</i>	gi4557093		6.00E-17
338	G1999	<i>Ipomoea nil</i>	gi10946337		2.80E-16
340	G2035	<i>Medicago truncatula</i>	AC140035		1.00E-115
340	G2035	<i>Brassica oleracea</i>	BZ428219		1.00E-106
340	G2035	<i>Oryza sativa</i> (japonica cultivar-group)	AK100495		1.00E-102
340	G2035	<i>Zea mays</i>	AX660947		1.00E-100
340	G2035	<i>Vitis vinifera</i>	CB979115		5.00E-96
340	G2035	<i>Oryza sativa</i>	AC084405		9.00E-95
340	G2035	<i>Glycine max</i>	AW186423		7.00E-92
340	G2035	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01010916		1.00E-89
340	G2035	<i>Lycopersicon esculentum</i>	BF113841		4.00E-82
340	G2035	<i>Lactuca sativa</i>	BQ865775		3.00E-81
340	G2035	<i>Oryza sativa</i>	gi24796797		4.60E-103

		(japonica cultivar-group)			
340	G2035	<i>Oryza sativa</i>	gi14140292		3.30E-09
340	G2035	<i>Populus tremula</i> x <i>Populus tremuloides</i>	gi9955730		4.10E-05
340	G2035	<i>Nicotiana paniculata</i>	gi5834502		5.20E-05
340	G2035	<i>Solanum tuberosum</i>	gi2225999		0.00011
340	G2035	<i>Samanea saman</i>	gi5081693		0.00029
340	G2035	<i>Chlamydomonas reinhardtii</i>	gi30025990		0.0011
340	G2035	<i>Vicia faba</i>	gi2293112		0.0045
340	G2035	<i>Triticum aestivum</i>	gi18616499		0.013
340	G2035	<i>Brassica napus</i>	gi22003730		0.022
341	G2041	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER244491_1	1105	
341	G2041	<i>Glycine max</i>	LIB4280-051-Q1-K1-E4	1106	
341	G2041	<i>Oryza sativa</i>	rsicem_7360.y1.abd	1107	
341	G2041	<i>Zea mays</i>	Zm_S11428605	1810	
341	G2041	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-47127	2046	
341	G2041	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-389924	2047	
342	G2041	<i>Glycine max</i>	AX196296		1.0e-999
342	G2041	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01023044		1.00E-161
342	G2041	<i>Oryza sativa</i> (japonica cultivar-group)	AP004333		1.00E-161
342	G2041	<i>Oryza sativa</i>	AC107085		8.00E-90
342	G2041	<i>Lotus corniculatus</i> var. <i>japonicus</i>	AP006426		7.00E-89
342	G2041	<i>Medicago truncatula</i>	BZ286591		9.00E-89
342	G2041	<i>Helianthus annuus</i>	CD853758		2.00E-88
342	G2041	<i>Lactuca sativa</i>	BQ853515		6.00E-87
342	G2041	<i>Capsicum annuum</i>	BM067036		3.00E-82
342	G2041	<i>Lycopersicon esculentum</i>	BI925244		8.00E-79
342	G2041	<i>Oryza sativa</i> (japonica cultivar-group)	gi33146888		1.50E-152
342	G2041	<i>Oryza sativa</i>	gi14140291		5.60E-34
342	G2041	<i>Zea mays</i>	gi18463957		1.50E-19
342	G2041	<i>Hordeum vulgare</i>	gi23193481		4.40E-08
342	G2041	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi23193479		1.40E-07
342	G2041	<i>Triticum monococcum</i>	gi23193487		2.60E-07
342	G2041	<i>Brassica napus</i>	gi4106378		0.12
342	G2041	<i>Medicago sativa</i>	gi1279563		1
342	G2041	<i>Nicotiana tabacum</i>	gi8096269		1
342	G2041	<i>Triticum aestivum</i>	gi32400814		1
343	G2051	<i>Medicago truncatula</i>	Mtr_S5387033	1705	
343	G2051	<i>Hordeum vulgare</i>	Hv_S171660	1740	
344	G2051	<i>Brassica oleracea</i>	BH456374		6.00E-78

344	G2051	<i>Petunia x hybrida</i>	AF509874		4.00E-69
344	G2051	<i>Lycopersicon esculentum</i>	AW222093		2.00E-57
344	G2051	<i>Oryza sativa</i>	AX654515		1.00E-51
344	G2051	<i>Medicago truncatula</i>	BQ165266		7.00E-51
344	G2051	<i>Sorghum bicolor</i>	BG933492		8.00E-50
344	G2051	<i>Oryza sativa (japonica cultivar- group)</i>	AK099540		5.00E-43
344	G2051	<i>Hordeum vulgare subsp. spontaneum</i>	BJ481205		5.00E-42
344	G2051	<i>Hordeum vulgare</i>	BQ469035		5.00E-42
344	G2051	<i>Hordeum vulgare subsp. vulgare</i>	BU967516		5.00E-42
344	G2051	<i>Petunia x hybrida</i>	gi21105751		9.50E-70
344	G2051	<i>Oryza sativa (japonica cultivar- group)</i>	gi19225018		3.40E-59
344	G2051	<i>Oryza sativa</i>	gi6730946		1.20E-45
344	G2051	<i>Brassica napus</i>	gi31322582		3.50E-41
344	G2051	<i>Lycopersicon esculentum</i>	gi6175246		8.40E-40
344	G2051	<i>Phaseolus vulgaris</i>	gi15148914		1.10E-39
344	G2051	<i>Solanum tuberosum</i>	gi14485513		3.30E-38
344	G2051	<i>Medicago truncatula</i>	gi7716952		3.30E-38
344	G2051	<i>Glycine max</i>	gi22597158		8.70E-38
344	G2051	<i>Triticum sp.</i>	gi4218537		8.70E-38
345	G2060	<i>Oryza sativa</i>	Os_S109370	1602	
345	G2060	<i>Medicago truncatula</i>	Mtr_S5408429	1706	
345	G2060	<i>Triticum aestivum</i>	Ta_S317703	1897	
346	G2060	<i>Oryza sativa</i>	AX653450		4.00E-49
346	G2060	<i>Brassica oleracea</i>	BH456149		7.00E-48
346	G2060	<i>Lycopersicon esculentum</i>	BI422854		1.00E-39
346	G2060	<i>Nicotiana tabacum</i>	AY220477		1.00E-36
346	G2060	<i>Citrus sinensis</i>	BQ625082		2.00E-35
346	G2060	<i>Lactuca sativa</i>	BQ870137		3.00E-35
346	G2060	<i>Hordeum vulgare</i>	BM370908		9.00E-35
346	G2060	<i>Medicago truncatula</i>	CB893379		2.00E-34
346	G2060	<i>Glycine max</i>	CA782643		8.00E-34
346	G2060	<i>Cryptomeria japonica</i>	AU083645		2.00E-33
346	G2060	<i>Oryza sativa</i>	gi11320830		2.60E-40
346	G2060	<i>Nicotiana tabacum</i>	gi30013667		5.30E-38
346	G2060	<i>Oryza sativa (japonica cultivar- group)</i>	gi20160973		2.10E-27
346	G2060	<i>Petroselinum crispum</i>	gi11493822		4.50E-21
346	G2060	<i>Avena fatua</i>	gi1159879		3.00E-19
346	G2060	<i>Oryza sativa (indica cultivar-group)</i>	gi23305051		2.60E-17
346	G2060	<i>Pimpinella</i>	gi3420906		2.60E-16

		<i>brachycarpa</i>			
346	G2060	<i>Avena sativa</i>	gi4894965		7.10E-16
346	G2060	<i>Ipomoea batatas</i>	gi1076685		1.20E-15
346	G2060	<i>Solanum tuberosum</i>	gi24745606		2.20E-15
348	G2063	<i>Brassica oleracea</i>	BH923036		3.00E-45
348	G2063	<i>Medicago truncatula</i>	AC139746		1.00E-18
348	G2063	<i>Lotus corniculatus</i> var. <i>japonicus</i>	AP006395		2.00E-18
348	G2063	<i>Gossypium arboreum</i>	BQ403135		2.00E-17
348	G2063	<i>Oryza sativa</i>	AP004093		4.00E-17
348	G2063	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AP004863		4.00E-17
348	G2063	<i>Lotus japonicus</i>	AP006142		5.00E-16
348	G2063	<i>Sorghum bicolor</i>	BZ627051		8.00E-16
348	G2063	<i>Zea mays</i>	CC690653		5.00E-15
348	G2063	<i>Brassica napus</i>	CD813986		1.00E-14
348	G2063	<i>Oryza sativa</i>	gi15290141		1.90E-17
348	G2063	<i>Antirrhinum majus</i>	gi264223		5.80E-17
348	G2063	<i>Picea abies</i>	gi25307922		2.00E-15
348	G2063	<i>Gossypium hirsutum</i>	gi19743774		3.20E-15
348	G2063	<i>Malus x domestica</i>	gi16973298		5.30E-15
348	G2063	<i>Phalaenopsis equestris</i>	gi18650789		1.10E-14
348	G2063	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi33090203		1.40E-14
348	G2063	<i>Petunia x hybrida</i>	gi17827467		1.80E-14
348	G2063	<i>Nicotiana tabacum</i>	gi3913007		1.80E-14
348	G2063	<i>Cucumis sativus</i>	gi13810204		2.30E-14
350	G2070	<i>Brassica oleracea</i>	BH598265		1.00E-44
350	G2070	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU870843		2.00E-14
350	G2070	<i>Lycopersicon esculentum</i>	BI922075		1.00E-12
350	G2070	<i>Brassica napus</i>	CD833815		1.00E-12
350	G2070	<i>Glycine max</i>	BM269595		6.00E-11
350	G2070	<i>Ipomoea nil</i>	BJ572296		2.00E-10
350	G2070	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAAA01003396		6.00E-10
350	G2070	<i>Prunus armeniaca</i>	CB821535		1.00E-09
350	G2070	<i>Nicotiana tabacum</i>	AY045572		1.00E-09
350	G2070	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AP005785		1.00E-09
350	G2070	<i>Nicotiana tabacum</i>	gi16580134		3.00E-12
350	G2070	<i>Phaseolus vulgaris</i>	gi13430400		1.00E-11
350	G2070	<i>Phaseolus acutifolius</i>	gi12829956		2.70E-11
350	G2070	<i>Petroselinum crispum</i>	gi9650826		1.00E-09
350	G2070	<i>Hordeum vulgare</i>	gi1869928		1.40E-09

350	G2070	<i>Antirrhinum majus</i>	gi2244742		3.60E-09
350	G2070	<i>Capsicum chinense</i>	gi4457221		9.40E-09
350	G2070	<i>Glycine max</i>	gi1905785		1.00E-08
350	G2070	<i>Oryza sativa</i>	gi18698991		1.10E-08
350	G2070	<i>Zea mays</i>	gi1060935		1.20E-08
352	G2071	<i>Vitis vinifera</i>	VVI237992		4.00E-87
352	G2071	<i>Phaseolus vulgaris</i>	AF369792		3.00E-77
352	G2071	<i>Brassica oleracea</i>	BZ007832		4.00E-75
352	G2071	<i>Nicotiana tabacum</i>	AB063648		2.00E-74
352	G2071	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK072062		9.00E-65
352	G2071	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	AY150676		3.00E-58
352	G2071	<i>Oryza sativa</i>	AB023288		1.00E-52
352	G2071	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01010740		4.00E-47
352	G2071	<i>Helianthus annuus</i>	AF001453		8.00E-40
352	G2071	<i>Triticum aestivum</i>	AF519804		6.00E-38
352	G2071	<i>Vitis vinifera</i>	gi7406677		2.30E-87
352	G2071	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi27469352		1.40E-64
352	G2071	<i>Nicotiana tabacum</i>	gi14571808		1.50E-58
352	G2071	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi33087069		3.20E-53
352	G2071	<i>Oryza sativa</i>	gi5821255		3.20E-53
352	G2071	<i>Phaseolus vulgaris</i>	gi13775111		1.80E-46
352	G2071	<i>Triticum aestivum</i>	gi21693585		2.50E-31
352	G2071	<i>Helianthus annuus</i>	gi2228771		1.10E-30
352	G2071	<i>Zea mays</i>	gi15422222		7.60E-08
352	G2071	<i>Populus x generosa</i>	gi13435335		2.50E-07
354	G2084	<i>Brassica oleracea</i>	BH426816		2.00E-77
354	G2084	<i>Triticum aestivum</i>	CD937226		3.00E-41
354	G2084	<i>Poncirus trifoliata</i>	CD574564		8.00E-41
354	G2084	<i>Vitis vinifera</i>	CB981408		1.00E-40
354	G2084	<i>Oryza sativa</i>	AP003314		5.00E-40
354	G2084	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01013746		5.00E-40
354	G2084	<i>Zea mays</i>	CD434392		9.00E-40
354	G2084	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK066561		1.00E-39
354	G2084	<i>Sorghum bicolor</i>	BE356071		1.00E-39
354	G2084	<i>Brassica napus</i>	CD837858		3.00E-37
354	G2084	<i>Oryza sativa</i>	gi11034559		3.20E-40
354	G2084	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi21104687		3.20E-40
354	G2084	<i>Pinus pinaster</i>	gi18129286		0.65
354	G2084	<i>Pinus thunbergii</i>	gi1262717		0.94
354	G2084	<i>Chloroplast Pinus thunbergii</i>	gi7484547		0.94
354	G2084	<i>Glycine max</i>	gi21439778		0.98
354	G2084	<i>Nicotiana tabacum</i>	gi478508		1
354	G2084	<i>Chloroplast</i>	gi544746		1

		<i>Nicotiana sylvestris</i>			
354	G2084	<i>Chloroplast Nicotiana tabacum</i>	gi544747		1
354	G2084	<i>Ipomoea batatas</i>	gi100467		1
355	G2085	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER62196_1	1108	
355	G2085	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER65589_1	1109	
355	G2085	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER65589_2	1110	
355	G2085	<i>Glycine max</i>	jC- gmXLIB3563P057de07d 2	1111	
355	G2085	<i>Oryza sativa</i>	OSC102337.C1.pl.fg	1112	
355	G2085	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER841917_1	1113	
355	G2085	<i>Medicago truncatula</i>	Mtr_S10820675	1707	
356	G2085	<i>Glycine max</i>	BI498544		1.00E-58
356	G2085	<i>Medicago truncatula</i>	CA991109		1.00E-54
356	G2085	<i>Vitis vinifera</i>	BM437375		1.00E-46
356	G2085	<i>Triticum aestivum</i>	BQ295376		1.00E-44
356	G2085	<i>Triticum monococcum</i>	BF199732		9.00E-44
356	G2085	<i>Oryza sativa (japonica cultivar- group)</i>	AK068931		2.00E-43
356	G2085	<i>Zea mays</i>	AY103800		3.00E-43
356	G2085	<i>Brassica oleracea</i>	BH723453		3.00E-40
356	G2085	<i>Hordeum vulgare</i>	BU993000		5.00E-39
356	G2085	<i>Ipomoea nil</i>	BJ572579		1.00E-38
356	G2085	<i>Oryza sativa</i>	gi13174240		3.90E-42
356	G2085	<i>Oryza sativa (japonica cultivar- group)</i>	gi24960749		1.80E-07
356	G2085	<i>Brassica rapa subsp. pekinensis</i>	gi28193631		2.90E-06
356	G2085	<i>Nicotiana tabacum</i>	gi12711287		0.00075
356	G2085	<i>Hordeum vulgare subsp. vulgare</i>	gi21655162		0.0033
356	G2085	<i>Nicotiana plumbaginifolia</i>	gi1076609		0.019
356	G2085	<i>Brassica nigra</i>	gi22854920		0.02
356	G2085	<i>Brassica napus</i>	gi30984027		0.091
356	G2085	<i>Raphanus sativus</i>	gi3341723		0.1
356	G2085	<i>Pisum sativum</i>	gi27530710		0.13
358	G2106	<i>Citrus sinensis</i>	BQ625052		8.00E-92
358	G2106	<i>Oryza sativa (japonica cultivar- group)</i>	AK106769		3.00E-88
358	G2106	<i>Zea mays</i>	AY103852		3.00E-74
358	G2106	<i>Brassica napus</i>	CD832004		6.00E-74
358	G2106	<i>Lycopersicon esculentum</i>	AW030921		3.00E-70
358	G2106	<i>Physcomitrella patens subsp. patens</i>	BJ178045		5.00E-68

358	G2106	<i>Glycine max</i>	CA783156		5.00E-67
358	G2106	<i>Oryza sativa</i>	AX555220		6.00E-66
358	G2106	<i>Nuphar advena</i>	CD475882		3.00E-65
358	G2106	<i>Lactuca sativa</i>	BQ864461		7.00E-58
358	G2106	<i>Brassica napus</i>	gi21069053		5.10E-65
358	G2106	<i>Oryza sativa</i>	gi25898749		7.40E-64
358	G2106	<i>Glycine max</i>	gi25898747		7.40E-64
358	G2106	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi20161013		2.00E-63
358	G2106	<i>Zea mays</i>	gi2652938		1.10E-62
358	G2106	<i>Antirrhinum majus</i>	gi28894443		1.90E-39
358	G2106	<i>Malus x domestica</i>	gi21717332		2.30E-35
358	G2106	<i>Hordeum vulgare</i>	gi18476518		2.40E-35
358	G2106	<i>Picea abies</i>	gi11181612		4.00E-34
358	G2106	<i>Petunia x hybrida</i>	gi5081555		7.20E-34
359	G2109	<i>Oryza sativa</i>	uC-osrM202145h04b1	1114	
359	G2109	<i>Zea mays</i>	LIB3066-034-Q1-K1-B12	1115	
359	G2109	<i>Oryza sativa</i>	Os_S114273	1603	
359	G2109	<i>Oryza sativa</i>	Os_S29604	1604	
359	G2109	<i>Zea mays</i>	Zm_S11374620	1811	
359	G2109	<i>Triticum aestivum</i>	Ta_S302577	1898	
360	G2109	<i>Brassica napus</i>	CD815586		1.00E-50
360	G2109	<i>Beta vulgaris</i>	BQ583447		5.00E-45
360	G2109	<i>Ceratopteris richardii</i>	BE643398		9.00E-33
360	G2109	<i>Nicotiana tabacum</i>	AY183721		2.00E-31
360	G2109	<i>Physcomitrella patens</i>	PPA419329		5.00E-28
360	G2109	<i>Physcomitrella patens</i> subsp. <i>patens</i>	AB067689		1.00E-22
360	G2109	<i>Brassica oleracea</i>	BH451078		6.00E-20
360	G2109	<i>Zinnia elegans</i>	AU287699		9.00E-17
360	G2109	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AC120888		1.00E-16
360	G2109	<i>Oryza sativa</i>	AC108870		1.00E-16
360	G2109	<i>Nicotiana tabacum</i>	gi27802107		1.40E-34
360	G2109	<i>Physcomitrella patens</i>	gi22474457		8.50E-32
360	G2109	<i>Physcomitrella patens</i> subsp. <i>patens</i>	gi22090622		9.30E-29
360	G2109	<i>Gerbera hybrid</i> cv. 'Terra Regina'	gi29500904		6.10E-21
360	G2109	<i>Triticum aestivum</i>	gi30721847		1.50E-20
360	G2109	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	gi10835358		1.70E-20
360	G2109	<i>Zea mays</i>	gi29372764		3.60E-20
360	G2109	<i>Triticum monococcum</i>	gi30090030		4.00E-20
360	G2109	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi31712055		4.20E-20
360	G2109	<i>Papaver nudicaule</i>	gi3170464		9.70E-20

362	G2111	<i>Glycine max</i>	AW508033		3.00E-35
362	G2111	<i>Brassica oleracea</i>	BH455618		2.00E-32
362	G2111	<i>Medicago truncatula</i>	AC137602		2.00E-29
362	G2111	<i>Antirrhinum majus</i>	AJ558896		9.00E-27
362	G2111	<i>Gossypium arboreum</i>	BE054256		4.00E-25
362	G2111	<i>Gossypium hirsutum</i>	BH023181		9.00E-24
362	G2111	<i>Zea mays</i>	CC654475		5.00E-23
362	G2111	<i>Oryza sativa</i>	AP002070		9.00E-22
362	G2111	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01000422		9.00E-22
362	G2111	<i>Lotus japonicus</i>	AP004625		2.00E-18
362	G2111	<i>Oryza sativa</i>	gi8096379		1.80E-23
362	G2111	<i>Gerbera hybrid cv. 'Terra Regina'</i>	gi29500904		7.70E-14
362	G2111	<i>Nicotiana tabacum</i>	gi4102113		1.30E-13
362	G2111	<i>Brassica oleracea var. botrytis</i>	gi23304676		1.60E-13
362	G2111	<i>Lycopersicon esculentum</i>	gi20219014		8.90E-13
362	G2111	<i>Sinapis alba</i>	gi1076477		1.10E-12
362	G2111	<i>Oryza sativa (japonica cultivar-group)</i>	gi21742221		1.80E-12
362	G2111	<i>Lolium perenne</i>	gi28630953		1.80E-12
362	G2111	<i>Triticum monococcum</i>	gi30090030		2.40E-12
362	G2111	<i>Triticum aestivum</i>	gi30721847		2.40E-12
364	G2129	<i>Brassica napus</i>	CD833815		8.00E-49
364	G2129	<i>Brassica oleracea</i>	BH972911		4.00E-38
364	G2129	<i>Populus balsamifera subsp. trichocarpa</i>	BU870843		4.00E-26
364	G2129	<i>Glycine max</i>	BM269595		3.00E-22
364	G2129	<i>Lycopersicon esculentum</i>	BF051268		3.00E-21
364	G2129	<i>Beta vulgaris</i>	BQ582406		2.00E-11
364	G2129	<i>Gossypium arboreum</i>	BQ407558		4.00E-11
364	G2129	<i>Medicago truncatula</i>	BG648225		4.00E-10
364	G2129	<i>Oryza sativa (japonica cultivar-group)</i>	AK098869		1.00E-09
364	G2129	<i>Oryza sativa (indica cultivar-group)</i>	CA759739		1.00E-09
364	G2129	<i>Nicotiana tabacum</i>	gi16580130		1.30E-11
364	G2129	<i>Petroselinum crispum</i>	gi9650828		2.70E-11
364	G2129	<i>Capsicum chinense</i>	gi24460973		4.40E-11
364	G2129	<i>Phaseolus vulgaris</i>	gi13430400		7.20E-11
364	G2129	<i>Lycopersicon esculentum</i>	gi5901747		7.20E-11
364	G2129	<i>Phaseolus acutifolius</i>	gi12829956		1.20E-10

364	G2129	<i>Antirrhinum majus</i>	gi2244742		1.20E-10
364	G2129	<i>Zea mays</i>	gi1352613		1.90E-10
364	G2129	<i>Glycine max</i>	gi22597162		3.10E-10
364	G2129	<i>Sorghum bicolor</i>	gi1076760		3.60E-10
365	G2142	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER10684_8	1116	
365	G2142	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER137024_1	1117	
365	G2142	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER49853_1	1118	
365	G2142	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER49853_4	1119	
365	G2142	<i>Glycine max</i>	LIB3242-451-P1-J1-G8	1120	
365	G2142	<i>Glycine max</i>	jC-gmXLIB3563P042ag07d1	1121	
365	G2142	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER54709_1	1122	
365	G2142	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER8097_1	1123	
365	G2142	<i>Zea mays</i>	700164501H1	1124	
365	G2142	<i>Glycine max</i>	Gma_S4891278	1666	
365	G2142	<i>Medicago truncatula</i>	Mtr_S5397469	1708	
365	G2142	<i>Zea mays</i>	Zm_S11527973	1812	
365	G2142	<i>Triticum aestivum</i>	Ta_S115402	1899	
365	G2142	<i>Triticum aestivum</i>	Ta_S146851	1900	
365	G2142	<i>Triticum aestivum</i>	Ta_S308126	1901	
365	G2142	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-48174	2048	
365	G2142	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-50424	2049	
365	G2142	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-56397	2050	
365	G2142	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-56608	2051	
366	G2142	<i>Brassica napus</i>	CD813318		8.00E-90
366	G2142	<i>Medicago truncatula</i>	BF650735		2.00E-59
366	G2142	<i>Populus tremula x Populus tremuloides</i>	BU837621		4.00E-59
366	G2142	<i>Glycine max</i>	BU080678		3.00E-58
366	G2142	<i>Beta vulgaris</i>	BQ594352		4.00E-54
366	G2142	<i>Solanum tuberosum</i>	BF186943		6.00E-53
366	G2142	<i>Lycopersicon esculentum</i>	AI490572		1.00E-52
366	G2142	<i>Oryza sativa (japonica cultivar-group)</i>	AK101896		7.00E-48
366	G2142	<i>Stevia rebaudiana</i>	BG524015		2.00E-44
366	G2142	<i>Hordeum vulgare subsp. vulgare</i>	BU989763		8.00E-42
366	G2142	<i>Pennisetum glaucum</i>	gi527655		3.10E-10
366	G2142	<i>Sorghum bicolor</i>	gi527665		3.90E-08
366	G2142	<i>Phyllostachys acuta</i>	gi527661		6.50E-08
366	G2142	<i>Tripsacum australe</i>	gi527663		1.80E-07

366	G2142	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi32488806		3.20E-07
366	G2142	<i>Oryza sativa</i>	gi15451582		3.50E-07
366	G2142	<i>Oryza rufipogon</i>	gi2130061		6.40E-07
366	G2142	<i>Oryza australiensis</i>	gi1086526		1.40E-06
366	G2142	<i>Oryza officinalis</i>	gi1086534		2.90E-06
366	G2142	<i>Oryza longistaminata</i>	gi1086530		3.80E-06
368	G2146	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BG543943		8.00E-48
368	G2146	<i>Brassica oleracea</i>	BH978369		2.00E-42
368	G2146	<i>Lotus japonicus</i>	BI418128		6.00E-29
368	G2146	<i>Glycine max</i>	CD398757		4.00E-28
368	G2146	<i>Poncirus trifoliata</i>	CD575942		2.00E-27
368	G2146	<i>Gossypium arboreum</i>	BE054359		8.00E-26
368	G2146	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK103709		1.00E-25
368	G2146	<i>Oryza sativa</i>	AF461424		1.00E-25
368	G2146	<i>Ipomoea nil</i>	BJ574783		7.00E-25
368	G2146	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU832777		3.00E-24
368	G2146	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi24059889		2.90E-23
368	G2146	<i>Oryza sativa</i>	gi5852091		0.015
368	G2146	<i>Tulipa gesneriana</i>	gi5923912		0.019
368	G2146	<i>Petunia x hybrida</i>	gi3127045		0.85
368	G2146	<i>Gerbera hybrida</i>	gi3650292		0.99
368	G2146	<i>Oryza rufipogon</i>	gi1086538		1
368	G2146	<i>Sorghum bicolor</i>	gi527667		1
370	G2184	<i>Petunia x hybrida</i>	AF509870		1.00E-113
370	G2184	<i>Brassica napus</i>	CD836672		4.00E-92
370	G2184	<i>Lactuca sativa</i>	BQ864249		3.00E-77
370	G2184	<i>Solanum tuberosum</i>	BG350410		9.00E-75
370	G2184	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU863110		2.00E-71
370	G2184	<i>Brassica oleracea</i>	BH526845		1.00E-65
370	G2184	<i>Medicago truncatula</i>	AW736414		1.00E-63
370	G2184	<i>Citrus sinensis</i>	CB293271		3.00E-62
370	G2184	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK099237		2.00E-57
370	G2184	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	CB633792		2.00E-57
370	G2184	<i>Petunia x hybrida</i>	gi21105742		1.10E-106
370	G2184	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi27452910		7.00E-58
370	G2184	<i>Medicago truncatula</i>	gi7716952		4.60E-52
370	G2184	<i>Oryza sativa</i>	gi6730946		8.30E-47
370	G2184	<i>Brassica napus</i>	gi31322578		2.20E-39

370	G2184	<i>Lycopersicon esculentum</i>	gi6175246		3.60E-39
370	G2184	<i>Phaseolus vulgaris</i>	gi15148914		1.20E-38
370	G2184	<i>Glycine max</i>	gi22597158		3.30E-38
370	G2184	<i>Triticum sp.</i>	gi4218537		2.90E-37
370	G2184	<i>Triticum monococcum</i>	gi6732160		2.90E-37
371	G2207	<i>Oryza sativa</i>	Os_S17837	1605	
371	G2207	<i>Oryza sativa</i>	Os_S6232	1606	
371	G2207	<i>Glycine max</i>	Gma_S5129383	1667	
371	G2207	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-50991	2052	
371	G2207	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-399437	2053	
372	G2207	<i>Oryza sativa (japonica cultivar- group)</i>	AK100046		1.00E-172
372	G2207	<i>Oryza sativa</i>	AX654056		1.00E-168
372	G2207	<i>Lotus japonicus</i>	LJA239041		1.00E-148
372	G2207	<i>Pisum sativum</i>	PSA493066		1.00E-130
372	G2207	<i>Brassica oleracea</i>	BZ078380		1.00E-123
372	G2207	<i>Oryza sativa (indica cultivar-group)</i>	AAAAA01002068		2.00E-76
372	G2207	<i>Brassica nigra</i>	AY061812		7.00E-71
372	G2207	<i>Zea mays</i>	CC644684		6.00E-70
372	G2207	<i>Gossypium arboreum</i>	BF269998		4.00E-58
372	G2207	<i>Lycopersicon esculentum</i>	BI931640		7.00E-55
372	G2207	<i>Oryza sativa (japonica cultivar- group)</i>	gi20503001		1.00E-166
372	G2207	<i>Lotus japonicus</i>	gi6448579		3.90E-160
372	G2207	<i>Pisum sativum</i>	gi23504759		4.50E-124
372	G2207	<i>Oryza sativa</i>	gi7339715		1.00E-122
372	G2207	<i>Chlamydomonas incerta</i>	gi2190980		4.70E-06
372	G2207	<i>Chlamydomonas reinhardtii</i>	gi1928929		0.00049
372	G2207	<i>Bromheadia finlaysoniana</i>	gi2108256		0.55
372	G2207	<i>Lycopersicon esculentum</i>	gi100214		0.73
372	G2207	<i>Nicotiana tabacum</i>	gi322758		0.81
372	G2207	<i>Oryza sativa (indica cultivar-group)</i>	gi2407271		0.96
374	G2213	<i>Brassica oleracea</i>	BH427528		2.00E-19
374	G2213	<i>Gossypium hirsutum</i>	AI726978		2.00E-18
374	G2213	<i>Zea mays</i>	AY106664		1.00E-16
374	G2213	<i>Glycine max</i>	BE821577		1.00E-15
374	G2213	<i>Triticum monococcum</i>	BQ802007		2.00E-15
374	G2213	<i>Oryza sativa (japonica cultivar- group)</i>	AP004258		7.00E-15
374	G2213	<i>Oryza sativa (indica)</i>	AAAAA01008029		7.00E-15

		cultivar-group)			
374	G2213	<i>Oryza sativa</i>	AP003933		7.00E-15
374	G2213	<i>Chlamydomonas reinhardtii</i>	BU648678		4.00E-12
374	G2213	<i>Hordeum vulgare</i>	BQ459689		2.00E-11
374	G2213	<i>Oryza sativa</i> (japonica cultivar-group)	gi20161719		3.80E-28
374	G2213	<i>Oryza sativa</i>	gi7339715		1.60E-08
374	G2213	<i>Chlamydomonas reinhardtii</i>	gi1928929		6.90E-07
374	G2213	<i>Chlamydomonas incerta</i>	gi2190980		2.50E-06
374	G2213	<i>Pisum sativum</i>	gi23504757		9.10E-05
374	G2213	<i>Lotus japonicus</i>	gi6448579		0.00014
374	G2213	<i>Cicer arietinum</i>	gi6002283		0.26
374	G2213	<i>Allium cepa</i>	gi19979631		0.82
374	G2213	<i>Brassica napus</i>	gi2809204		0.82
376	G2226	<i>Thellungiella halophila</i>	BM985667		3.00E-71
376	G2226	<i>Brassica napus</i>	CD834580		9.00E-70
376	G2226	<i>Glycine max</i>	CA784214		2.00E-52
376	G2226	<i>Gossypium arboreum</i>	BF278307		4.00E-47
376	G2226	<i>Gossypium hirsutum</i>	AI727363		3.00E-46
376	G2226	<i>Medicago truncatula</i>	BF648350		7.00E-46
376	G2226	<i>Lactuca sativa</i>	BU010488		1.00E-37
376	G2226	<i>Solanum tuberosum</i>	BG599025		5.00E-37
376	G2226	<i>Capsicum annuum</i>	CA525749		2.00E-36
376	G2226	<i>Hevea brasiliensis</i>	CB376421		2.00E-35
376	G2226	<i>Thellungiella halophila</i>	gi20340241		2.30E-69
376	G2226	<i>Oryza sativa</i> (japonica cultivar-group)	gi32488512		4.90E-12
376	G2226	<i>Oryza sativa</i>	gi6069662		2.70E-11
376	G2226	<i>Cucumis melo</i>	gi28558782		1.00E-08
376	G2226	<i>Medicago sativa</i>	gi23451086		1.20E-08
376	G2226	<i>Glycine max</i>	gi22597166		2.70E-08
376	G2226	<i>Hordeum vulgare</i>	gi2894379		5.80E-08
376	G2226	<i>Pisum sativum</i>	gi4240031		2.30E-07
376	G2226	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152976		2.60E-07
376	G2226	<i>Zea mays</i>	gi21645888		2.80E-07
378	G2227	<i>Brassica oleracea</i>	BZ520300		1.00E-123
378	G2227	<i>Medicago truncatula</i>	AC144609		2.00E-87
378	G2227	<i>Oryza sativa</i>	AC079022		3.00E-81
378	G2227	<i>Oryza sativa</i> (japonica cultivar-group)	AK067221		7.00E-69
378	G2227	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01002581		7.00E-69
378	G2227	<i>Lycopersicon esculentum</i>	AW035988		1.00E-67

378	G2227	<i>Lactuca sativa</i>	BQ858069		6.00E-67
378	G2227	<i>Vitis aestivalis</i>	CB288974		9.00E-66
378	G2227	<i>Glycine max</i>	BM188705		5.00E-62
378	G2227	<i>Zea mays</i>	CC429342		1.00E-60
378	G2227	<i>Oryza sativa</i>	gi14719329		1.20E-79
378	G2227	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi29893617		6.70E-63
378	G2227	<i>Cicer arietinum</i>	gi4651204		5.10E-21
378	G2227	<i>Tulipa gesneriana</i>	gi23386073		6.30E-19
378	G2227	<i>Cucumis melo</i>	gi28558782		8.40E-10
378	G2227	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152976		1.40E-07
378	G2227	<i>Thellungiella halophila</i>	gi20340241		9.80E-07
378	G2227	<i>Glycine max</i>	gi22597166		3.70E-06
378	G2227	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	gi29164825		8.60E-06
378	G2227	<i>Medicago sativa</i>	gi23451086		1.70E-05
379	G2239	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER12957_1	1125	
379	G2239	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER12957_2	1126	
379	G2239	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER12957_5	1127	
379	G2239	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER135837_1	1128	
379	G2239	<i>Glycine max</i>	uC-gmflIB3275P131g04a1	1129	
379	G2239	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER139279_1	1130	
379	G2239	<i>Oryza sativa</i>	OSC100308.C1.p4.fg	1131	
379	G2239	<i>Oryza sativa</i>	OSC101055.C1.p3.fg	1132	
379	G2239	<i>Oryza sativa</i>	OSC102053.C1.p4.fg	1133	
379	G2239	<i>Oryza sativa</i>	OSC20507.C1.p2.fg	1134	
379	G2239	<i>Zea mays</i>	LIB4828-050-R1-N1-D2	1135	
379	G2239	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER495748_1	1136	
380	G2239	<i>Brassica oleracea</i>	BH582110		1.00E-120
380	G2239	<i>Cucumis melo</i>	AF499727		3.00E-73
380	G2239	<i>Medicago truncatula</i>	AC136503		4.00E-71
380	G2239	<i>Poncirus trifoliata</i>	CD576402		8.00E-57
380	G2239	<i>Citrus sinensis</i>	CB290516		1.00E-56
380	G2239	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01004423		4.00E-55
380	G2239	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AP005399		4.00E-55
380	G2239	<i>Oryza sativa</i>	AX653298		5.00E-51
380	G2239	<i>Gossypium hirsutum</i>	AI730749		6.00E-51
380	G2239	<i>Capsicum annuum</i>	BM063816		1.00E-49
380	G2239	<i>Cucumis melo</i>	gi28558782		3.30E-70
380	G2239	<i>Oryza sativa</i>	gi21740711		2.10E-38
380	G2239	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi24756877		4.00E-33

		group)			
380	G2239	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152976		3.50E-21
380	G2239	<i>Nicotiana tabacum</i>	gi12003386		2.20E-20
380	G2239	<i>Medicago sativa</i>	gi23451086		2.20E-17
380	G2239	<i>Zea mays</i>	gi21645888		1.20E-16
380	G2239	<i>Hordeum vulgare</i>	gi2894379		3.20E-16
380	G2239	<i>Solanum tuberosum</i>	gi24745601		4.70E-16
380	G2239	<i>Thellungiella</i> <i>halophila</i>	gi20340241		4.30E-10
382	G2251	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BG543052		2.00E-67
382	G2251	<i>Populus tremula</i>	BU893088		4.00E-48
382	G2251	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU894285		3.00E-47
382	G2251	<i>Glycine max</i>	BE440750		5.00E-45
382	G2251	<i>Gossypium</i> <i>hirsutum</i>	AI729600		2.00E-44
382	G2251	<i>Lycopersicon</i> <i>esculentum</i>	AW034559		8.00E-44
382	G2251	<i>Capsicum annuum</i>	CA847343		1.00E-43
382	G2251	<i>Lactuca sativa</i>	BQ849490		2.00E-43
382	G2251	<i>Brassica oleracea</i>	BZ013045		4.00E-43
382	G2251	<i>Ipomoea nil</i>	BJ572086		3.00E-42
382	G2251	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi32488512		3.50E-29
382	G2251	<i>Oryza sativa</i>	gi6069662		3.50E-18
382	G2251	<i>Thellungiella</i> <i>halophila</i>	gi20340241		6.20E-12
382	G2251	<i>Medicago sativa</i>	gi23451086		7.00E-12
382	G2251	<i>Cucumis melo</i>	gi28558782		3.00E-10
382	G2251	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152976		3.10E-10
382	G2251	<i>Zea mays</i>	gi21645888		3.70E-08
382	G2251	<i>Glycine max</i>	gi1076498		1.00E-07
382	G2251	<i>Hordeum vulgare</i>	gi2894379		8.20E-07
382	G2251	<i>Nicotiana tabacum</i>	gi12003386		9.40E-07
384	G2269	<i>Brassica oleracea</i>	BH433947		7.00E-72
384	G2269	<i>Brassica napus</i>	CD838796		1.00E-67
384	G2269	<i>Gossypium</i> <i>hirsutum</i>	AI727683		8.00E-60
384	G2269	<i>Glycine max</i>	CA939042		8.00E-60
384	G2269	<i>Gossypium</i> <i>arboreum</i>	BG444995		1.00E-56
384	G2269	<i>Zea mays</i>	CC694850		2.00E-47
384	G2269	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AC109596		4.00E-47
384	G2269	<i>Oryza sativa</i>	AC108499		4.00E-47
384	G2269	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01000476		7.00E-45
384	G2269	<i>Ipomoea nil</i>	BJ568099		1.00E-42
384	G2269	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi20160500		2.30E-44

384	G2269	<i>Gossypium barbadense</i>	gi30983938		3.00E-21
384	G2269	<i>Oryza sativa</i>	gi5091511		9.50E-16
384	G2269	<i>Nicotiana tabacum</i>	gi12003386		1.10E-12
384	G2269	<i>Cucumis melo</i>	gi28558782		3.20E-12
384	G2269	<i>Hordeum vulgare</i>	gi2894379		4.10E-12
384	G2269	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152976		6.00E-12
384	G2269	<i>Medicago sativa</i>	gi23451086		2.00E-11
384	G2269	<i>Zea mays</i>	gi21645888		4.40E-09
384	G2269	<i>Cicer arietinum</i>	gi4651204		6.60E-09
386	G2298	<i>Brassica oleracea</i>	BH498020		2.00E-69
386	G2298	<i>Beta vulgaris</i>	BQ487577		9.00E-35
386	G2298	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU861348		2.00E-34
386	G2298	<i>Lycopersicon esculentum</i>	AI489478		1.00E-33
386	G2298	<i>Glycine max</i>	BE807652		1.00E-33
386	G2298	<i>Lotus japonicus</i>	AV424732		8.00E-33
386	G2298	<i>Phaseolus vulgaris</i>	BQ481785		1.00E-32
386	G2298	<i>Solanum tuberosum</i>	BI920063		1.00E-32
386	G2298	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i> x <i>Populus deltoides</i>	CA826218		4.00E-32
386	G2298	<i>Brassica napus</i>	CD819945		1.00E-30
386	G2298	<i>Atriplex hortensis</i>	gi8571476		1.20E-21
386	G2298	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi21742362		1.80E-21
386	G2298	<i>Oryza sativa</i>	gi14140155		6.40E-21
386	G2298	<i>Zea mays</i>	gi21908036		1.90E-19
386	G2298	<i>Prunus armeniaca</i>	gi3264767		2.30E-19
386	G2298	<i>Lycopersicon esculentum</i>	gi27436378		4.50E-18
386	G2298	<i>Glycine max</i>	gi31324058		4.50E-18
386	G2298	<i>Stylosanthes hamata</i>	gi4099914		1.70E-17
386	G2298	<i>Nicotiana tabacum</i>	gi10798644		1.10E-16
386	G2298	<i>Triticum aestivum</i>	gi15488459		1.70E-16
388	G2311	<i>Brassica napus</i>	CD822731		1.00E-57
388	G2311	<i>Gossypium arboreum</i>	BE053309		2.00E-51
388	G2311	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	OSA495797		1.00E-47
388	G2311	<i>Zea mays</i>	AF461815		1.00E-45
388	G2311	<i>Glycine max</i>	BU761883		1.00E-44
388	G2311	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU827154		2.00E-42
388	G2311	<i>Petroselinum crispum</i>	PCU67132		1.00E-41
388	G2311	<i>Medicago truncatula</i>	AW329290		6.00E-41
388	G2311	<i>Ipomoea nil</i>	BJ554376		3.00E-39
388	G2311	<i>Triticum aestivum</i>	CA502640		5.00E-38
388	G2311	<i>Oryza sativa</i>	gi20804653		4.00E-49

		(japonica cultivar-group)			
388	G2311	<i>Zea mays</i>	gi18463961		2.90E-46
388	G2311	<i>Petroselinum crispum</i>	gi2224897		2.00E-22
388	G2311	<i>Fritillaria liliacea</i>	gi15281594		8.70E-11
388	G2311	<i>Triticum aestivum</i>	gi2980891		2.30E-09
388	G2311	<i>Euphorbia esula</i>	gi6752901		5.50E-09
388	G2311	<i>Vicia faba</i>	gi30420970		2.60E-08
388	G2311	<i>Fritillaria agrestis</i>	gi2641211		3.00E-08
388	G2311	<i>Pisum sativum</i>	gi4106696		7.10E-08
388	G2311	<i>Lathyrus aphaca</i>	gi21465093		7.30E-08
389	G2317	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER2162_3	1137	
389	G2317	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER2162_4	1138	
389	G2317	<i>Oryza sativa</i>	Os_S96262	1607	
389	G2317	<i>Glycine max</i>	Gma_S4915353	1668	
389	G2317	<i>Medicago truncatula</i>	Mtr_SS363423	1709	
389	G2317	<i>Hordeum vulgare</i>	Hv_S60108	1741	
389	G2317	<i>Lycopersicon esculentum</i>	Les_S5190181	1933	
390	G2317	<i>Medicago truncatula</i>	BG453991		5.00E-51
390	G2317	<i>Zinnia elegans</i>	AU292197		2.00E-42
390	G2317	<i>Triticum aestivum</i>	BT009406		1.00E-41
390	G2317	<i>Solanum tuberosum</i>	BM110307		1.00E-41
390	G2317	<i>Oryza sativa</i>	AX658868		3.00E-41
390	G2317	<i>Glycine max</i>	BM093706		6.00E-41
390	G2317	<i>Lycopersicon esculentum</i>	AI774224		1.00E-39
390	G2317	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BJ472642		7.00E-39
390	G2317	<i>Oryza sativa</i> (japonica cultivar-group)	AK101209		4.00E-37
390	G2317	<i>Sorghum bicolor</i>	CD219576		7.00E-37
390	G2317	<i>Phaseolus vulgaris</i>	gi21213868		2.60E-36
390	G2317	<i>Oryza sativa</i> (japonica cultivar-group)	gi21742243		5.50E-36
390	G2317	<i>Oryza sativa</i>	gi15528628		6.00E-23
390	G2317	<i>Hordeum vulgare</i>	gi12406993		1.10E-07
390	G2317	<i>Hevea brasiliensis</i>	gi12005328		4.90E-07
390	G2317	<i>Antirrhinum majus</i>	gi18874263		1.80E-06
390	G2317	<i>Malus xiaojinensis</i>	gi28629811		3.80E-06
390	G2317	<i>Glycine max</i>	gi19911577		3.90E-06
390	G2317	<i>Zea mays</i>	gi20067661		1.00E-05
390	G2317	<i>Lycopersicon esculentum</i>	gi6688529		2.60E-05
391	G2319	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER33063_1	1139	
391	G2319	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER33063_2	1140	
391	G2319	<i>Glycine max</i>	GLYMA-28NOV01-	1141	

			CLUSTER33063_4		
391	G2319	<i>Glycine max</i>	jC-gmst024169f06b1	1142	
391	G2319	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-335798	2054	
392	G2319	<i>Lycopersicon esculentum</i>	BI921951		7.00E-93
392	G2319	<i>Triticum aestivum</i>	BT008954		2.00E-71
392	G2319	<i>Gossypium arboreum</i>	BQ403368		4.00E-71
392	G2319	<i>Zea mays</i>	AX756404		8.00E-70
392	G2319	<i>Mesembryanthemu m crystallinum</i>	CA840558		7.00E-69
392	G2319	<i>Citrus sinensis</i>	CB290239		2.00E-65
392	G2319	<i>Populus tremula x Populus tremuloides</i>	BU887003		1.00E-62
392	G2319	<i>Glycine max</i>	CD487127		2.00E-58
392	G2319	<i>Hordeum vulgare subsp. vulgare</i>	AV909036		1.00E-56
392	G2319	<i>Medicago truncatula</i>	BF005534		7.00E-55
392	G2319	<i>Oryza sativa</i>	gi15528628		2.70E-38
392	G2319	<i>Oryza sativa (japonica cultivar- group)</i>	gi21742243		1.80E-25
392	G2319	<i>Phaseolus vulgaris</i>	gi21213868		5.00E-25
392	G2319	<i>Hordeum vulgare</i>	gi12406993		8.80E-08
392	G2319	<i>Hevea brasiliensis</i>	gi12005328		2.50E-06
392	G2319	<i>Glycine max</i>	gi19911577		3.30E-06
392	G2319	<i>Lycopersicon esculentum</i>	gi6688529		5.20E-06
392	G2319	<i>Solanum tuberosum</i>	gi7705206		9.00E-06
392	G2319	<i>Zea mays</i>	gi20067661		1.90E-05
392	G2319	<i>Malus xiaojinensis</i>	gi28629811		2.00E-05
393	G2334	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-57794	2055	
394	G2334	<i>Brassica oleracea</i>	BZ428330		5.00E-61
394	G2334	<i>Medicago truncatula</i>	AW981431		1.00E-30
394	G2334	<i>Glycine max</i>	BI786182		3.00E-30
394	G2334	<i>Solanum tuberosum</i>	BE922572		7.00E-30
394	G2334	<i>Oryza sativa (japonica cultivar- group)</i>	AK110934		7.00E-30
394	G2334	<i>Amborella trichopoda</i>	CD483211		3.00E-29
394	G2334	<i>Lycopersicon esculentum</i>	AW650563		4.00E-29
394	G2334	<i>Oryza sativa</i>	AF201895		6.00E-29
394	G2334	<i>Hordeum vulgare subsp. vulgare</i>	CA029723		6.00E-29
394	G2334	<i>Zea mays</i>	CA828910		2.00E-28
394	G2334	<i>Oryza sativa</i>	gi6573149		6.20E-37
394	G2334	<i>Oryza sativa (japonica cultivar- group)</i>	gi24413958		1.80E-35
394	G2334	<i>Sorghum bicolor</i>	gi18390099		6.00E-33
394	G2334	<i>Solanum</i>	gi32470646		5.90E-32

		<i>bulbocastanum</i>			
394	G2334	<i>Nicotiana alata</i>	gi1087017		0.79
394	G2334	<i>Petunia x hybrida</i>	gi14522848		0.94
394	G2334	<i>Picea abies</i>	gi10764150		0.98
394	G2334	<i>Oryza sativa (indica cultivar-group)</i>	gi4680183		1
394	G2334	<i>Lycopersicon esculentum</i>	gi1418988		1
394	G2334	<i>Pyrus pyrifolia</i>	gi8698889		1
396	G2371	<i>Brassica oleracea</i>	BH518264		2.00E-83
396	G2371	<i>Brassica napus</i>	CD815763		8.00E-71
396	G2371	<i>Capsicum annuum</i>	BM063508		7.00E-50
396	G2371	<i>Oryza sativa (japonica cultivar-group)</i>	AK072663		2.00E-45
396	G2371	<i>Solanum tuberosum</i>	BQ115437		9.00E-45
396	G2371	<i>Lycopersicon esculentum</i>	BI921667		3.00E-44
396	G2371	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01005658		1.00E-43
396	G2371	<i>Triticum aestivum</i>	BE499367		3.00E-43
396	G2371	<i>Glycine max</i>	AW781777		4.00E-43
396	G2371	<i>Lycopersicon pennellii</i>	AW617994		6.00E-41
396	G2371	<i>Oryza sativa (japonica cultivar-group)</i>	gi21426118		2.20E-42
396	G2371	<i>Marchantia polymorpha</i>	gi25272004		7.20E-32
396	G2371	<i>Oryza sativa</i>	gi19352041		3.20E-07
396	G2371	<i>Mangifera indica</i>	gi31747324		5.40E-06
396	G2371	<i>Prunus persica</i>	gi27450533		7.40E-06
396	G2371	<i>Eragrostis tef</i>	gi17906977		9.80E-06
396	G2371	<i>Hordeum vulgare subsp. vulgare</i>	gi1730475		1.30E-05
396	G2371	<i>Phaseolus vulgaris</i>	gi1046278		5.70E-05
396	G2371	<i>Mesembryanthemum crystallinum</i>	gi3219155		0.00012
396	G2371	<i>Zea mays</i>	gi100922		0.00015
398	G2372	<i>Oryza sativa</i>	AB071299		3.00E-97
398	G2372	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01008877		3.00E-97
398	G2372	<i>Oryza sativa (japonica cultivar-group)</i>	AK100322		2.00E-96
398	G2372	<i>Physcomitrella patens</i>	AX288142		5.00E-93
398	G2372	<i>Brassica oleracea</i>	BZ495025		1.00E-87
398	G2372	<i>Lotus japonicus</i>	AP004505		5.00E-77
398	G2372	<i>Gossypium arboreum</i>	BG443827		2.00E-68
398	G2372	<i>Zea mays</i>	CC657791		2.00E-66
398	G2372	<i>Vitis vinifera</i>	CB979491		7.00E-59
398	G2372	<i>Medicago truncatula</i>	BG646821		3.00E-58
398	G2372	<i>Oryza sativa (japonica cultivar-</i>	gi13384374		3.10E-97

		group)			
398	G2372	<i>Oryza sativa</i>	gi19352051		1.50E-95
398	G2372	<i>Prunus persica</i>	gi27450533		1.60E-50
398	G2372	<i>Oryza sativa</i> (indica cultivar-group)	gi26251300		3.40E-46
398	G2372	<i>Mangifera indica</i>	gi30027167		1.10E-42
398	G2372	<i>Marchantia polymorpha</i>	gi25272004		1.30E-10
398	G2372	<i>Chamaecyparis nootkatensis</i>	gi30421190		0.97
400	G2375	<i>Brassica oleracea</i>	BH685171		2.00E-84
400	G2375	<i>Medicago truncatula</i>	BG648693		1.00E-56
400	G2375	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01004311		6.00E-42
400	G2375	<i>Nicotiana tabacum</i>	E64987		1.00E-28
400	G2375	<i>Malus x domestica</i>	AU301396		2.00E-28
400	G2375	<i>Pinus taeda</i>	BG040491		7.00E-26
400	G2375	<i>Zea mays</i>	AY109868		3.00E-25
400	G2375	<i>Lycopersicon esculentum</i>	BG123901		1.00E-24
400	G2375	<i>Solanum tuberosum</i>	BQ118023		1.00E-23
400	G2375	<i>Oryza sativa</i>	OSJN00077		7.00E-23
400	G2375	<i>Oryza sativa</i> (japonica cultivar-group)	gi21740920		4.60E-48
400	G2375	<i>Oryza sativa</i>	gi20249		4.90E-15
400	G2375	<i>Nicotiana tabacum</i>	gi170271		2.20E-14
400	G2375	<i>Oryza sativa</i> (indica cultivar-group)	gi27368895		3.40E-12
400	G2375	<i>Pisum sativum</i>	gi13646986		1.20E-11
400	G2375	<i>Glycine max</i>	gi18182311		5.40E-07
400	G2375	<i>Cucurbita maxima</i>	gi17221648		3.70E-06
400	G2375	<i>Lycopersicon esculentum</i>	gi9858781		0.00023
400	G2375	<i>Daucus carota</i>	gi2190187		0.00051
400	G2375	<i>Fagopyrum urophyllum</i>	gi31088123		0.007
401	G2382	<i>Medicago truncatula</i>	Mtr_S7091755	1710	
401	G2382	<i>Triticum aestivum</i>	Ta_S282850	1902	
401	G2382	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-47842	2056	
401	G2382	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-57633	2057	
402	G2382	<i>Brassica oleracea</i>	BH542030		1.00E-104
402	G2382	<i>Brassica napus</i>	CD814588		2.00E-63
402	G2382	<i>Vitis vinifera</i>	CB347529		2.00E-57
402	G2382	<i>Ipomoea nil</i>	BJ575415		4.00E-45
402	G2382	<i>Lycopersicon esculentum</i>	AW441337		2.00E-40
402	G2382	<i>Medicago truncatula</i>	CA921647		6.00E-40
402	G2382	<i>Lactuca sativa</i>	BU006964		3.00E-39
402	G2382	<i>Vitis aestivalis</i>	CB289221		1.00E-34
402	G2382	<i>Oryza sativa</i>	AP003453		9.00E-34

402	G2382	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01000618		8.00E-32
402	G2382	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi15624003		4.00E-33
402	G2382	<i>Nicotiana tabacum</i>	gi18149189		6.90E-23
402	G2382	<i>Oryza sativa</i>	gi12597883		3.80E-08
402	G2382	<i>Chloroplast Panicum koolauense</i>	gi16551225		8.60E-07
402	G2382	<i>Chloroplast Paspalum fimbriatum</i>	gi16551261		5.90E-05
402	G2382	<i>Chloroplast Mesosetum chaseae</i>	gi16551247		0.00022
402	G2382	<i>Chloroplast Thrasya petrosa</i>	gi16551309		0.00027
402	G2382	<i>Chloroplast Tatianyx arnacites</i>	gi16551305		0.00072
402	G2382	<i>Chloroplast Altoparadisium chapadense</i>	gi16551207		0.00078
402	G2382	<i>Chloroplast Thrasya glaziovii</i>	gi16551307		0.0011
404	G2394	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK071804		1.00E-108
404	G2394	<i>Zea mays</i>	BG837939		2.00E-85
404	G2394	<i>Oryza sativa</i>	AX699700		3.00E-72
404	G2394	<i>Triticum aestivum</i>	BJ319065		7.00E-72
404	G2394	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	CB634885		3.00E-69
404	G2394	<i>Lactuca sativa</i>	BQ852089		4.00E-69
404	G2394	<i>Lycopersicon esculentum</i>	BI921710		1.00E-67
404	G2394	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	AL505242		9.00E-64
404	G2394	<i>Hordeum vulgare</i>	BU991885		3.00E-60
404	G2394	<i>Solanum tuberosum</i>	BQ512426		3.00E-57
404	G2394	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi15289774		1.50E-74
404	G2394	<i>Phacelia tanacetifolia</i>	gi5002214		1.50E-24
404	G2394	<i>Oryza sativa</i>	gi14164470		1.40E-13
404	G2394	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152976		1.80E-12
404	G2394	<i>Cicer arietinum</i>	gi10334499		6.90E-12
404	G2394	<i>Cucumis melo</i>	gi17016985		8.10E-12
404	G2394	<i>Thellungiella halophila</i>	gi20340241		7.80E-11
404	G2394	<i>Nicotiana tabacum</i>	gi12003386		8.80E-10
404	G2394	<i>Zea mays</i>	gi21645888		1.10E-09
404	G2394	<i>Hordeum vulgare</i>	gi2894379		2.30E-09
406	G2404	<i>Brassica oleracea</i>	BH418639		3.00E-61
406	G2404	<i>Descurainia sophia</i>	BU238407		1.00E-47
406	G2404	<i>Medicago</i>	BQ148493		3.00E-45

		<i>truncatula</i>			
406	G2404	<i>Brassica napus</i>	CD815525		3.00E-41
406	G2404	<i>Vitis vinifera</i>	CB983093		1.00E-39
406	G2404	<i>Glycine max</i>	BQ741279		6.00E-39
406	G2404	<i>Nicotiana tabacum</i>	BP129655		3.00E-36
406	G2404	<i>Solanum tuberosum</i>	BQ507078		5.00E-36
406	G2404	<i>Populus tremula x</i> <i>Populus tremuloides</i>	BI131425		5.00E-33
406	G2404	<i>Oryza sativa</i>	AU101377		2.00E-31
406	G2404	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi18565429		3.90E-41
406	G2404	<i>Pisum sativum</i>	gi4240031		8.40E-29
406	G2404	<i>Lotus japonicus</i>	gi1086225		3.10E-27
406	G2404	<i>Oryza sativa</i>	gi8570055		5.10E-26
406	G2404	<i>Glycine max</i>	gi1076498		1.00E-25
406	G2404	<i>Cicer arietinum</i>	gi10334499		1.80E-14
406	G2404	<i>Thellungiella</i> <i>halophila</i>	gi20340241		9.50E-09
406	G2404	<i>Cucumis melo</i>	gi17016985		1.20E-07
406	G2404	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	gi29164825		1.50E-07
406	G2404	<i>Hordeum vulgare</i>	gi2894379		4.80E-06
407	G2432	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER68229_1	1143	
407	G2432	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER68229_2	1144	
407	G2432	<i>Oryza sativa</i>	OSC2225.C1.p2.fg	1145	
407	G2432	<i>Oryza sativa</i>	Os_S60255	1608	
407	G2432	<i>Lycopersicon</i> <i>esculentum</i>	SGN-UNIGENE- SINGLET-18277	2058	
408	G2432	<i>Brassica oleracea</i>	BH959523		7.00E-85
408	G2432	<i>Brassica napus</i>	CD824503		6.00E-76
408	G2432	<i>Populus</i> <i>balsamifera</i> subsp. <i>trichocarpa</i>	BU868493		7.00E-47
408	G2432	<i>Lycopersicon</i> <i>esculentum</i>	AW648389		7.00E-39
408	G2432	<i>Vitis vinifera</i>	CA810654		1.00E-36
408	G2432	<i>Medicago</i> <i>truncatula</i>	BE323614		2.00E-35
408	G2432	<i>Glycine max</i>	BE474759		3.00E-31
408	G2432	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	HVU312330		1.00E-30
408	G2432	<i>Beta vulgaris</i>	BQ584245		2.00E-29
408	G2432	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	CB622873		3.00E-29
408	G2432	<i>Oryza sativa</i>	gi15451553		3.40E-33
408	G2432	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi31431991		3.40E-33
408	G2432	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi21538791		3.70E-30
408	G2432	<i>Cucurbita maxima</i>	gi1669341		1.10E-28
408	G2432	<i>Dendrobium</i> grex <i>Madame Thong-In</i>	gi3929325		6.60E-24
408	G2432	<i>Hordeum vulgare</i>	gi3777436		1.20E-22

408	G2432	<i>Zea mays</i>	gi1346559		2.00E-22
408	G2432	<i>Pisum sativum</i>	gi6092016		5.40E-22
408	G2432	<i>Nicotiana tabacum</i>	gi3341468		1.10E-21
408	G2432	<i>Triticum aestivum</i>	gi3790264		1.10E-21
410	G2443	<i>Brassica napus</i>	A50832		1.00E-148
410	G2443	<i>Brassica nigra</i>	AF269127		1.00E-131
410	G2443	<i>Brassica oleracea</i>	BH650127		1.00E-93
410	G2443	<i>Ipomoea nil</i>	AF300700		2.00E-86
410	G2443	<i>Oryza sativa</i>	AB041838		1.00E-65
410	G2443	<i>Malus domestica</i>	AF052585		7.00E-62
410	G2443	<i>Raphanus sativus</i>	AF052690		2.00E-59
410	G2443	<i>Pinus radiata</i>	AF001136		2.00E-58
410	G2443	<i>Medicago truncatula</i>	AC127169		7.00E-57
410	G2443	<i>Mesembryanthemum crystallinum</i>	BM300894		2.00E-54
410	G2443	<i>Brassica napus</i>	gi2303681		1.80E-140
410	G2443	<i>Brassica nigra</i>	gi11037308		9.00E-139
410	G2443	<i>Oryza sativa</i>	gi11094203		1.90E-65
410	G2443	<i>Oryza sativa</i> (japonica cultivar-group)	gi23589949		1.90E-65
410	G2443	<i>Hordeum vulgare</i>	gi21667475		1.10E-60
410	G2443	<i>Malus x domestica</i>	gi4091804		2.10E-59
410	G2443	<i>Raphanus sativus</i>	gi3341723		1.80E-56
410	G2443	<i>Ipomoea nil</i>	gi10946337		1.90E-51
410	G2443	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi21655154		6.60E-51
410	G2443	<i>Pinus radiata</i>	gi4557093		2.90E-39
411	G2453	<i>Glycine max</i>	BF070025.1	1146	
411	G2453	<i>Oryza sativa</i>	Os_S112425	1609	
411	G2453	<i>Zea mays</i>	Zm_S11447234	1813	
412	G2453	<i>Chrysanthemum x morifolium</i>	AY173066		1.00E-33
412	G2453	<i>Lactuca sativa</i>	BQ995044		3.00E-33
412	G2453	<i>Glycine max</i>	CA935182		1.00E-32
412	G2453	<i>Hordeum vulgare</i>	BI949633		2.00E-32
412	G2453	<i>Antirrhinum majus</i>	AJ559762		6.00E-32
412	G2453	<i>Lycopersicon esculentum</i>	BI931349		1.00E-31
412	G2453	<i>Solanum tuberosum</i>	BQ117114		1.00E-31
412	G2453	<i>Mentha x piperita</i>	AW255624		2.00E-31
412	G2453	<i>Oryza sativa</i> (japonica cultivar-group)	AU094883		2.00E-31
412	G2453	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BU968850		2.00E-31
412	G2453	<i>Chrysanthemum x morifolium</i>	gi27804377		1.70E-34
412	G2453	<i>Zea mays</i>	gi32330681		2.00E-34
412	G2453	<i>Oryza sativa</i> (japonica cultivar-group)	gi22267600		1.40E-33
412	G2453	<i>Oryza sativa</i>	gi11280864		3.60E-32
412	G2453	<i>Daucus carota</i>	gi3551257		0.81
412	G2453	<i>Vicia faba</i>	gi2104679		0.82

412	G2453	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi29123372		0.9
412	G2453	<i>Nicotiana tabacum</i>	gi2196548		0.97
412	G2453	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	gi23345287		1
412	G2453	<i>Narcissus</i> <i>pseudonarcissus</i>	gi18419623		1
414	G2455	<i>Brassica napus</i>	CD830903		3.00E-63
414	G2455	<i>Lycopersicon</i> <i>esculentum</i>	BM410884		3.00E-58
414	G2455	<i>Glycine max</i>	BU579031		2.00E-56
414	G2455	<i>Populus</i> <i>balsamifera</i> subsp. <i>trichocarpa</i>	BU871780		9.00E-56
414	G2455	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU864185		2.00E-53
414	G2455	<i>Prunus persica</i>	BU044242		3.00E-50
414	G2455	<i>Cycas rumphii</i>	CB093475		1.00E-48
414	G2455	<i>Nuphar advena</i>	CD472928		9.00E-48
414	G2455	<i>Antirrhinum majus</i>	AJ559762		1.00E-46
414	G2455	<i>Triticum aestivum</i>	BJ264502		5.00E-44
414	G2455	<i>Chrysanthemum</i> x <i>morifolium</i>	gi27804377		5.60E-43
414	G2455	<i>Zea mays</i>	gi32330677		6.40E-43
414	G2455	<i>Oryza sativa</i>	gi11280864		7.10E-43
414	G2455	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi33146736		9.10E-43
414	G2455	<i>Glycine max</i>	gi5019730		0.16
414	G2455	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi29123372		0.2
414	G2455	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	gi2570503		0.69
416	G2456	<i>Glycine max</i>	CA800830		3.00E-67
416	G2456	<i>Chrysanthemum</i> x <i>morifolium</i>	AY173066		5.00E-63
416	G2456	<i>Lycopersicon</i> <i>esculentum</i>	AW623191		6.00E-62
416	G2456	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU830431		5.00E-61
416	G2456	<i>Solanum tuberosum</i>	BQ117114		2.00E-58
416	G2456	<i>Zea mays</i>	AY313904		6.00E-58
416	G2456	<i>Lactuca sativa</i>	BQ995044		1.00E-57
416	G2456	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AK106784		2.00E-57
416	G2456	<i>Nuphar advena</i>	CD475930		1.00E-52
416	G2456	<i>Populus tremuloides</i>	CA931450		8.00E-50
416	G2456	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi22267600		1.20E-61
416	G2456	<i>Zea mays</i>	gi32330681		8.50E-61
416	G2456	<i>Chrysanthemum</i> x <i>morifolium</i>	gi27804377		8.80E-61
416	G2456	<i>Oryza sativa</i>	gi11280863		7.90E-37
416	G2456	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi29123372		0.027

416	G2456	<i>Triticum aestivum</i>	gi32400832		0.037
416	G2456	<i>Solanum tuberosum</i>	gi9954112		0.038
416	G2456	<i>Phaseolus vulgaris</i>	gi457750		0.04
416	G2456	<i>Volvox carteri f. nagariensis</i>	gi6523547		0.22
416	G2456	<i>Capsella rubella</i>	gi8919877		0.45
417	G2457	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER62346_1	1147	
417	G2457	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER47850_1	1148	
417	G2457	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER504_1	1149	
417	G2457	<i>Oryza sativa</i>	OSC102186.C1.p13.fg	1150	
417	G2457	<i>Oryza sativa</i>	OSC29392.C1.p1.fg	1151	
417	G2457	<i>Oryza sativa</i>	OSC7136.C1.p1.fg	1152	
417	G2457	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER603_35	1153	
417	G2457	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER779_19	1154	
417	G2457	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER779_20	1155	
417	G2457	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER779_24	1156	
417	G2457	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER779_9	1157	
417	G2457	<i>Hordeum vulgare</i>	Hv_S18520	1742	
417	G2457	<i>Zea mays</i>	Zm_S11528333	1814	
417	G2457	<i>Triticum aestivum</i>	Ta_S241823	1903	
417	G2457	<i>Triticum aestivum</i>	Ta_S417975	1904	
418	G2457	<i>Antirrhinum majus</i>	AJ559642		6.00E-55
418	G2457	<i>Lycopersicon esculentum</i>	AI483816		7.00E-53
418	G2457	<i>Hedyotis centranthoides</i>	CB088054		9.00E-53
418	G2457	<i>Zea mays</i>	AY104291		1.00E-41
418	G2457	<i>Triticum aestivum</i>	BT008985		5.00E-41
418	G2457	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BQ462679		3.00E-40
418	G2457	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU880953		5.00E-30
418	G2457	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK104918		5.00E-30
418	G2457	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU864185		5.00E-30
418	G2457	<i>Prunus persica</i>	BU043103		2.00E-29
418	G2457	<i>Zea mays</i>	gi32330677		8.50E-32
418	G2457	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi22267600		9.50E-31
418	G2457	<i>Oryza sativa</i>	gi11280863		4.70E-30
418	G2457	<i>Chrysanthemum</i> x <i>morifolium</i>	gi27804377		1.70E-18
418	G2457	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi29123372		1.70E-16
418	G2457	<i>Sesbania rostrata</i>	gi169880		0.3

418	G2457	<i>Lycopersicon esculentum</i>	gi4467884		0.45
418	G2457	<i>Dianthus caryophyllus</i>	gi2406586		0.63
418	G2457	<i>Vicia faba</i>	gi4468042		0.81
418	G2457	<i>Pisum sativum</i>	gi100057		0.96
419	G2459	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER62346 1	1147	
419	G2459	<i>Oryza sativa</i>	LIB4370-016-R1-K1-B3	1158	
419	G2459	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER47850 1	1148	
419	G2459	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER504 1	1149	
419	G2459	<i>Oryza sativa</i>	OSC102186.C1.p13.fg	1150	
419	G2459	<i>Oryza sativa</i>	OSC29392.C1.p1.fg	1151	
419	G2459	<i>Oryza sativa</i>	OSC7136.C1.p1.fg	1152	
419	G2459	<i>Oryza sativa</i>	jC-osfLIB3479001b04b1	1159	
419	G2459	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER603 34	1160	
419	G2459	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER603 35	1153	
419	G2459	<i>Triticum aestivum</i>	Ta_S241823	1903	
419	G2459	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-70658	2059	
420	G2459	<i>Brassica napus</i>	CD830187		4.00E-84
420	G2459	<i>Glycine max</i>	CA800542		4.00E-68
420	G2459	<i>Lycopersicon esculentum</i>	AI484101		2.00E-66
420	G2459	<i>Antirrhinum majus</i>	AJ559762		6.00E-61
420	G2459	<i>Mentha x piperita</i>	AW255624		4.00E-58
420	G2459	<i>Solanum tuberosum</i>	BQ516639		2.00E-56
420	G2459	<i>Ipomoea nil</i>	BJ575190		6.00E-51
420	G2459	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU880953		2.00E-49
420	G2459	<i>Populus tremula x Populus tremuloides</i>	BU864185		2.00E-48
420	G2459	<i>Nuphar advena</i>	CD474192		1.00E-47
420	G2459	<i>Oryza sativa</i>	gi11280864		1.30E-45
420	G2459	<i>Zea mays</i>	gi32330677		7.30E-44
420	G2459	<i>Oryza sativa (japonica cultivar- group)</i>	gi22267600		1.20E-43
420	G2459	<i>Chrysanthemum x morifolium</i>	gi27804377		1.20E-26
420	G2459	<i>Brassica rapa subsp. pekinensis</i>	gi29123372		0.013
420	G2459	<i>Nicotiana tabacum</i>	gi4206787		0.68
420	G2459	<i>Narcissus pseudonarcissus</i>	gi18419623		1
420	G2459	<i>Pinus koraiensis</i>	gi29469765		1
422	G2467	<i>Brassica oleracea</i>	BH657157		7.00E-72
422	G2467	<i>Citrus sinensis</i>	CB291749		8.00E-63
422	G2467	<i>Oryza sativa</i>	AX653477		1.00E-59
422	G2467	<i>Oryza sativa (japonica cultivar- group)</i>	AK068660		2.00E-59

422	G2467	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	AV833112		5.00E-51
422	G2467	<i>Lycopersicon</i> <i>peruvianum</i>	LPHSF30		3.00E-50
422	G2467	<i>Medicago</i> <i>truncatula</i>	BE319312		2.00E-49
422	G2467	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01016817		5.00E-49
422	G2467	<i>Zea mays</i>	CC610706		5.00E-49
422	G2467	<i>Helianthus annuus</i>	BQ916240		9.00E-48
422	G2467	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi28971956		2.20E-58
422	G2467	<i>Lycopersicon</i> <i>peruvianum</i>	gi100265		5.70E-50
422	G2467	<i>Helianthus annuus</i>	gi25052685		7.90E-44
422	G2467	<i>Glycine max</i>	gi2129828		9.10E-43
422	G2467	<i>Oryza sativa</i>	gi16580739		1.70E-42
422	G2467	<i>Phaseolus</i> <i>acutifolius</i>	gi16118447		6.20E-37
422	G2467	<i>Nicotiana tabacum</i>	gi5821138		1.00E-36
422	G2467	<i>Lycopersicon</i> <i>esculentum</i>	gi100225		1.30E-36
422	G2467	<i>Medicago sativa</i>	gi20162459		1.10E-35
422	G2467	<i>Pisum sativum</i>	gi3550552		4.50E-34
424	G2492	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AK073195		1.00E-126
424	G2492	<i>Pisum sativum</i>	PSPD3BIPR		3.00E-72
424	G2492	<i>Vicia sativa</i>	VSENBPIGN		2.00E-71
424	G2492	<i>Lactuca sativa</i>	BU008717		4.00E-69
424	G2492	<i>Vitis vinifera</i>	CB348303		8.00E-67
424	G2492	<i>Mesembryanthemum</i> <i>crystallinum</i>	CA838861		9.00E-65
424	G2492	<i>Zea mays</i>	AY106688		2.00E-64
424	G2492	<i>Brassica oleracea</i>	BH582293		1.00E-60
424	G2492	<i>Triphysaria</i> <i>versicolor</i>	BM357136		1.00E-60
424	G2492	<i>Ipomoea nil</i>	BJ577989		6.00E-59
424	G2492	<i>Medicago</i> <i>truncatula</i>	gi11358945		2.50E-153
424	G2492	<i>Pisum sativum</i>	gi2213540		3.00E-151
424	G2492	<i>Vicia sativa</i>	gi1360637		1.30E-150
424	G2492	<i>Nicotiana tabacum</i>	gi8096269		7.20E-10
424	G2492	<i>Brassica oleracea</i>	gi15054376		9.90E-08
424	G2492	<i>Oryza sativa</i>	gi6942229		6.40E-06
424	G2492	<i>Zea mays</i>	gi4138732		3.90E-05
424	G2492	<i>Saccharum hybrid</i> cultivar CP72-2086	gi21902142		0.00016
424	G2492	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi29367369		0.00062
424	G2492	<i>Saccharum hybrid</i> cultivar CP65-357	gi18873729		0.0016
425	G2505	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER81568 1	1161	
425	G2505	<i>Zea mays</i>	LIB5116-010-A1-PF1-D6	1162	

426	G2505	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU879250		7.00E-72
426	G2505	<i>Medicago truncatula</i>	BF645892		5.00E-70
426	G2505	<i>Sorghum bicolor</i>	CD230282		6.00E-68
426	G2505	<i>Oryza sativa</i> (japonica cultivar-group)	AK109860		2.00E-67
426	G2505	<i>Oryza sativa</i>	AB028186		6.00E-66
426	G2505	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i> x <i>Populus deltoides</i>	CA826386		2.00E-63
426	G2505	<i>Lycopersicon esculentum</i>	BF098091		5.00E-62
426	G2505	<i>Triticum aestivum</i>	BQ483881		7.00E-62
426	G2505	<i>Hordeum vulgare</i>	BE060921		4.00E-61
426	G2505	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01001925		1.00E-56
426	G2505	<i>Oryza sativa</i>	gi11875152		1.70E-66
426	G2505	<i>Oryza sativa</i> (japonica cultivar-group)	gi28190666		1.70E-66
426	G2505	<i>Petunia x hybrida</i>	gi1279640		5.80E-48
426	G2505	<i>Glycine max</i>	gi22597158		7.50E-48
426	G2505	<i>Zea mays</i>	gi32527660		4.50E-46
426	G2505	<i>Phaseolus vulgaris</i>	gi15148914		6.00E-46
426	G2505	<i>Triticum sp.</i>	gi4218537		5.40E-45
426	G2505	<i>Triticum monococcum</i>	gi6732156		5.40E-45
426	G2505	<i>Lycopersicon esculentum</i>	gi6175246		1.30E-43
426	G2505	<i>Brassica napus</i>	gi31322582		3.10E-42
428	G2515	<i>Betula pendula</i>	BPMADS5GN		1.00E-59
428	G2515	<i>Vitis vinifera</i>	AY275713		1.00E-56
428	G2515	<i>Petunia x hybrida</i>	AF176782		2.00E-55
428	G2515	<i>Petunia sp.</i>	A81451		2.00E-55
428	G2515	<i>Chrysanthemum x morifolium</i>	AY173055		2.00E-55
428	G2515	<i>Nicotiana tabacum</i>	AF385746		4.00E-55
428	G2515	<i>Capsicum annuum</i>	AF130118		4.00E-55
428	G2515	<i>Eucalyptus globulus</i>	AF306349		1.00E-54
428	G2515	<i>Antirrhinum majus</i>	AY040247		2.00E-54
428	G2515	<i>Daucus carota</i>	DCA271147		3.00E-54
428	G2515	<i>Betula pendula</i>	gi1483232		6.40E-58
428	G2515	<i>Vitis vinifera</i>	gi30526323		8.40E-56
428	G2515	<i>Chrysanthemum x morifolium</i>	gi27804357		2.60E-54
428	G2515	<i>Capsicum annuum</i>	gi14518447		2.60E-54
428	G2515	<i>Petunia x hybrida</i>	gi6634708		3.30E-54
428	G2515	<i>Petunia sp.</i>	gi6731756		3.30E-54
428	G2515	<i>Nicotiana tabacum</i>	gi27373049		5.30E-54
428	G2515	<i>Eucalyptus globulus</i>	gi11120557		6.80E-54
428	G2515	<i>Nicotiana glauca</i>	gi5070142		2.30E-53
428	G2515	<i>Daucus carota</i>	gi22091473		2.90E-53

430	G2525	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AC145379		3.00E-86
430	G2525	<i>Solanum tuberosum</i>	BQ115041		6.00E-76
430	G2525	<i>Suaeda maritima</i> subsp. <i>salsa</i>	BE231373		2.00E-69
430	G2525	<i>Brassica oleracea</i>	BH432132		2.00E-67
430	G2525	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	CB878456		3.00E-65
430	G2525	<i>Lactuca sativa</i>	BU013946		1.00E-63
430	G2525	<i>Medicago truncatula</i>	BE325206		1.00E-62
430	G2525	<i>Gossypium hirsutum</i>	AI728383		6.00E-60
430	G2525	<i>Zea mays</i>	CC641341		2.00E-58
430	G2525	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01009282		5.00E-58
430	G2525	<i>Oryza sativa</i>	gi18873845		1.20E-44
430	G2525	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi31433498		1.20E-44
430	G2525	<i>Spermatozopsis similis</i>	gi3417441		0.14
430	G2525	<i>Nicotiana tabacum</i>	gi237857		0.3
430	G2525	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	gi5679839		0.46
430	G2525	<i>Chlamydomonas reinhardtii</i>	gi3342148		0.58
430	G2525	<i>Brassica juncea</i>	gi32527767		0.94
430	G2525	<i>Zea mays</i>	gi100920		0.99
430	G2525	<i>Helianthus praecox</i>	gi18073228		1
430	G2525	<i>Helianthus niveus</i>	gi27526450		1
431	G2536	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER325924_1	1163	
431	G2536	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER325924_2	1164	
431	G2536	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER325924_3	1165	
431	G2536	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER90132_1	1166	
431	G2536	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER90912_1	1167	
431	G2536	<i>Oryza sativa</i>	BE039729.1	1168	
431	G2536	<i>Oryza sativa</i>	BE039742.1	1169	
431	G2536	<i>Oryza sativa</i>	OSC12121.C1.p10.fg	1170	
431	G2536	<i>Oryza sativa</i>	OSC8882.C1.p8.fg	1171	
431	G2536	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER460898_1	1172	
431	G2536	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-56029	2060	
431	G2536	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-36423	2061	
432	G2536	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU815065		5.00E-57
432	G2536	<i>Nicotiana tabacum</i>	AB021178		1.00E-53
432	G2536	<i>Medicago truncatula</i>	BG647353		2.00E-52

432	G2536	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i> x <i>Populus deltoides</i>	CA825708		1.00E-48
432	G2536	<i>Lycopersicon esculentum</i>	AW030267		3.00E-47
432	G2536	<i>Brassica oleracea</i>	BZ032987		1.00E-45
432	G2536	<i>Glycine max</i>	BM886486		1.00E-45
432	G2536	<i>Lactuca sativa</i>	BQ875839		4.00E-44
432	G2536	<i>Oryza sativa</i> (japonica cultivar-group)	AK063703		2.00E-43
432	G2536	<i>Zea mays</i>	CC673415		2.00E-42
432	G2536	<i>Nicotiana tabacum</i>	gi25457840		1.00E-50
432	G2536	<i>Oryza sativa</i>	gi15290110		6.50E-45
432	G2536	<i>Brassica napus</i>	gi31322582		5.10E-30
432	G2536	<i>Oryza sativa</i> (japonica cultivar-group)	gi24899399		8.10E-28
432	G2536	<i>Petunia x hybrida</i>	gi21105734		3.40E-27
432	G2536	<i>Solanum tuberosum</i>	gi14485513		1.20E-26
432	G2536	<i>Glycine max</i>	gi22597158		1.50E-26
432	G2536	<i>Lycopersicon esculentum</i>	gi6175246		1.50E-26
432	G2536	<i>Phaseolus vulgaris</i>	gi15148914		6.40E-26
432	G2536	<i>Triticum sp.</i>	gi4218535		8.50E-24
434	G2543	<i>Phalaenopsis sp.</i> SM9108	PSU34743		1.0e-999
434	G2543	<i>Picea abies</i>	AF172931		1.0e-999
434	G2543	<i>Oryza sativa</i> (japonica cultivar-group)	AB101645		1.00E-173
434	G2543	<i>Gossypium hirsutum</i>	AF530914		1.00E-173
434	G2543	<i>Oryza sativa</i>	AB077993		1.00E-172
434	G2543	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01007245		1.00E-170
434	G2543	<i>Zea mays</i>	ZMA250987		1.00E-170
434	G2543	<i>Malus domestica</i>	AF067961		1.00E-146
434	G2543	<i>Helianthus annuus</i>	HNNHAHR		1.00E-118
434	G2543	<i>Vitis vinifera</i>	CB002690		2.00E-93
434	G2543	<i>Phalaenopsis sp.</i> SM9108	gi1173622		5.10E-175
434	G2543	<i>Phalaenopsis sp.</i>	gi2147484		5.10E-175
434	G2543	<i>Picea abies</i>	gi12002853		4.80E-172
434	G2543	<i>Oryza sativa</i> (japonica cultivar-group)	gi32488795		4.70E-165
434	G2543	<i>Gossypium hirsutum</i>	gi22475197		6.00E-165
434	G2543	<i>Sorghum bicolor</i>	gi18481701		7.70E-165
434	G2543	<i>Oryza sativa</i>	gi19072102		5.40E-164
434	G2543	<i>Zea mays</i>	gi8920427		4.40E-162
434	G2543	<i>Malus x domestica</i>	gi3925363		2.10E-139
434	G2543	<i>Helianthus annuus</i>	gi1208940		1.90E-106
435	G2550	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER39853 1	1173	

435	G2550	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER39853_2	1174	
435	G2550	<i>Oryza sativa</i>	uC-osroM202005g06b1	1175	
435	G2550	<i>Oryza sativa</i>	Os_S107153	1610	
435	G2550	<i>Medicago truncatula</i>	Mtr_S5360919	1711	
435	G2550	<i>Medicago truncatula</i>	Mtr_S7094331	1712	
435	G2550	<i>Zea mays</i>	Zm_S11465618	1815	
435	G2550	<i>Triticum aestivum</i>	Ta_S146249	1905	
436	G2550	<i>Solanum tuberosum</i>	AF406703		9.00E-90
436	G2550	<i>Oryza sativa (japonica cultivar- group)</i>	AK069994		6.00E-89
436	G2550	<i>Brassica oleracea</i>	BZ485520		1.00E-82
436	G2550	<i>Lycopersicon esculentum</i>	AF375966		2.00E-77
436	G2550	<i>Sorghum bicolor</i>	BM324585		5.00E-74
436	G2550	<i>Malus x domestica</i>	AF053769		2.00E-70
436	G2550	<i>Oryza minuta</i>	CB213421		3.00E-70
436	G2550	<i>Hordeum vulgare</i>	BG344928		5.00E-70
436	G2550	<i>Medicago truncatula</i>	AW688195		8.00E-67
436	G2550	<i>Oryza sativa (indica cultivar-group)</i>	CB618008		3.00E-66
436	G2550	<i>Solanum tuberosum</i>	gi22652127		1.40E-87
436	G2550	<i>Oryza sativa</i>	gi12656811		1.60E-84
436	G2550	<i>Oryza sativa (japonica cultivar- group)</i>	gi20219036		1.20E-83
436	G2550	<i>Lycopersicon esculentum</i>	gi31323447		4.40E-75
436	G2550	<i>Hordeum vulgare</i>	gi13752407		1.70E-72
436	G2550	<i>Malus x domestica</i>	gi7239157		9.40E-72
436	G2550	<i>Gnetum gnemon</i>	gi31746344		5.50E-66
436	G2550	<i>Oryza sativa (indica cultivar-group)</i>	gi19352101		4.00E-49
436	G2550	<i>Zea mays</i>	gi19743685		1.90E-42
436	G2550	<i>Helianthus annuus</i>	gi20977644		6.30E-12
438	G2559	<i>Solanum tuberosum</i>	STU72489		1.00E-59
438	G2559	<i>Lycopersicon esculentum</i>	AF123265		2.00E-59
438	G2559	<i>Antirrhinum majus</i>	AJ559687		3.00E-54
438	G2559	<i>Vitis vinifera</i>	CB344101		2.00E-53
438	G2559	<i>Glycine max</i>	CA799179		3.00E-53
438	G2559	<i>Ipomoea nil</i>	BJ573275		9.00E-53
438	G2559	<i>Citrus sinensis</i>	CB292623		2.00E-52
438	G2559	<i>Gossypium arboreum</i>	BQ411282		6.00E-52
438	G2559	<i>Oryza sativa (japonica cultivar- group)</i>	AK105097		8.00E-52
438;	G2559	<i>Medicago truncatula</i>	BM779097		1.00E-51
438	G2559	<i>Solanum tuberosum</i>	gi1881585		7.10E-59
438	G2559	<i>Lycopersicon esculentum</i>	gi4731573		3.90E-58

438	G2559	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi32489830		1.50E-51
438	G2559	<i>Lotus japonicus</i>	gi2367429		9.80E-05
438	G2559	<i>Zea mays</i>	gi23928441		0.00023
438	G2559	<i>Plastid Oenothera elata</i> subsp. <i>hookeri</i>	gi13276714		0.00077
438	G2559	<i>Oenothera elata</i> subsp. <i>hookeri</i>	gi23822375		0.00077
438	G2559	<i>Nicotiana tabacum</i>	gi8096269		0.0013
438	G2559	<i>Cicer arietinum</i>	gi3129939		0.0014
438	G2559	<i>Solanum berthaultii</i>	gi1216214		0.002
440	G2565	<i>Mesembryanthemum crystallinum</i>	AF219972		5.00E-67
440	G2565	<i>Nicotiana tabacum</i>	AB017693		1.00E-60
440	G2565	<i>Triticum aestivum</i>	BQ806133		3.00E-55
440	G2565	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK109510		6.00E-55
440	G2565	<i>Beta vulgaris</i>	BQ587750		1.00E-52
440	G2565	<i>Medicago truncatula</i>	AW684291		1.00E-51
440	G2565	<i>Zea mays</i>	AY107734		2.00E-51
440	G2565	<i>Glycine max</i>	AW507631		2.00E-51
440	G2565	<i>Lycopersicon esculentum</i>	AW030183		8.00E-51
440	G2565	<i>Hordeum vulgare</i>	BU993345		8.00E-46
440	G2565	<i>Mesembryanthemum crystallinum</i>	gi6942190		3.50E-66
440	G2565	<i>Nicotiana tabacum</i>	gi4519671		2.80E-57
440	G2565	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi29647445		3.90E-42
440	G2565	<i>Solanum bulbocastanum</i>	gi32470629		6.00E-30
440	G2565	<i>Chlamydomonas reinhardtii</i>	gi5916207		2.30E-24
440	G2565	<i>Oryza sativa</i>	gi11034542		1.30E-09
440	G2565	<i>Zea mays</i>	gi15667625		2.60E-08
440	G2565	<i>Oryza glaberrima</i>	gi31338862		2.70E-07
440	G2565	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	gi31338860		7.40E-07
440	G2565	<i>Pachysandra terminalis</i>	gi32478053		0.0038
441	G2567	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER105903_1	1176	
441	G2567	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER25797_1	1177	
441	G2567	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER25797_2	1178	
441	G2567	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER25797_4	1179	
441	G2567	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER30315_1	1180	
441	G2567	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER67014_1	1181	
441	G2567	<i>Oryza sativa</i>	ORYSA-22JAN02-	1182	

			CLUSTER14787_2		
441	G2567	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER14787_3	1183	
441	G2567	<i>Oryza sativa</i>	OSC100544.C1.p6.fg	1184	
441	G2567	<i>Oryza sativa</i>	OSC100702.C1.p11.fg	1185	
441	G2567	<i>Oryza sativa</i>	OSC19346.C1.p18.fg	1186	
441	G2567	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER28837_1	1187	
441	G2567	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER536_1816	1188	
441	G2567	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER536_BYHAND_1816	1189	
441	G2567	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER64018_1	1190	
441	G2567	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER64018_4	1191	
441	G2567	<i>Oryza sativa</i>	Os_S45221	1611	
441	G2567	<i>Oryza sativa</i>	Os_S99383	1612	
441	G2567	<i>Glycine max</i>	Gma_S5079377	1669	
441	G2567	<i>Hordeum vulgare</i>	Hv_S31206	1743	
441	G2567	<i>Zea mays</i>	Zm_S11521593	1816	
441	G2567	<i>Triticum aestivum</i>	Ta_S114520	1906	
441	G2567	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-357264	2062	
441	G2567	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-360651	2063	
441	G2567	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-463424	2064	
442	G2567	<i>Oryza sativa</i> (japonica cultivar-group)	AK100322		1.0e-999
442	G2567	<i>Oryza sativa</i>	AB071299		1.0e-999
442	G2567	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01008877		1.00E-172
442	G2567	<i>Lotus japonicus</i>	AP004505		1.00E-140
442	G2567	<i>Physcomitrella patens</i>	AX288142		1.00E-131
442	G2567	<i>Brassica oleracea</i>	BZ016919		1.00E-124
442	G2567	<i>Medicago truncatula</i>	BG646821		1.00E-104
442	G2567	<i>Brassica napus</i>	CD843527		1.00E-100
442	G2567	<i>Zea mays</i>	CC657791		2.00E-99
442	G2567	<i>Vitis vinifera</i>	CB979491		2.00E-90
442	G2567	<i>Oryza sativa</i> (japonica cultivar-group)	gi13384374		3.80E-186
442	G2567	<i>Oryza sativa</i>	gi19352051		3.30E-164
442	G2567	<i>Prunus persica</i>	gi27450533		8.50E-72
442	G2567	<i>Oryza sativa</i> (indica cultivar-group)	gi26251300		4.30E-70
442	G2567	<i>Mangifera indica</i>	gi30027167		2.00E-68
442	G2567	<i>Marchantia polymorpha</i>	gi25272004		5.40E-13
442	G2567	<i>Mirabilis jalapa</i>	gi23343944		3.20E-05
442	G2567	<i>Zea mays</i>	gi18697008		0.014
442	G2567	<i>Cucumis sativus</i>	gi6136830		0.049

442	G2567	<i>Nicotiana tabacum</i>	gi4887014		0.087
444	G2570	<i>Brassica oleracea</i>	BH973299		3.00E-49
444	G2570	<i>Zea mays</i>	AB060130		3.00E-32
444	G2570	<i>Oryza sativa</i> (japonica cultivar-group)	AK101165		1.00E-28
444	G2570	<i>Oryza sativa</i> (indica cultivar-group)	CB630542		1.00E-25
444	G2570	<i>Medicago truncatula</i>	CB891281		3.00E-22
444	G2570	<i>Brassica napus</i>	QD825309		2.00E-20
444	G2570	<i>Solanum tuberosum</i>	BM407041		3.00E-20
444	G2570	<i>Triticum aestivum</i>	BQ743733		2.00E-17
444	G2570	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	CA014844		5.00E-17
444	G2570	<i>Stevia rebaudiana</i>	BG525366		9.00E-17
444	G2570	<i>Zea mays</i>	gi13661174		3.10E-31
444	G2570	<i>Oryza sativa</i> (japonica cultivar-group)	gi24308616		4.60E-31
444	G2570	<i>Oryza glaberrima</i>	gi31338862		1.90E-23
444	G2570	<i>Oryza sativa</i> (indica cultivar-group)	gi31338860		2.50E-23
444	G2570	<i>Oryza sativa</i>	gi15289981		4.10E-16
444	G2570	<i>Dianthus caryophyllus</i>	gi13173408		1.50E-08
444	G2570	<i>Chlamydomonas reinhardtii</i>	gi5916207		2.40E-07
444	G2570	<i>Solanum bulbocastanum</i>	gi32470629		8.30E-06
444	G2570	<i>Nicotiana tabacum</i>	gi4519671		1.50E-05
444	G2570	<i>Mesembryanthemum crystallinum</i>	gi6942190		0.00022
445	G2571	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER96988 1	1192	
445	G2571	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER96988 2	1193	
445	G2571	<i>Oryza sativa</i>	OSC1398.C1.p2.fg	1194	
445	G2571	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-56732	2065	
446	G2571	<i>Brassica oleracea</i>	BZ432711		1.00E-103
446	G2571	<i>Glycine max</i>	AW759250		2.00E-48
446	G2571	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01008818		6.00E-48
446	G2571	<i>Oryza sativa</i>	AC104284		8.00E-48
446	G2571	<i>Medicago truncatula</i>	BQ140137		1.00E-44
446	G2571	<i>Zea mays</i>	CC342129		8.00E-41
446	G2571	<i>Lactuca sativa</i>	BQ849477		2.00E-38
446	G2571	<i>Sorghum bicolor</i>	CD236030		3.00E-38
446	G2571	<i>Atriplex hortensis</i>	AF274033		3.00E-34
446	G2571	<i>Prunus persica</i>	BU046010		2.00E-33
446	G2571	<i>Oryza sativa</i> (japonica cultivar-group)	gi19920190		2.60E-36
446	G2571	<i>Atriplex hortensis</i>	gi8571476		1.90E-35
446	G2571	<i>Lycopersicon</i>	gi27436378		1.30E-34

		<i>esculentum</i>			
446	G2571	<i>Zea mays</i>	gi21908036		9.10E-27
446	G2571	<i>Oryza sativa</i>	gi5091503		3.90E-26
446	G2571	<i>Solanum tuberosum</i>	gi1688233		1.30E-20
446	G2571	<i>Nicotiana sylvestris</i>	gi8809571		5.50E-20
446	G2571	<i>Nicotiana tabacum</i>	gi1208498		1.50E-19
446	G2571	<i>Glycine max</i>	gi21304712		1.10E-18
446	G2571	<i>Prunus armeniaca</i>	gi3264767		7.70E-18
448	G2574	<i>Brassica oleracea</i>	BZ016708		1.00E-82
448	G2574	<i>Oryza sativa</i>	AX653450		5.00E-80
448	G2574	<i>Nicotiana tabacum</i>	AY220477		3.00E-68
448	G2574	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01001635		2.00E-64
448	G2574	<i>Lycopersicon esculentum</i>	BI922133		6.00E-56
448	G2574	<i>Hordeum vulgare</i>	BM370908		2.00E-47
448	G2574	<i>Medicago truncatula</i>	CB893379		4.00E-47
448	G2574	<i>Glycine max</i>	BU926713		4.00E-44
448	G2574	<i>Citrus sinensis</i>	BQ625082		4.00E-44
448	G2574	<i>Zea mays</i>	AX660892		6.00E-44
448	G2574	<i>Oryza sativa</i>	gi11320830		4.10E-61
448	G2574	<i>Nicotiana tabacum</i>	gi30013667		5.60E-59
448	G2574	<i>Oryza sativa (japonica cultivar-group)</i>	gi20160973		4.10E-37
448	G2574	<i>Petroselinum crispum</i>	gi11493822		6.80E-30
448	G2574	<i>Avena fatua</i>	gi1159879		5.10E-26
448	G2574	<i>Avena sativa</i>	gi4894965		2.10E-22
448	G2574	<i>Glycine max</i>	gi32493108		2.20E-20
448	G2574	<i>Ipomoea batatas</i>	gi1076685		5.20E-20
448	G2574	<i>Capsella rubella</i>	gi32454266		8.00E-20
448	G2574	<i>Lycopersicon esculentum</i>	gi13620227		2.20E-18
450	G2575	<i>Lycopersicon esculentum</i>	BI205259		1.00E-48
450	G2575	<i>Medicago truncatula</i>	BI308031		5.00E-45
450	G2575	<i>Vitis vinifera</i>	CD010167		1.00E-44
450	G2575	<i>Sorghum bicolor</i>	BE362650		2.00E-43
450	G2575	<i>Oryza sativa</i>	AX653470		2.00E-43
450	G2575	<i>Triticum aestivum</i>	CD883886		7.00E-42
450	G2575	<i>Amborella trichopoda</i>	CD483414		1.00E-41
450	G2575	<i>Oryza sativa (japonica cultivar-group)</i>	AK108745		3.00E-41
450	G2575	<i>Glycine max</i>	CA784851		3.00E-41
450	G2575	<i>Populus tremula x Populus tremuloides</i>	BU884581		3.00E-38
450	G2575	<i>Oryza sativa</i>	gi11761085		6.50E-45
450	G2575	<i>Oryza sativa (japonica cultivar-group)</i>	gi22830985		4.30E-36
450	G2575	<i>Nicotiana tabacum</i>	gi25348323		2.00E-30

450	G2575	<i>Solanum tuberosum</i>	gi24745606		3.00E-28
450	G2575	<i>Oryza sativa</i> (indica cultivar-group)	gi23305051		6.80E-28
450	G2575	<i>Lycopersicon esculentum</i>	gi13620227		9.90E-27
450	G2575	<i>Cucumis sativus</i>	gi7484759		1.70E-26
450	G2575	<i>Pimpinella brachycarpa</i>	gi3420906		1.80E-26
450	G2575	<i>Avena fatua</i>	gi1159877		1.90E-26
450	G2575	<i>Avena sativa</i>	gi4894965		2.10E-26
451	G2579	<i>Oryza sativa</i>	OSC101983.C1.p6.fg	1195	
451	G2579	<i>Zea mays</i>	LIB3076-043-Q1-K1-H9	1196	
451	G2579	<i>Zea mays</i>	Zm_S11519895	1817	
452	G2579	<i>Brassica oleracea</i>	BZ471318		2.00E-82
452	G2579	<i>Oryza sativa</i>	AP004016		3.00E-34
452	G2579	<i>Oryza sativa</i> (japonica cultivar-group)	AP004570		3.00E-34
452	G2579	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01001296		3.00E-34
452	G2579	<i>Zea mays</i>	AY178191		1.00E-32
452	G2579	<i>Sorghum bicolor</i>	BZ338708		1.00E-23
452	G2579	<i>Medicago truncatula</i>	AC119414		1.00E-21
452	G2579	<i>Beta vulgaris</i>	BQ488935		1.00E-19
452	G2579	<i>Lotus japonicus</i>	AV411846		2.00E-19
452	G2579	<i>Glycine max</i>	BE059333		7.00E-19
452	G2579	<i>Zea mays</i>	gi27802487		5.50E-38
452	G2579	<i>Oryza sativa</i> (japonica cultivar-group)	gi23307521		1.50E-35
452	G2579	<i>Stylosanthes hamata</i>	gi4099921		1.30E-19
452	G2579	<i>Cicer arietinum</i>	gi24817250		5.50E-19
452	G2579	<i>Nicotiana tabacum</i>	gi4587373		8.70E-19
452	G2579	<i>Oryza sativa</i>	gi12597874		1.90E-18
452	G2579	<i>Lycopersicon esculentum</i>	gi2213785		5.90E-18
452	G2579	<i>Prunus armeniaca</i>	gi3264767		5.90E-18
452	G2579	<i>Thellungiella halophila</i>	gi20340233		9.90E-18
452	G2579	<i>Nicotiana glauca</i>	gi8809573		1.30E-17
453	G2585	<i>Oryza sativa</i>	OSC102182.C1.p9.fg	1197	
453	G2585	<i>Oryza sativa</i>	OSC5912.C1.p4.fg	1198	
453	G2585	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER221367_1	1199	
454	G2585	<i>Brassica oleracea</i>	BH574869		1.00E-71
454	G2585	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU814191		9.00E-23
454	G2585	<i>Glycine max</i>	BQ612521		8.00E-22
454	G2585	<i>Lycopersicon esculentum</i>	BG127023		4.00E-21
454	G2585	<i>Solanum tuberosum</i>	BQ118881		1.00E-19
454	G2585	<i>Medicago truncatula</i>	AW776895		2.00E-19
454	G2585	<i>Gossypium hirsutum</i>	CA992948		2.00E-19

454	G2585	<i>Nicotiana tabacum</i>	AF193771		3.00E-19
454	G2585	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AC144737		5.00E-18
454	G2585	<i>Oryza sativa (indica</i> cultivar-group)	AAAA01016983		5.00E-18
454	G2585	<i>Nicotiana tabacum</i>	gi11358951		3.30E-22
454	G2585	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi18844822		5.30E-17
454	G2585	<i>Matricaria</i> <i>chamomilla</i>	gi17385638		6.50E-17
454	G2585	<i>Solanum tuberosum</i>	gi24745606		1.90E-12
454	G2585	<i>Oryza sativa</i>	gi14209559		1.20E-11
454	G2585	<i>Petroselinum</i> <i>crispum</i>	gi11493824		1.70E-11
454	G2585	<i>Retama raetam</i>	gi18158619		1.10E-09
454	G2585	<i>Oryza sativa (indica</i> cultivar-group)	gi23305051		3.30E-09
454	G2585	<i>Solanum dulcamara</i>	gi16588566		8.20E-09
454	G2585	<i>Capsella rubella</i>	gi27817201		1.10E-08
456	G2587	<i>Lycopersicon</i> <i>esculentum</i>	BG642706		5.00E-23
456	G2587	<i>Solanum tuberosum</i>	BE472874		1.00E-22
456	G2587	<i>Medicago</i> <i>truncatula</i>	AW560120		6.00E-22
456	G2587	<i>Populus tremula x</i> <i>Populus tremuloides</i>	BU816132		1.00E-20
456	G2587	<i>Glycine max</i>	BQ612521		3.00E-20
456	G2587	<i>Nicotiana tabacum</i>	AF193770		6.00E-19
456	G2587	<i>Gossypium</i> <i>hirsutum</i>	CA992948		7.00E-18
456	G2587	<i>Triticum aestivum</i>	BG605176		2.00E-16
456	G2587	<i>Vitis vinifera</i>	CA813725		6.00E-16
456	G2587	<i>Lactuca sativa</i>	BQ875950		8.00E-16
456	G2587	<i>Nicotiana tabacum</i>	gi7406995		5.40E-22
456	G2587	<i>Matricaria</i> <i>chamomilla</i>	gi17385638		1.10E-16
456	G2587	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi18844816		5.90E-16
456	G2587	<i>Petroselinum</i> <i>crispum</i>	gi11493824		5.20E-13
456	G2587	<i>Oryza sativa</i>	gi15289994		1.30E-11
456	G2587	<i>Solanum tuberosum</i>	gi24745606		3.00E-11
456	G2587	<i>Capsella rubella</i>	gi27817201		2.90E-09
456	G2587	<i>Solanum dulcamara</i>	gi16588566		5.10E-09
456	G2587	<i>Avena fatua</i>	gi1159879		1.80E-08
456	G2587	<i>Dactylis glomerata</i>	gi11993901		2.20E-08
458	G2592	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK103583		1.00E-154
458	G2592	<i>Lemna paucicostata</i>	AB023895		1.00E-131
458	G2592	<i>Zea mays</i>	AY109994		1.00E-128
458	G2592	<i>Cicer arietinum</i>	CAR400860		1.00E-105
458	G2592	<i>Solanum tuberosum</i>	BG351697		1.00E-104

458	G2592	<i>Lotus japonicus</i>	AP004525		1.00E-103
458	G2592	<i>Medicago truncatula</i>	CB894562		1.00E-100
458	G2592	<i>Helianthus annuus</i>	BQ970590		3.00E-96
458	G2592	<i>Gossypium arboreum</i>	BQ406633		3.00E-93
458	G2592	<i>Oryza sativa</i>	AC105318		7.00E-93
458	G2592	<i>Oryza sativa</i> (japonica cultivar-group)	gi32480039		1.10E-146
458	G2592	<i>Oryza sativa</i>	gi5777631		1.10E-146
458	G2592	<i>Lemna paucicostata</i>	gi5689214		2.90E-124
458	G2592	<i>Cicer arietinum</i>	gi7635492		7.70E-101
458	G2592	<i>Pyrus communis</i>	gi18252343		2.90E-56
458	G2592	<i>Chloroplast Pinus thunbergii</i>	gi1262738		1
460	G2597	<i>Brassica oleracea</i>	BH974513		6.00E-35
460	G2597	<i>Vitis vinifera</i>	CB977099		6.00E-35
460	G2597	<i>Glycine max</i>	AW760239		2.00E-33
460	G2597	<i>Helianthus annuus</i>	BQ966485		9.00E-33
460	G2597	<i>Lactuca sativa</i>	BQ853988		1.00E-32
460	G2597	<i>Lotus corniculatus</i> var. japonicus	CB827195		2.00E-32
460	G2597	<i>Medicago truncatula</i>	BI309254		2.00E-31
460	G2597	<i>Lycopersicon esculentum</i>	AI895129		4.00E-30
460	G2597	<i>Solanum tuberosum</i>	BE919865		7.00E-30
460	G2597	<i>Lupinus albus</i>	CA410490		8.00E-29
460	G2597	<i>Oryza sativa</i> (japonica cultivar-group)	gi23495868		4.20E-39
460	G2597	<i>Lemna paucicostata</i>	gi5689214		5.90E-35
460	G2597	<i>Oryza sativa</i>	gi5777631		3.60E-33
460	G2597	<i>Cicer arietinum</i>	gi7635492		4.70E-33
460	G2597	<i>Pyrus communis</i>	gi18252343		0.018
462	G2603	<i>Oryza sativa</i> (japonica cultivar-group)	AK060587		1.00E-116
462	G2603	<i>Brassica oleracea</i>	BZ462499		3.00E-95
462	G2603	<i>Zea mays</i>	AY106234		9.00E-95
462	G2603	<i>Lemna paucicostata</i>	AB023895		2.00E-92
462	G2603	<i>Cicer arietinum</i>	CAR400860		3.00E-92
462	G2603	<i>Descurainia sophia</i>	BU238485		1.00E-84
462	G2603	<i>Brassica napus</i>	CD819805		2.00E-83
462	G2603	<i>Medicago truncatula</i>	BF004440		2.00E-76
462	G2603	<i>Vitis vinifera</i>	CB977099		3.00E-75
462	G2603	<i>Triticum aestivum</i>	CA485505		6.00E-73
462	G2603	<i>Oryza sativa</i> (japonica cultivar-group)	gi23495868		9.40E-112
462	G2603	<i>Lemna paucicostata</i>	gi5689214		4.80E-91
462	G2603	<i>Cicer arietinum</i>	gi7635492		1.90E-88
462	G2603	<i>Oryza sativa</i>	gi5777631		2.70E-84
462	G2603	<i>Pyrus communis</i>	gi18252343		6.90E-61

464	G2604	<i>Medicago truncatula</i>	BF519786		2.00E-74
464	G2604	<i>Solanum tuberosum</i>	BQ118459		8.00E-74
464	G2604	<i>Lycopersicon esculentum</i>	BF051817		5.00E-73
464	G2604	<i>Populus tremula x Populus tremuloides</i>	BU863675		5.00E-73
464	G2604	<i>Populus tremula</i>	BU892953		5.00E-73
464	G2604	<i>Glycine max</i>	CD487599		3.00E-72
464	G2604	<i>Helianthus paradoxus</i>	CF079899		2.00E-70
464	G2604	<i>Oryza sativa (japonica cultivar-group)</i>	CB680709		9.00E-67
464	G2604	<i>Sorghum propinquum</i>	BG488424		6.00E-66
464	G2604	<i>Triticum aestivum</i>	BJ302536		6.00E-66
464	G2604	<i>Oryza sativa (japonica cultivar-group)</i>	gi29467554		6.50E-65
464	G2604	<i>Zea mays</i>	gi13509835		3.40E-43
464	G2604	<i>Brassica oleracea</i>	gi17981380		2.40E-35
464	G2604	<i>Triticum aestivum</i>	gi32400832		2.20E-25
464	G2604	<i>Oryza sativa</i>	gi11034561		1.80E-21
464	G2604	<i>Hordeum vulgare subsp. vulgare</i>	gi23954355		0.067
464	G2604	<i>Phaseolus vulgaris</i>	gi6863082		0.087
464	G2604	<i>Vigna angularis</i>	gi224356		0.18
464	G2604	<i>Gossypium barbadense</i>	gi28274033		0.18
464	G2604	<i>Lycopersicon esculentum</i>	gi575950		0.18
466	G2616	<i>Brassica oleracea</i>	BH511341		2.00E-47
466	G2616	<i>Populus tremula x Populus tremuloides</i>	BD194427		6.00E-37
466	G2616	<i>Lycopersicon esculentum</i>	BI930760		1.00E-36
466	G2616	<i>Solanum tuberosum</i>	BE472904		4.00E-36
466	G2616	<i>Oryza sativa (japonica cultivar-group)</i>	AK102788		2.00E-35
466	G2616	<i>Helianthus annuus</i>	AJ412302		2.00E-35
466	G2616	<i>Prunus persica</i>	BU045784		9.00E-35
466	G2616	<i>Hordeum vulgare subsp. vulgare</i>	CA032614		2.00E-34
466	G2616	<i>Glycine max</i>	BM520826		4.00E-34
466	G2616	<i>Medicago truncatula</i>	BE202697		1.00E-33
466	G2616	<i>Populus tremula x Populus tremuloides</i>	gi3955021		2.60E-38
466	G2616	<i>Oryza sativa</i>	gi15128400		1.30E-36
466	G2616	<i>Oryza sativa (japonica cultivar-group)</i>	gi21104626		4.80E-19
466	G2616	<i>Petunia x hybrida</i>	gi22087128		1.80E-11
466	G2616	<i>Lycopersicon esculentum</i>	gi28070968		3.20E-11

466	G2616	<i>Narcissus pseudonarcissus</i>	gi18419580		7.20E-11
466	G2616	<i>Ceratopteris richardii</i>	gi3868847		0.00018
466	G2616	<i>Craterostigma plantagineum</i>	gi3171739		0.002
466	G2616	<i>Capsella rubella</i>	gi8919876		0.0025
466	G2616	<i>Physcomitrella patens</i>	gi7415620		0.0068
467	G2617	<i>Oryza sativa</i>	jc-osroLIB3475060d09b1	1200	
468	G2617	<i>Brassica oleracea</i>	BH732988		3.00E-66
468	G2617	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BZ614339		2.00E-54
468	G2617	<i>Medicago truncatula</i>	AC135233		2.00E-19
468	G2617	<i>Oryza sativa</i>	AC133008		4.00E-19
468	G2617	<i>Glycine max</i>	BG363109		4.00E-19
468	G2617	<i>Oryza sativa</i> (japonica cultivar-group)	AK108829		7.00E-19
468	G2617	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01006129		7.00E-19
468	G2617	<i>Zea mays</i>	BZ735433		2.00E-18
468	G2617	<i>Hordeum vulgare</i>	BF255914		9.00E-16
468	G2617	<i>Helianthus annuus</i>	BQ977193		1.00E-13
468	G2617	<i>Oryza sativa</i> (japonica cultivar-group)	gi32489630		2.60E-18
468	G2617	<i>Zea ramosa</i>	gi18674684		6.20E-14
468	G2617	<i>Petunia x hybrida</i>	gi14275902		9.10E-12
468	G2617	<i>Oryza sativa</i>	gi15528588		1.80E-05
468	G2617	<i>Sorghum bicolor</i>	gi18390109		0.00014
468	G2617	<i>Datisca glomerata</i>	gi4666360		0.006
468	G2617	<i>Pisum sativum</i>	gi2129892		0.0097
468	G2617	<i>Triticum aestivum</i>	gi485814		0.02
468	G2617	<i>Brassica rapa</i>	gi2058504		0.021
468	G2617	<i>Glycine max</i>	gi1763063		0.029
470	G2628	<i>Brassica oleracea</i>	BH962006		1.00E-21
470	G2628	<i>Mesembryanthemum crystallinum</i>	BF479304		4.00E-08
470	G2628	<i>Lycopersicon esculentum</i>	BE450859		9.00E-08
470	G2628	<i>Nicotiana tabacum</i>	BP130848		3.00E-07
470	G2628	<i>Glycine max</i>	BF595900		3.00E-07
470	G2628	<i>Phaseolus vulgaris</i>	AF350505		8.00E-07
470	G2628	<i>Lotus japonicus</i>	BI417596		1.00E-06
470	G2628	<i>Rosa chinensis</i>	BI977302		1.00E-06
470	G2628	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01003396		1.00E-06
470	G2628	<i>Medicago truncatula</i>	BE943475		2.00E-06
470	G2628	<i>Phaseolus vulgaris</i>	gi13430400		6.40E-10
470	G2628	<i>Phaseolus acutifolius</i>	gi12829956		1.70E-09
470	G2628	<i>Raphanus sativus</i>	gi1033059		2.70E-08

470	G2628	<i>Sinapis alba</i>	gi2995462		5.00E-08
470	G2628	<i>Petroselinum crispum</i>	gi9650826		1.80E-07
470	G2628	<i>Brassica napus</i>	gi633154		2.40E-07
470	G2628	<i>Glycine max</i>	gi169961		3.20E-07
470	G2628	<i>Oryza sativa</i>	gi13365774		4.40E-07
470	G2628	<i>Nicotiana tabacum</i>	gi10241920		6.00E-07
470	G2628	<i>Oryza sativa</i> (japonica cultivar-group)	gi18844791		1.80E-06
472	G2632	<i>Brassica napus</i>	BNU33885		1.00E-121
472	G2632	<i>Brassica oleracea</i>	BZ466456		2.00E-61
472	G2632	<i>Medicago truncatula</i>	BI263541		2.00E-53
472	G2632	<i>Citrus sinensis</i>	BQ624240		1.00E-48
472	G2632	<i>Prunus dulcis</i>	BU573158		1.00E-48
472	G2632	<i>Helianthus paradoxus</i>	CF082573		1.00E-38
472	G2632	<i>Amborella trichopoda</i>	CD484119		5.00E-36
472	G2632	<i>Oryza sativa</i> (japonica cultivar-group)	AK069854		8.00E-36
472	G2632	<i>Lycopersicon esculentum</i>	BF113081		1.00E-35
472	G2632	<i>Triticum aestivum</i>	BT009512		5.00E-34
472	G2632	<i>Brassica napus</i>	gi1173618		1.10E-115
472	G2632	<i>Oryza sativa</i> (japonica cultivar-group)	gi27552556		5.30E-38
472	G2632	<i>Vitis riparia</i>	gi7141243		1.50E-30
472	G2632	<i>Oryza sativa</i>	gi2826786		2.00E-29
472	G2632	<i>Nicotiana tabacum</i>	gi4731314		7.00E-20
472	G2632	<i>Triticum aestivum</i>	gi1076781		0.05
472	G2632	<i>Antirrhinum majus</i>	gi28894445		0.056
472	G2632	<i>Solanum tuberosum</i>	gi7688355		0.27
472	G2632	<i>Vigna unguiculata</i>	gi9857292		0.38
472	G2632	<i>Zea mays</i>	gi829240		0.79
474	G2633	<i>Medicago truncatula</i>	AC121232		1.00E-160
474	G2633	<i>Oryza sativa</i> (japonica cultivar-group)	AE017084		1.00E-159
474	G2633	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01002412		1.00E-159
474	G2633	<i>Oryza sativa</i>	AP003747		1.00E-154
474	G2633	<i>Zea mays</i>	AY109543		1.00E-145
474	G2633	<i>Vitis vinifera</i>	CB980495		1.00E-124
474	G2633	<i>Solanum tuberosum</i>	BG595264		1.00E-103
474	G2633	<i>Brassica oleracea</i>	BH591768		1.00E-103
474	G2633	<i>Glycine max</i>	CA800623		1.00E-102
474	G2633	<i>Lycopersicon esculentum</i>	BI422927		4.00E-94
474	G2633	<i>Oryza sativa</i> (japonica cultivar-group)	gi20043021		8.30E-152

474	G2633	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	gi28143934		9.60E-71
474	G2633	<i>Vitis vinifera</i>	gi20334379		6.90E-61
474	G2633	<i>Lycopersicon</i> <i>esculentum</i>	gi31322802		1.10E-60
474	G2633	<i>Lilium longiflorum</i>	gi32813435		3.80E-60
474	G2633	<i>Oryza sativa</i>	gi14719333		2.20E-57
474	G2633	<i>Gossypium</i> <i>hirsutum</i>	gi29122893		7.30E-57
474	G2633	<i>Argyroxiphium</i> <i>sandwicense</i> subsp. <i>macrocephalum</i>	gi20257438		9.40E-57
474	G2633	<i>Wilkesia</i> <i>gymnoxiphium</i>	gi20257432		1.50E-56
474	G2633	<i>Calycadenia</i> <i>multiglandulosa</i>	gi20257451		1.50E-56
476	G2636	<i>Petunia x hybrida</i>	PHRNANAM		5.00E-80
476	G2636	<i>Lactuca sativa</i>	BQ994853		1.00E-71
476	G2636	<i>Medicago</i> <i>truncatula</i>	BI308121		2.00E-70
476	G2636	<i>Glycine max</i>	AF532619		1.00E-68
476	G2636	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AP004679		7.00E-65
476	G2636	<i>Oryza sativa</i>	AP003542		7.00E-65
476	G2636	<i>Brassica napus</i>	CD830372		6.00E-62
476	G2636	<i>Thellungiella</i> <i>halophila</i>	BM985861		1.00E-61
476	G2636	<i>Lycopersicon</i> <i>esculentum</i>	AI898478		1.00E-61
476	G2636	<i>Solanum tuberosum</i>	BQ518471		1.00E-61
476	G2636	<i>Petunia x hybrida</i>	gi1279640		1.60E-75
476	G2636	<i>Glycine max</i>	gi22597158		3.00E-67
476	G2636	<i>Oryza sativa</i>	gi27529810		1.30E-59
476	G2636	<i>Zea mays</i>	gi32527660		5.50E-58
476	G2636	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi28411877		7.50E-58
476	G2636	<i>Triticum sp.</i>	gi4218537		4.20E-54
476	G2636	<i>Triticum</i> <i>monococcum</i>	gi6732160		4.20E-54
476	G2636	<i>Phaseolus vulgaris</i>	gi15148912		1.70E-50
476	G2636	<i>Lycopersicon</i> <i>esculentum</i>	gi6175246		3.00E-44
476	G2636	<i>Brassica napus</i>	gi31322568		7.90E-44
478	G2639	<i>Brassica oleracea</i>	BH678678		1.00E-67
478	G2639	<i>Medicago</i> <i>truncatula</i>	BE998137		7.00E-47
478	G2639	<i>Populus tremula x</i> <i>Populus tremuloides</i>	BU826518		2.00E-43
478	G2639	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AK102444		3.00E-41
478	G2639	<i>Lycopersicon</i> <i>esculentum</i>	BI208719		2.00E-38
478	G2639	<i>Oryza sativa</i>	AP003683		5.00E-38
478	G2639	<i>Oryza sativa (indica)</i>	AAAA01008013		5.00E-38

		cultivar-group)			
478	G2639	<i>Hevea brasiliensis</i>	CB376600		1.00E-37
478	G2639	<i>Zea mays</i>	CC628094		4.00E-36
478	G2639	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	CA029965		1.00E-33
478	G2639	<i>Oryza sativa</i>	gi15528818		2.20E-41
478	G2639	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi20161862		2.20E-41
478	G2639	<i>Pinus pinaster</i>	gi18129286		0.68
478	G2639	<i>Zea mays</i>	gi7489714		0.74
478	G2639	<i>Triticum aestivum</i>	gi170732		1
478	G2639	<i>Populus tremuloides</i>	gi9651406		1
480	G2640	<i>Brassica oleracea</i>	BH678678		1.00E-107
480	G2640	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU826518		1.00E-54
480	G2640	<i>Medicago</i> <i>truncatula</i>	BE998137		1.00E-52
480	G2640	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK102444		1.00E-42
480	G2640	<i>Hevea brasiliensis</i>	CB376600		2.00E-40
480	G2640	<i>Lycopersicon</i> <i>esculentum</i>	BI205918		3.00E-40
480	G2640	<i>Oryza sativa</i>	AP003683		4.00E-40
480	G2640	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01008013		4.00E-40
480	G2640	<i>Zea mays</i>	CC628094		2.00E-37
480	G2640	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	CA029965		7.00E-35
480	G2640	<i>Oryza sativa</i>	gi15528818		1.90E-45
480	G2640	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi20161862		1.90E-45
480	G2640	<i>Zea mays</i>	gi7248461		0.00063
480	G2640	<i>Brassica napus</i>	gi17821		0.0011
480	G2640	<i>Triticum aestivum</i>	gi21322752		0.0012
480	G2640	<i>Chlamydomonas</i> <i>reinhardtii</i>	gi32454910		0.0022
480	G2640	<i>Phaseolus vulgaris</i>	gi121628		0.0042
480	G2640	<i>Lycopersicon</i> <i>esculentum</i>	gi19322		0.0051
480	G2640	<i>Nicotiana glauca</i>	gi121631		0.0061
480	G2640	<i>Physcomitrella</i> <i>patens</i>	gi21388660		0.01
482	G2649	<i>Brassica oleracea</i>	BH593456		8.00E-72
482	G2649	<i>Hevea brasiliensis</i>	CB376600		3.00E-71
482	G2649	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK102444		9.00E-66
482	G2649	<i>Lycopersicon</i> <i>esculentum</i>	AW216650		9.00E-65
482	G2649	<i>Oryza sativa</i>	AP004319		4.00E-62
482	G2649	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01008013		1.00E-61
482	G2649	<i>Glycine max</i>	BG155693		3.00E-54
482	G2649	<i>Zea mays</i>	CC628094		1.00E-51

482	G2649	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	CA029965		3.00E-44
482	G2649	<i>Medicago truncatula</i>	BG645979		3.00E-36
482	G2649	<i>Oryza sativa</i>	gi15528818		5.80E-64
482	G2649	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi20161862		5.80E-64
482	G2649	<i>Nicotiana tabacum</i>	gi395147		0.7
482	G2649	<i>Zea mays</i>	gi100922		0.79
482	G2649	<i>Physcomitrella patens</i>	gi14597654		0.91
482	G2649	<i>Lycopersicon esculentum</i>	gi1345532		0.95
482	G2649	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	gi10241429		0.96
482	G2649	<i>Chlamydomonas reinhardtii</i>	gi21218057		0.99
482	G2649	<i>Pisum sativum</i>	gi3426304		1
483	G2650	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER427_60	1201	
483	G2650	<i>Oryza sativa</i>	OSC2212.C1.p1.fg	1202	
483	G2650	<i>Oryza sativa</i>	uC-osrocyp034e01a1	1203	
483	G2650	<i>Zea mays</i>	LIB4740-140-A1-K1-E11	1204	
483	G2650	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER112147_1	1205	
483	G2650	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER112147_3	1206	
483	G2650	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER36738_1	1207	
483	G2650	<i>Oryza sativa</i>	Os_S23789	1613	
483	G2650	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-50042	2066	
483	G2650	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-453738	2067	
484	G2650	<i>Brassica oleracea</i>	BH937292		2.00E-40
484	G2650	<i>Lotus japonicus</i>	AG245821		9.00E-31
484	G2650	<i>Glycine max</i>	CA799031		3.00E-29
484	G2650	<i>Oryza sativa</i>	AU096089		5.00E-29
484	G2650	<i>Hordeum vulgare</i>	BG301195		8.00E-29
484	G2650	<i>Zea mays</i>	CC637450		1.00E-28
484	G2650	<i>Lactuca sativa</i>	BU003054		1.00E-28
484	G2650	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	CB680333		1.00E-28
484	G2650	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01007185		1.00E-28
484	G2650	<i>Medicago truncatula</i>	BF521010		2.00E-28
484	G2650	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi20804689		2.90E-30
484	G2650	<i>Lupinus albus</i>	gi20269127		2.00E-17
484	G2650	<i>Oryza sativa</i>	gi14164473		3.50E-17
484	G2650	<i>Lycopersicon esculentum</i>	gi12002867		3.90E-17
484	G2650	<i>Pueraria montana</i>	gi21624281		4.00E-17

		var. <i>lobata</i>			
484	G2650	<i>Arundinella hirta</i>	gi13649854		6.10E-13
484	G2650	<i>Linaria vulgaris</i>	gi29788739		6.80E-12
484	G2650	<i>Digitalis purpurea</i>	gi29788741		6.80E-12
484	G2650	<i>Leymus triticoides</i>	gi23307807		1.30E-11
484	G2650	<i>Linaria canadensis</i>	gi29788737		1.50E-11
486	G2655	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK107555		4.00E-66
486	G2655	<i>Brassica oleracea</i>	BH589305		2.00E-64
486	G2655	<i>Lactuca sativa</i>	BQ995023		1.00E-60
486	G2655	<i>Robinia pseudoacacia</i>	BI677665		1.00E-52
486	G2655	<i>Glycine max</i>	BE021887		1.00E-49
486	G2655	<i>Medicago truncatula</i>	CA920255		5.00E-49
486	G2655	<i>Zea mays</i>	CC617212		3.00E-47
486	G2655	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01002332		9.00E-47
486	G2655	<i>Cicer arietinum</i>	CAR011013		3.00E-42
486	G2655	<i>Arachis hypogaea</i>	CD038481		3.00E-41
486	G2655	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi19920107		2.00E-61
486	G2655	<i>Cucumis melo</i>	gi28558779		1.70E-50
486	G2655	<i>Cicer arietinum</i>	gi3641870		5.00E-42
486	G2655	<i>Zea mays</i>	gi1420924		9.00E-12
486	G2655	<i>Phaseolus vulgaris</i>	gi1142621		2.50E-11
486	G2655	<i>Petunia x hybrida</i>	gi10998404		6.80E-10
486	G2655	<i>Oryza sativa</i>	gi12643064		2.70E-08
486	G2655	<i>Perilla frutescens</i>	gi28375728		7.90E-08
486	G2655	<i>Tripsacum australe</i>	gi527663		8.90E-08
486	G2655	<i>Mesembryanthemum crystallinum</i>	gi4206118		2.20E-07
487	G2661	<i>Oryza sativa</i>	OSC5501.C1.p4.fg	1208	
488	G2661	<i>Brassica oleracea</i>	BH704648		1.00E-29
488	G2661	<i>Sorghum bicolor</i>	BZ341609		1.00E-20
488	G2661	<i>Oryza sativa</i>	AP003252		2.00E-20
488	G2661	<i>Zea mays</i>	CC336314		2.00E-20
488	G2661	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01005031		5.00E-20
488	G2661	<i>Hordeum vulgare</i>	BF263465		3.00E-15
488	G2661	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	AT002234		5.00E-15
488	G2661	<i>Glycine max</i>	CA783614		7.00E-15
488	G2661	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK106119		9.00E-15
488	G2661	<i>Medicago truncatula</i>	AC144431		1.00E-14
488	G2661	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi20160648		1.60E-22
488	G2661	<i>Oryza sativa</i>	gi15528743		2.50E-16
488	G2661	<i>Tulipa gesneriana</i>	gi5923912		2.70E-07
488	G2661	<i>Pinus taeda</i>	gi6166283		3.50E-07

488	G2661	<i>Petunia x hybrida</i>	gi3127045		4.20E-07
488	G2661	<i>Glycine max</i>	gi3399777		1.10E-05
488	G2661	<i>Perilla frutescens</i>	gi4519199		2.70E-05
488	G2661	<i>Lycopersicon esculentum</i>	gi6175252		5.20E-05
488	G2661	<i>Antirrhinum majus</i>	gi166428		7.60E-05
488	G2661	<i>Sorghum bicolor</i>	gi527665		0.00017
490	G2679	<i>Glycine max</i>	BM525733		2.00E-71
490	G2679	<i>Lycopersicon esculentum</i>	BI421583		2.00E-60
490	G2679	<i>Hordeum vulgare</i>	CD054855		4.00E-55
490	G2679	<i>Brassica oleracea</i>	BZ508263		2.00E-53
490	G2679	<i>Triticum aestivum</i>	CA600208		5.00E-52
490	G2679	<i>Beta vulgaris</i>	BQ583502		3.00E-40
490	G2679	<i>Triticum monococcum</i>	BQ800694		4.00E-40
490	G2679	<i>Medicago truncatula</i>	BI308837		7.00E-39
490	G2679	<i>Oryza sativa (indica cultivar-group)</i>	CB626016		7.00E-38
490	G2679	<i>Oryza sativa (japonica cultivar- group)</i>	AK071493		2.00E-37
490	G2679	<i>Oryza sativa (japonica cultivar- group)</i>	gi14587305		3.10E-33
490	G2679	<i>Glycine max</i>	gi4218187		2.60E-30
490	G2679	<i>Zea mays</i>	gi20152907		0.0046
490	G2679	<i>Oryza sativa</i>	gi22535907		0.066
490	G2679	<i>Oryza sativa (indica cultivar-group)</i>	gi29565495		0.066
490	G2679	<i>Ambrosia trifida</i>	gi114091		0.085
490	G2679	<i>Aster tripolium</i>	gi28804507		0.17
490	G2679	<i>Helianthus tuberosus</i>	gi18491030		0.39
490	G2679	<i>Casuarina glauca</i>	gi1223652		0.39
490	G2679	<i>Musa acuminata</i>	gi12006148		0.4
492	G2682	<i>Glycine max</i>	BM525733		4.00E-33
492	G2682	<i>Brassica oleracea</i>	BH435758		1.00E-31
492	G2682	<i>Hordeum vulgare</i>	CD054855		2.00E-31
492	G2682	<i>Oryza sativa (japonica cultivar- group)</i>	AK071493		1.00E-30
492	G2682	<i>Lycopersicon esculentum</i>	BI421583		5.00E-30
492	G2682	<i>Triticum aestivum</i>	CA600208		2.00E-26
492	G2682	<i>Zea mays</i>	AY103668		2.00E-24
492	G2682	<i>Medicago truncatula</i>	BI308837		1.00E-23
492	G2682	<i>Oryza sativa (indica cultivar-group)</i>	CB626016		2.00E-20
492	G2682	<i>Zinnia elegans</i>	AU294482		2.00E-20
492	G2682	<i>Glycine max</i>	gi4218187		5.90E-28
492	G2682	<i>Oryza sativa (japonica cultivar- group)</i>	gi14587305		2.10E-21

492	G2682	<i>Ambrosia trifida</i>	gi114091		0.03
492	G2682	<i>Zea mays</i>	gi20152909		0.037
492	G2682	<i>Vigna angularis</i>	gi350610		0.078
492	G2682	<i>Fritillaria agrestis</i>	gi2754855		0.089
492	G2682	<i>Vitis vinifera</i>	gi7406673		0.16
492	G2682	<i>Amburana acreana</i>	gi25453051		0.24
492	G2682	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi29786353		0.35
492	G2682	<i>Oryza sativa</i>	gi22535907		0.6
494	G2686	<i>Lycopersicon</i> <i>esculentum</i>	BG127023		6.00E-21
494	G2686	<i>Solanum tuberosum</i>	BE472874		5.00E-20
494	G2686	<i>Glycine max</i>	BQ612521		2.00E-19
494	G2686	<i>Vitis vinifera</i>	CA813725		4.00E-19
494	G2686	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU815822		2.00E-18
494	G2686	<i>Nicotiana tabacum</i>	AF193770		4.00E-18
494	G2686	<i>Lactuca sativa</i>	BQ875950		4.00E-17
494	G2686	<i>Brassica oleracea</i>	BH574869		6.00E-17
494	G2686	<i>Capsicum annuum</i>	CA847397		5.00E-16
494	G2686	<i>Medicago</i> <i>truncatula</i>	AW560120		5.00E-16
494	G2686	<i>Nicotiana tabacum</i>	gi7406995		3.40E-20
494	G2686	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi20303630		1.90E-16
494	G2686	<i>Matricaria</i> <i>chamomilla</i>	gi17385638		1.60E-15
494	G2686	<i>Oryza sativa</i>	gi15290030		5.60E-14
494	G2686	<i>Petroselinum</i> <i>crispum</i>	gi11493824		2.10E-12
494	G2686	<i>Solanum tuberosum</i>	gi24745606		6.20E-12
494	G2686	<i>Capsella rubella</i>	gi27817201		9.20E-09
494	G2686	<i>Avena sativa</i>	gi4894963		4.60E-08
494	G2686	<i>Retama raetam</i>	gi18158619		2.40E-07
494	G2686	<i>Solanum dulcamara</i>	gi16588566		4.20E-07
496	G2690	<i>Brassica oleracea</i>	BH516775		1.00E-105
496	G2690	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AK065008		5.00E-39
496	G2690	<i>Oryza sativa</i>	AP002913		5.00E-39
496	G2690	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01002497		1.00E-35
496	G2690	<i>Helianthus annuus</i>	BQ971511		4.00E-35
496	G2690	<i>Triticum aestivum</i>	BT009310		2.00E-34
496	G2690	<i>Zea mays</i>	CC616336		3.00E-33
496	G2690	<i>Brassica napus</i>	CB686050		3.00E-33
496	G2690	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BU994579		4.00E-28
496	G2690	<i>Gossypium</i> <i>arboreum</i>	BQ405698		7.00E-27
496	G2690	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi12328553		9.90E-39
496	G2690	<i>Marchantia</i> <i>polymorpha</i>	gi25272004		9.70E-15

496	G2690	<i>Solanum tuberosum</i>	gi1688233		3.60E-07
496	G2690	<i>Lycopersicon esculentum</i>	gi28274830		4.00E-07
496	G2690	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi1730475		5.00E-07
496	G2690	<i>Eragrostis tef</i>	gi17906977		1.10E-06
496	G2690	<i>Atriplex hortensis</i>	gi8571476		1.20E-06
496	G2690	<i>Daucus carota</i>	gi5578746		1.20E-06
496	G2690	<i>Nicotiana tabacum</i>	gi3065895		1.80E-06
496	G2690	<i>Zea mays</i>	gi21908036		1.90E-06
498	G2691	<i>Brassica oleracea</i>	BH591758		7.00E-29
498	G2691	<i>Beta vulgaris</i>	BQ591872		2.00E-15
498	G2691	<i>Lycopersicon esculentum</i>	BD194704		1.00E-14
498	G2691	<i>Gossypium arboreum</i>	BF279235		7.00E-13
498	G2691	<i>Nicotiana tabacum</i>	AF058827		7.00E-13
498	G2691	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BQ791746		2.00E-12
498	G2691	<i>Brassica napus</i>	BQ704534		3.00E-11
498	G2691	<i>Medicago truncatula</i>	AJ503842		9.00E-11
498	G2691	<i>Lactuca sativa</i>	BQ873772		9.00E-11
498	G2691	<i>Helianthus argophyllus</i>	CF091307		1.00E-10
498	G2691	<i>Lycopersicon esculentum</i>	gi2213785		5.00E-19
498	G2691	<i>Nicotiana tabacum</i>	gi3065895		5.10E-17
498	G2691	<i>Oryza sativa</i>	gi9049421		3.70E-11
498	G2691	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi33087061		1.10E-08
498	G2691	<i>Thellungiella halophila</i>	gi20340233		2.00E-07
498	G2691	<i>Narcissus pseudonarcissus</i>	gi18266198		2.50E-07
498	G2691	<i>Solanum tuberosum</i>	gi28268684		4.00E-07
498	G2691	<i>Prunus armeniaca</i>	gi3264767		3.50E-06
498	G2691	<i>Fagus sylvatica</i>	gi18496063		6.60E-06
498	G2691	<i>Zea mays</i>	gi27802487		1.00E-05
500	G2694	<i>Zea mays</i>	BZ743538		4.4
500	G2694	<i>Sorghum bicolor</i>	CD463350		5.8
500	G2694	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi32479831		0.04
502	G2699	<i>Lotus japonicus</i>	AP006085		1.00E-137
502	G2699	<i>Medicago truncatula</i>	AC137703		1.00E-132
502	G2699	<i>Oryza sativa</i>	AP003823		1.00E-123
502	G2699	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AP005149		1.00E-123
502	G2699	<i>Oryza sativa (indica</i> cultivar-group)	AAAA01000614		1.00E-123
502	G2699	<i>Brassica oleracea</i>	BH956190		8.00E-65
502	G2699	<i>Zea mays</i>	CC730365		2.00E-62
502	G2699	<i>Solanum tuberosum</i>	BF052580		9.00E-50

502	G2699	<i>Lycopersicon esculentum</i>	BG123921		2.00E-45
502	G2699	<i>Glycine max</i>	BE473856		2.00E-33
502	G2699	<i>Oryza sativa</i> (japonica cultivar- group)	gi28564823		4.10E-118
502	G2699	<i>Lycopersicon esculentum</i>	gi13620224		8.30E-33
502	G2699	<i>Brassica napus</i>	gi13170126		2.20E-27
502	G2699	<i>Oryza sativa</i>	gi13937306		3.90E-27
502	G2699	<i>Zea mays</i>	gi5640155		4.00E-27
502	G2699	<i>Lilium longiflorum</i>	gi32813435		4.80E-27
502	G2699	<i>Capsella rubella</i>	gi13620166		1.10E-26
502	G2699	<i>Triticum aestivum</i>	gi5640157		1.70E-26
502	G2699	<i>Hordeum vulgare</i>	gi18254373		4.30E-26
502	G2699	<i>Dubautia menziesii</i>	gi20257471		2.90E-25
504	G2702	<i>Glycine max</i>	AW234074		3.00E-52
504	G2702	<i>Triticum aestivum</i>	CA730325		8.00E-47
504	G2702	<i>Medicago truncatula</i>	BI311137		2.00E-46
504	G2702	<i>Oryza sativa</i> (japonica cultivar- group)	BP184381		3.00E-46
504	G2702	<i>Oryza sativa</i>	AX699721		5.00E-46
504	G2702	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BU998112		9.00E-46
504	G2702	<i>Lycopersicon esculentum</i>	LETHM1		2.00E-45
504	G2702	<i>Eschscholzia californica</i>	CD480267		3.00E-45
504	G2702	<i>Sorghum bicolor</i>	CD226268		6.00E-45
504	G2702	<i>Triphysaria versicolor</i>	BM356984		6.00E-45
504	G2702	<i>Oryza sativa</i> (japonica cultivar- group)	gi20146436		7.50E-48
504	G2702	<i>Oryza sativa</i>	gi13486737		2.00E-47
504	G2702	<i>Lycopersicon esculentum</i>	gi1167486		7.70E-46
504	G2702	<i>Dendrobium sp.</i> XMW-2002-2	gi28628949		6.20E-44
504	G2702	<i>Hordeum vulgare</i>	gi19059		1.60E-43
504	G2702	<i>Gossypium hirsutum</i>	gi13346194		2.90E-43
504	G2702	<i>Nicotiana tabacum</i>	gi6552389		1.20E-40
504	G2702	<i>Fragaria x ananassa</i>	gi15082210		2.50E-40
504	G2702	<i>Antirrhinum majus</i>	gi82310		4.40E-40
504	G2702	<i>Petunia x hybrida</i>	gi20561		5.20E-40
505	G2717	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER16793_1	1209	
505	G2717	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER16793_3	1210	
505	G2717	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER23207_1	1211	
505	G2717	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER30577_1	1212	

505	G2717	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER30577 4	1213	
505	G2717	<i>Glycine max</i>	LIB3053-003-Q1-N1-A7	1214	
505	G2717	<i>Glycine max</i>	jC-gmle01810024c12a1	1215	
505	G2717	<i>Oryza sativa</i>	AU075998.1	1216	
505	G2717	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER275001 1	1217	
505	G2717	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER62825 1	1218	
505	G2717	<i>Oryza sativa</i>	OSC100863.C1.p7.fg	1219	
505	G2717	<i>Oryza sativa</i>	OSC17223.C1.p2.fg	1220	
505	G2717	<i>Oryza sativa</i>	OSC21325.C1.p9.fg	1221	
505	G2717	<i>Zea mays</i>	LIB3689-236-Q1-K6-H9	1222	
505	G2717	<i>Zea mays</i>	LIB4758-055-R2-K1-G11	1223	
505	G2717	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER25294 1	1224	
505	G2717	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER25294 2	1225	
505	G2717	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER304 164	1226	
505	G2717	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER304 172	1227	
505	G2717	<i>Oryza sativa</i>	Os_S96374	1614	
505	G2717	<i>Glycine max</i>	Gma_S4993926	1670	
505	G2717	<i>Hordeum vulgare</i>	Hv_S134310	1744	
505	G2717	<i>Zea mays</i>	Zm_S11527070	1818	
505	G2717	<i>Triticum aestivum</i>	Ta_S167441	1907	
505	G2717	<i>Triticum aestivum</i>	Ta_S275432	1908	
505	G2717	<i>Triticum aestivum</i>	Ta_S88094	1909	
505	G2717	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-51988	2068	
505	G2717	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-393701	2069	
506	G2717	<i>Brassica napus</i>	CD814949		7.00E-90
506	G2717	<i>Oryza sativa</i> (japonica cultivar-group)	AK100618		2.00E-74
506	G2717	<i>Lycopersicon esculentum</i>	BG127613		3.00E-65
506	G2717	<i>Vitis vinifera</i>	CB007263		5.00E-63
506	G2717	<i>Ipomoea nil</i>	BJ563043		2.00E-61
506	G2717	<i>Medicago truncatula</i>	BF003720		3.00E-61
506	G2717	<i>Pennisetum ciliare</i>	BM084769		2.00E-58
506	G2717	<i>Glycine max</i>	BU964889		3.00E-55
506	G2717	<i>Solanum tuberosum</i>	BQ119267		2.00E-54
506	G2717	<i>Hordeum vulgare</i>	BM816006		4.00E-52
506	G2717	<i>Oryza sativa</i> (japonica cultivar-group)	gi20146249		1.10E-69
506	G2717	<i>Zea mays</i>	gi18463961		1.80E-39
506	G2717	<i>Petroselinum crispum</i>	gi2224899		7.80E-21
506	G2717	<i>Nicotiana tabacum</i>	gi1084419		2.20E-14
506	G2717	<i>Triticum aestivum</i>	gi283024		5.10E-14

506	G2717	<i>Fritillaria liliacea</i>	gi15281590		1.10E-13
506	G2717	<i>Lycopersicon esculentum</i>	gi3021487		5.40E-13
506	G2717	<i>Fritillaria agrestis</i>	gi2641211		2.70E-12
506	G2717	<i>Medicago truncatula</i>	gi32966575		3.10E-11
506	G2717	<i>Lens culinaris</i>	gi13540405		6.10E-11
507	G2718	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER31802 1	1057	
507	G2718	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER586 102	1058	
507	G2718	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER586 116	1059	
507	G2718	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER8724 1	1060	
507	G2718	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER8724 2	1061	
507	G2718	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER30974 3	1063	
507	G2718	<i>Oryza sativa</i>	OSC20053.C1.p5.fg	1064	
507	G2718	<i>Oryza sativa</i>	OSC20055.C1.p5.fg	1065	
507	G2718	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER69699 1	1066	
507	G2718	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER69699 2	1067	
507	G2718	<i>Glycine max</i>	Gma_S4901946	1663	
507	G2718	<i>Triticum aestivum</i>	Ta_S45274	1883	
508	G2718	<i>Brassica oleracea</i>	BH961028		1.00E-24
508	G2718	<i>Populus tremula x Populus tremuloides</i>	BU831849		3.00E-21
508	G2718	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU872107		3.00E-21
508	G2718	<i>Vitis vinifera</i>	BM437313		6.00E-20
508	G2718	<i>Vitis aestivalis</i>	CB289238		3.00E-19
508	G2718	<i>Glycine max</i>	BI699876		2.00E-18
508	G2718	<i>Pinus pinaster</i>	AL750151		4.00E-16
508	G2718	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	AV911235		1.00E-12
508	G2718	<i>Nuphar advena</i>	CD473522		2.00E-12
508	G2718	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	CB684618		4.00E-12
508	G2718	<i>Solanum tuberosum</i>	gi9954118		7.20E-11
508	G2718	<i>Vitis labrusca x Vitis vinifera</i>	gi22266671		3.10E-10
508	G2718	<i>Gossypium hirsutum</i>	gi23476287		3.10E-10
508	G2718	<i>Gossypium rainondii</i>	gi23476291		3.10E-10
508	G2718	<i>Gossypium herbaceum</i>	gi23476293		3.10E-10
508	G2718	<i>Gossypoides kirkii</i>	gi23476295		3.10E-10
508	G2718	<i>Fragaria x ananassa</i>	gi15082210		5.00E-10
508	G2718	<i>Oryza sativa</i>	gi19072770		6.40E-10
508	G2718	<i>Zea luxurians</i>	gi15042120		8.20E-10

508	G2718	<i>Zea mays</i>	gi19548449		8.20E-10
509	G2723	<i>Oryza sativa</i>	rsicek_8958.y1.abd	1228	
510	G2723	<i>Brassica rapa</i>	L38243		8.00E-40
510	G2723	<i>Vitis vinifera</i>	CB920052		1.00E-26
510	G2723	<i>Populus tremula</i>	BU890694		2.00E-26
510	G2723	<i>Phaseolus coccineus</i>	CA897021		6.00E-25
510	G2723	<i>Eucalyptus grandis</i>	CD669972		3.00E-24
510	G2723	<i>Glycine max</i>	BG726181		5.00E-24
510	G2723	<i>Lycopersicon esculentum</i>	AJ320067		3.00E-23
510	G2723	<i>Lotus japonicus</i>	AP004546		3.00E-23
510	G2723	<i>Solanum tuberosum</i>	BI433702		7.00E-23
510	G2723	<i>Capsicum annuum</i>	BM060888		6.00E-22
510	G2723	<i>Lycopersicon esculentum</i>	gi7981380		2.50E-24
510	G2723	<i>Oryza sativa</i> (japonica cultivar-group)	gi20161824		1.10E-21
510	G2723	<i>Oryza sativa</i>	gi5091605		3.80E-21
510	G2723	<i>Hevea brasiliensis</i>	gi12005328		1.20E-14
510	G2723	<i>Antirrhinum majus</i>	gi18874265		7.30E-14
510	G2723	<i>Glycine max</i>	gi19911577		5.40E-13
510	G2723	<i>Solanum demissum</i>	gi15209176		8.30E-13
510	G2723	<i>Lilium longiflorum</i>	gi31442292		0.0034
510	G2723	<i>Volvox carteri</i> f. nagariensis	gi4633127		0.012
510	G2723	<i>Oryza sativa</i> (indica cultivar-group)	gi10443488		0.64
511	G2741	<i>Glycine max</i>	BG508638.1	1229	
511	G2741	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER5654_1	1230	
511	G2741	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER5654_2	1231	
511	G2741	<i>Oryza sativa</i>	OSC102289.C1.p18.fg	1232	
511	G2741	<i>Oryza sativa</i>	OSC5384.C1.p5.fg	1233	
511	G2741	<i>Oryza sativa</i>	rsicen_25533.y1.abd	1234	
511	G2741	<i>Oryza sativa</i>	rsicen_8566.y1.abd	1235	
511	G2741	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER73638_1	1236	
511	G2741	<i>Glycine max</i>	Gma_S4922181	1671	
511	G2741	<i>Hordeum vulgare</i>	Hv_S24580	1745	
511	G2741	<i>Zea mays</i>	Zm_S11434269	1819	
511	G2741	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-50878	2070	
511	G2741	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-356106	2071	
512	G2741	<i>Oryza sativa</i>	AP003277		2.00E-56
512	G2741	<i>Brassica oleracea</i>	BZ506408		6.00E-48
512	G2741	<i>Zea mays</i>	BZ709707		1.00E-47
512	G2741	<i>Glycine max</i>	CA953428		4.00E-45
512	G2741	<i>Lycopersicon esculentum</i>	BE432293		3.00E-39
512	G2741	<i>Oryza sativa</i> (japonica cultivar-group)	AC130607		7.00E-39

512	G2741	<i>Hordeum vulgare</i>	BE559431		2.00E-37
512	G2741	<i>Oryza minuta</i>	CB210034		2.00E-34
512	G2741	<i>Oryza sativa (indica cultivar-group)</i>	AAAAA01011300		5.00E-34
512	G2741	<i>Lactuca sativa</i>	BU000462		1.00E-33
512	G2741	<i>Oryza sativa</i>	gi15289981		3.20E-57
512	G2741	<i>Oryza sativa (japonica cultivar-group)</i>	gi20160613		9.30E-29
512	G2741	<i>Zea mays</i>	gi13661174		3.00E-25
512	G2741	<i>Oryza glaberrima</i>	gi31338862		2.50E-13
512	G2741	<i>Oryza sativa (indica cultivar-group)</i>	gi31338860		7.60E-13
512	G2741	<i>Chlamydomonas reinhardtii</i>	gi5916207		3.20E-11
512	G2741	<i>Mesembryanthemum crystallinum</i>	gi6942190		7.90E-11
512	G2741	<i>Nicotiana tabacum</i>	gi4519671		1.20E-09
512	G2741	<i>Solanum bulbocastanum</i>	gi32470629		4.30E-09
512	G2741	<i>Pisum sativum</i>	gi23504755		0.063
514	G2743	<i>Medicago truncatula</i>	CF068634		3.00E-50
514	G2743	<i>Oryza sativa (japonica cultivar-group)</i>	AK064355		2.00E-49
514	G2743	<i>Solanum tuberosum</i>	BQ513305		2.00E-40
514	G2743	<i>Lycopersicon pennellii</i>	AW398166		7.00E-40
514	G2743	<i>Populus tremuloides</i>	CA926221		4.00E-38
514	G2743	<i>Brassica oleracea</i>	BH485910		9.00E-37
514	G2743	<i>Lycopersicon esculentum</i>	BE450553		3.00E-36
514	G2743	<i>Glycine max</i>	BM524732		3.00E-33
514	G2743	<i>Hordeum vulgare subsp. vulgare</i>	BU988945		1.00E-30
514	G2743	<i>Prunus armeniaca</i>	CB820349		4.00E-27
514	G2743	<i>Oryza sativa</i>	gi11034542		1.50E-49
514	G2743	<i>Oryza sativa (japonica cultivar-group)</i>	gi31415946		4.50E-41
514	G2743	<i>Zea mays</i>	gi14189890		4.30E-12
514	G2743	<i>Chlamydomonas reinhardtii</i>	gi5916207		5.00E-12
514	G2743	<i>Mesembryanthemum crystallinum</i>	gi6942190		1.80E-10
514	G2743	<i>Solanum bulbocastanum</i>	gi32470629		2.40E-09
514	G2743	<i>Nicotiana tabacum</i>	gi4519671		4.80E-09
514	G2743	<i>Oryza glaberrima</i>	gi31338862		1.30E-08
514	G2743	<i>Oryza sativa (indica cultivar-group)</i>	gi31338860		8.10E-08
514	G2743	<i>Hordeum vulgare</i>	gi12406993		0.079
516	G2747	<i>Brassica oleracea</i>	BH542430		1.00E-110
516	G2747	<i>Oryza sativa (indica cultivar-group)</i>	AAAAA01011764		1.00E-51
516	G2747	<i>Lycopersicon</i>	BI934304		3.00E-51

		<i>esculentum</i>			
516	G2747	<i>Oryza sativa</i>	AX654655		7.00E-51
516	G2747	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK106367		3.00E-50
516	G2747	<i>Lactuca sativa</i>	BU005803		1.00E-49
516	G2747	<i>Zea mays</i>	AC144718		9.00E-44
516	G2747	<i>Solanum tuberosum</i>	BQ119486		1.00E-43
516	G2747	<i>Capsicum annuum</i>	BM063508		1.00E-42
516	G2747	<i>Glycine max</i>	AW760132		3.00E-39
516	G2747	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi21426118		2.80E-52
516	G2747	<i>Marchantia polymorpha</i>	gi25272004		7.10E-39
516	G2747	<i>Oryza sativa</i>	gi19352041		2.30E-09
516	G2747	<i>Prunus persica</i>	gi27450533		7.10E-09
516	G2747	<i>Mangifera indica</i>	gi31747324		3.60E-08
516	G2747	<i>Eragrostis tef</i>	gi17906977		7.70E-08
516	G2747	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi1730475		1.00E-07
516	G2747	<i>Phaseolus vulgaris</i>	gi1046278		9.40E-07
516	G2747	<i>Pisum sativum</i>	gi22335711		1.20E-06
516	G2747	<i>Zea mays</i>	gi100922		4.00E-06
517	G2754	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER34285 1	1237	
517	G2754	<i>Glycine max</i>	LIB4167-054-R1-K1-B3	1238	
517	G2754	<i>Oryza sativa</i>	AU062733.2	1239	
517	G2754	<i>Oryza sativa</i>	LIB4309-004-Q1-K1-B9	1240	
517	G2754	<i>Oryza sativa</i>	OSC13803.C1.pl.fg	1241	
517	G2754	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER33736 2	1242	
517	G2754	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER41889 1	1243	
517	G2754	<i>Oryza sativa</i>	Os_S24071	1615	
517	G2754	<i>Hordeum vulgare</i>	Hv_S103555	1746	
517	G2754	<i>Zea mays</i>	Zm_S11456823	1820	
517	G2754	<i>Zea mays</i>	Zm_S11521388	1821	
517	G2754	<i>Zea mays</i>	Zm_S11523999	1822	
517	G2754	<i>Triticum aestivum</i>	Ta_S210098	1910	
517	G2754	<i>Triticum aestivum</i>	Ta_S272733	1911	
518	G2754	<i>Zea mays</i>	AF461813		1.0e-999
518	G2754	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK100732		1.00E-128
518	G2754	<i>Chenopodium amaranticolor</i>	AX652119		1.00E-111
518	G2754	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01000051		2.00E-92
518	G2754	<i>Triticum aestivum</i>	CA499811		6.00E-90
518	G2754	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	CB882737		4.00E-86
518	G2754	<i>Lactuca sativa</i>	BU006379		7.00E-86
518	G2754	<i>Oryza sativa</i>	AP004006		6.00E-84
518	G2754	<i>Medicago truncatula</i>	BQ122721		1.00E-83

518	G2754	<i>Nicotiana tabacum</i>	BP129768		6.00E-77
518	G2754	<i>Zea mays</i>	gi18463957		3.30E-251
518	G2754	<i>Oryza sativa</i>	gi12083522		1.70E-132
518	G2754	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi21952816		5.30E-86
518	G2754	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi23193479		1.20E-83
518	G2754	<i>Hordeum vulgare</i>	gi23193481		5.60E-82
518	G2754	<i>Triticum monococcum</i>	gi23193487		1.20E-81
518	G2754	<i>Glycine max</i>	gi25172762		3.30E-15
518	G2754	<i>Nicotiana tabacum</i>	gi8096269		0.54
518	G2754	<i>Lycopersicon esculentum</i>	gi4731573		0.87
518	G2754	<i>Alnus glutinosa</i>	gi2467082		0.9
520	G2757	<i>Brassica napus</i>	CD833979		1.00E-109
520	G2757	<i>Brassica oleracea</i>	BH475285		3.00E-85
520	G2757	<i>Glycine max</i>	AI494758		4.00E-29
520	G2757	<i>Medicago truncatula</i>	CB891664		2.00E-27
520	G2757	<i>Ipomoea nil</i>	BJ553668		4.00E-26
520	G2757	<i>Oryza sativa</i>	AC084763		1.00E-25
520	G2757	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AE017120		1.00E-25
520	G2757	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01000681		1.00E-25
520	G2757	<i>Zea mays</i>	BZ420052		5.00E-25
520	G2757	<i>Lycopersicon esculentum</i>	BG132323		1.00E-24
520	G2757	<i>Oryza sativa</i>	gi12597883		3.90E-39
520	G2757	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi31433545		3.90E-39
520	G2757	<i>Nicotiana tabacum</i>	gi18149189		1.50E-14
520	G2757	<i>Zea mays</i>	gi5731354		0.97
520	G2757	<i>Glycine max</i>	gi18182311		0.99
520	G2757	<i>Zinnia elegans</i>	gi531098		0.99
520	G2757	<i>Chloroplast</i> <i>Phaseolus vulgaris</i>	gi21309708		1
520	G2757	<i>Phalaenopsis</i> sp. SM9108	gi1173628		1
520	G2757	<i>Ranunculus ficaria</i>	gi27995073		1
520	G2757	<i>Cucumis melo</i>	gi7595346		1
521	G2763	<i>Hordeum vulgare</i>	Hv_S114962	1747	
522	G2763	<i>Brassica oleracea</i>	BH560418		3.00E-75
522	G2763	<i>Thellungiella halophila</i>	BM986046		3.00E-73
522	G2763	<i>Poncirus trifoliata</i>	CD575942		3.00E-54
522	G2763	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU896429		2.00E-50
522	G2763	<i>Ipomoea nil</i>	BJ574783		1.00E-48
522	G2763	<i>Solanum tuberosum</i>	BG351877		2.00E-47
522	G2763	<i>Glycine max</i>	CD415130		8.00E-43
522	G2763	<i>Lycopersicon</i>	BM409924		9.00E-42

		<i>esculentum</i>			
522	G2763	<i>Medicago truncatula</i>	AC135100		9.00E-42
522	G2763	<i>Theobroma cacao</i>	CA797288		4.00E-41
522	G2763	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi24059889		4.80E-21
522	G2763	<i>Tulipa gesneriana</i>	gi5923912		0.03
522	G2763	<i>Ananas comosus</i>	gi25044805		0.034
522	G2763	<i>Oryza sativa</i>	gi5852091		0.29
522	G2763	<i>Oryza longistaminata</i>	gi1086530		0.66
522	G2763	<i>Zea mays</i>	gi1244653		0.76
522	G2763	<i>Oryza rufipogon</i>	gi1086536		0.85
522	G2763	<i>Quercus robur</i>	gi33111961		0.98
522	G2763	<i>Triticum monococcum</i>	gi30090030		1
522	G2763	<i>Glycine max</i>	gi3399777		1
524	G2765	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK106649		4.00E-61
524	G2765	<i>Lycopersicon esculentum</i>	AI488313		5.00E-60
524	G2765	<i>Brassica oleracea</i>	BH582059		4.00E-51
524	G2765	<i>Glycine max</i>	BE020519		2.00E-50
524	G2765	<i>Oryza sativa</i> subsp. <i>japonica</i>	AU093196		4.00E-49
524	G2765	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU813371		1.00E-37
524	G2765	<i>Medicago truncatula</i>	BF647687		2.00E-37
524	G2765	<i>Pinus pinaster</i>	BX252556		1.00E-32
524	G2765	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU869748		4.00E-32
524	G2765	<i>Zea mays</i>	BZ644709		3.00E-31
524	G2765	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi32129332		2.30E-30
524	G2765	<i>Oryza sativa</i>	gi10800070		3.80E-28
524	G2765	<i>Pennisetum glaucum</i>	gi527655		8.40E-09
524	G2765	<i>Perilla frutescens</i>	gi28375728		1.30E-08
524	G2765	<i>Sorghum bicolor</i>	gi527665		1.40E-08
524	G2765	<i>Oryza australiensis</i>	gi1086526		1.80E-08
524	G2765	<i>Oryza rufipogon</i>	gi1086536		2.30E-08
524	G2765	<i>Phyllostachys acuta</i>	gi527661		3.80E-08
524	G2765	<i>Oryza longistaminata</i>	gi1086530		4.90E-08
524	G2765	<i>Oryza officinalis</i>	gi1086534		1.00E-07
525	G2768	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER48270_1	1244	
525	G2768	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER48270_2	1245	
525	G2768	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER48270_6	1246	
525	G2768	<i>Glycine max</i>	GLYMA-28NOV01-	1247	

			CLUSTER777019_1		
525	G2768	<i>Glycine max</i>	LIB4165-033-Q1-K1-E7	1248	
525	G2768	<i>Glycine max</i>	jC-gmle01810065e09d1	1249	
525	G2768	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER22_6	1250	
525	G2768	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER22_7	1251	
525	G2768	<i>Oryza sativa</i>	OSC10851.C1.p4.fg	1252	
525	G2768	<i>Oryza sativa</i>	OSC19157.C1.p4.fg	1253	
525	G2768	<i>Oryza sativa</i>	OSC32936.C1.p1.fg	1254	
525	G2768	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER21189_1	1255	
525	G2768	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER21189_3	1256	
525	G2768	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER35998_1	1257	
525	G2768	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER692790_1	1258	
525	G2768	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER697_56	1259	
525	G2768	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER697_59	1260	
525	G2768	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER697_60	1261	
525	G2768	<i>Hordeum vulgare</i>	Hv_S30775	1748	
525	G2768	<i>Triticum aestivum</i>	Ta_S127458	1912	
525	G2768	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-49806	2072	
525	G2768	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-51288	2073	
525	G2768	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-13430	2074	
526	G2768	<i>Oryza sativa</i> (japonica cultivar-group)	AK106568		1.00E-146
526	G2768	<i>Beta vulgaris</i>	BQ589936		7.00E-72
526	G2768	<i>Brassica oleracea</i>	BZ518223		2.00E-64
526	G2768	<i>Medicago truncatula</i>	AC119408		2.00E-56
526	G2768	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BQ758728		2.00E-56
526	G2768	<i>Sorghum bicolor</i>	CD222928		9.00E-56
526	G2768	<i>Lycopersicon esculentum</i>	BI931469		3.00E-53
526	G2768	<i>Oryza sativa</i>	AC087545		2.00E-49
526	G2768	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01000530		2.00E-49
526	G2768	<i>Ceratopteris richardii</i>	BE640922		1.00E-35
526	G2768	<i>Oryza sativa</i> (japonica cultivar-group)	gi31432245		9.90E-155
526	G2768	<i>Oryza sativa</i>	gi14028993		2.00E-08
526	G2768	<i>Nicotiana glauca</i>	gi3850823		1.50E-07
526	G2768	<i>Lycopersicon esculentum</i>	gi9858779		3.70E-06
526	G2768	<i>Cucurbita maxima</i>	gi17221648		1.10E-05

526	G2768	<i>Ipomoea nil</i>	gi11127996		3.80E-05
526	G2768	<i>Rosa hybrid cultivar</i>	gi15029364		0.0001
526	G2768	<i>Pisum sativum</i>	gi7688063		0.00022
526	G2768	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi520943		0.00053
526	G2768	<i>Hordeum vulgare</i>	gi629788		0.00053
528	G2771	<i>Glycine max</i>	CA783908		1.00E-35
528	G2771	<i>Brassica oleracea</i>	BZ510921		3.00E-33
528	G2771	<i>Lycopersicon</i> <i>esculentum</i>	BE431510		1.00E-30
528	G2771	<i>Amborella</i> <i>trichopoda</i>	CD482068		1.00E-29
528	G2771	<i>Prunus dulcis</i>	BU574318		2.00E-29
528	G2771	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AK060505		6.00E-28
528	G2771	<i>Solanum tuberosum</i>	BG591063		4.00E-27
528	G2771	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU866069		4.00E-27
528	G2771	<i>Oryza minuta</i>	CB209966		1.00E-26
528	G2771	<i>Sorghum bicolor</i>	BE598711		2.00E-26
528	G2771	<i>Oryza sativa</i>	gi31043851		6.10E-27
528	G2771	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi23495742		3.10E-25
528	G2771	<i>Tulipa gesneriana</i>	gi5923912		1.40E-14
528	G2771	<i>Oryza rufipogon</i>	gi1086538		1.70E-07
528	G2771	<i>Pennisetum</i> <i>glauca</i>	gi527653		1.70E-07
528	G2771	<i>Phyllostachys acuta</i>	gi527661		1.70E-07
528	G2771	<i>Sorghum bicolor</i>	gi527665		1.70E-07
528	G2771	<i>Gossypium</i> <i>hirsutum</i>	gi13346180		1.10E-06
528	G2771	<i>Zea mays</i>	gi100921		1.20E-06
528	G2771	<i>Oryza officinalis</i>	gi1086534		1.20E-06
529	G2776	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER10667_1	1262	
529	G2776	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER249_1	1263	
529	G2776	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER27648_1	1264	
529	G2776	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER318_3	1265	
529	G2776	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER318_5	1266	
529	G2776	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER362284_1	1267	
529	G2776	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER38253_1	1268	
529	G2776	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER92523_2	1269	
529	G2776	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER92523_4	1270	
529	G2776	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER278119_1	1271	
529	G2776	<i>Oryza sativa</i>	OSC21904.C1.p3.fg	1272	
529	G2776	<i>Oryza sativa</i>	OSC22826.C1.p11.fg	1273	

529	G2776	<i>Oryza sativa</i>	OSC6897.C1.p1.fg	1274	
529	G2776	<i>Oryza sativa</i>	OSC9960.C1.p2.fg	1275	
529	G2776	<i>Oryza sativa</i>	OSC9961.C1.p3.fg	1276	
529	G2776	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER607309 1	1277	
529	G2776	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER81320 1	1278	
529	G2776	<i>Glycine max</i>	Gma_S4925755	1672	
529	G2776	<i>Glycine max</i>	Gma_S5146563	1673	
529	G2776	<i>Triticum aestivum</i>	Ta_S121078	1913	
529	G2776	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-49159	2075	
529	G2776	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-357057	2076	
530	G2776	<i>Brassica oleracea</i>	BZ437288		5.00E-48
530	G2776	<i>Glycine max</i>	AF069738		2.00E-47
530	G2776	<i>Lotus japonicus</i>	AI967554		4.00E-46
530	G2776	<i>Lycopersicon esculentum</i>	AI896266		1.00E-45
530	G2776	<i>Populus tremula x Populus tremuloides</i>	BU884552		4.00E-43
530	G2776	<i>Medicago truncatula</i>	AW775712		4.00E-40
530	G2776	<i>Mesembryanthemum crystallinum</i>	AF097665		2.00E-38
530	G2776	<i>Oryza sativa (japonica cultivar-group)</i>	AC145380		2.00E-33
530	G2776	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01000416		2.00E-33
530	G2776	<i>Triticum aestivum</i>	BQ483543		2.00E-30
530	G2776	<i>Glycine max</i>	gi3399777		1.40E-48
530	G2776	<i>Mesembryanthemum crystallinum</i>	gi4206118		7.40E-41
530	G2776	<i>Oryza sativa (japonica cultivar-group)</i>	gi29788848		4.70E-33
530	G2776	<i>Oryza sativa</i>	gi18542931		6.60E-24
530	G2776	<i>Phaseolus vulgaris</i>	gi1142619		6.10E-19
530	G2776	<i>Lycopersicon esculentum</i>	gi6175252		5.80E-16
530	G2776	<i>Zea mays</i>	gi4321762		4.70E-15
530	G2776	<i>Petunia x hybrida</i>	gi10998404		2.30E-14
530	G2776	<i>Pennisetum glaucum</i>	gi527653		2.80E-12
530	G2776	<i>Phyllostachys acuta</i>	gi527661		7.80E-12
532	G2777	<i>Medicago truncatula</i>	BF521311		1.00E-64
532	G2777	<i>Brassica napus</i>	CD813382		1.00E-64
532	G2777	<i>Citrus sinensis</i>	CB293518		6.00E-56
532	G2777	<i>Oryza sativa (japonica cultivar-group)</i>	AK071315		2.00E-53
532	G2777	<i>Glycine max</i>	AW832440		5.00E-53
532	G2777	<i>Lactuca sativa</i>	BQ870016		1.00E-52
532	G2777	<i>Brassica rapa subsp. pekinensis</i>	BG544499		3.00E-52

532	G2777	<i>Populus tremula x Populus tremuloides</i>	BU831324		4.00E-40
532	G2777	<i>Brassica oleracea</i>	BZ432234		4.00E-38
532	G2777	<i>Lycopersicon esculentum</i>	BI926824		5.00E-37
532	G2777	<i>Phyllostachys acuta</i>	gi527661		1.20E-06
532	G2777	<i>Pennisetum glaucum</i>	gi527655		2.00E-06
532	G2777	<i>Lycopersicon esculentum</i>	gi23600383		2.10E-06
532	G2777	<i>Sorghum bicolor</i>	gi527665		5.30E-06
532	G2777	<i>Oryza sativa (japonica cultivar-group)</i>	gi22758263		6.10E-06
532	G2777	<i>Tripsacum australe</i>	gi527663		6.80E-06
532	G2777	<i>Phaseolus vulgaris</i>	gi1142621		8.60E-06
532	G2777	<i>Oryza rufipogon</i>	gi1086536		8.70E-06
532	G2777	<i>Oryza australiensis</i>	gi1086526		1.80E-05
532	G2777	<i>Oryza sativa</i>	gi15451582		2.10E-05
534	G2779	<i>Glycine max</i>	BE347561		4.00E-47
534	G2779	<i>Populus tremula x Populus tremuloides</i>	BU811904		2.00E-43
534	G2779	<i>Medicago truncatula</i>	CB066613		1.00E-29
534	G2779	<i>Oryza sativa (japonica cultivar-group)</i>	AK059041		2.00E-29
534	G2779	<i>Triticum aestivum</i>	BJ211785		5.00E-29
534	G2779	<i>Zea mays</i>	CB604124		1.00E-28
534	G2779	<i>Lycopersicon esculentum</i>	AI490119		3.00E-28
534	G2779	<i>Lotus corniculatus var. japonicus</i>	CB828026		3.00E-28
534	G2779	<i>Hordeum vulgare subsp. vulgare</i>	CA003238		7.00E-28
534	G2779	<i>Capsicum annuum</i>	CA522636		7.00E-28
534	G2779	<i>Oryza sativa (japonica cultivar-group)</i>	gi20804997		1.20E-30
534	G2779	<i>Tulipa gesneriana</i>	gi5923912		2.30E-30
534	G2779	<i>Oryza sativa</i>	gi11862964		7.90E-28
534	G2779	<i>Pinus taeda</i>	gi6166283		4.20E-10
534	G2779	<i>Glycine max</i>	gi3399777		3.00E-05
534	G2779	<i>Gossypium hirsutum</i>	gi13346182		5.30E-05
534	G2779	<i>Sorghum bicolor</i>	gi527665		0.00018
534	G2779	<i>Brassica napus</i>	gi27650307		0.00023
534	G2779	<i>Petunia x hybrida</i>	gi10998404		0.0005
534	G2779	<i>Phaseolus vulgaris</i>	gi1142621		0.00071
536	G2783	<i>Nicotiana glauca</i>	NPL292767		1.00E-127
536	G2783	<i>Zea mays</i>	AY107267		1.00E-125
536	G2783	<i>Oryza sativa (japonica cultivar-group)</i>	AK101593		1.00E-124
536	G2783	<i>Gossypium hirsutum</i>	CA993585		1.00E-113

536	G2783	<i>Beta vulgaris</i>	BVU313097		1.00E-110
536	G2783	<i>Medicago truncatula</i>	CB893695		1.00E-104
536	G2783	<i>Triticum aestivum</i>	BT009299		1.00E-102
536	G2783	<i>Nicotiana tabacum</i>	AF029351		3.00E-97
536	G2783	<i>Glycine max</i>	CA784546		1.00E-96
536	G2783	<i>Gossypium arboreum</i>	BF278029		8.00E-94
536	G2783	<i>Nicotiana plumbaginifolia</i>	gi9663767		9.00E-123
536	G2783	<i>Oryza sativa</i>	gi12583812		2.50E-120
536	G2783	<i>Oryza sativa</i> (japonica cultivar-group)	gi32488785		2.50E-120
536	G2783	<i>Beta vulgaris</i>	gi30524689		1.60E-107
536	G2783	<i>Nicotiana tabacum</i>	gi2708532		3.70E-94
536	G2783	<i>Sorghum bicolor</i>	gi22208507		2.70E-28
536	G2783	<i>Zea mays</i>	gi23928438		5.10E-25
536	G2783	<i>Solanum tuberosum</i>	gi17432522		7.90E-22
536	G2783	<i>Nicotiana glauca</i>	gi100293		5.40E-19
536	G2783	<i>Cucumis sativus</i>	gi7528270		6.70E-18
537	G2784	<i>Glycine max</i>	Gma_S5128871	1674	
537	G2784	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-68213	2077	
538	G2784	<i>Brassica oleracea</i>	BH966813		6.00E-65
538	G2784	<i>Mesembryanthemum crystallinum</i>	BE034373		2.00E-62
538	G2784	<i>Glycine max</i>	BE659785		2.00E-60
538	G2784	<i>Populus tremula</i>	BU821418		1.00E-42
538	G2784	<i>Lycopersicon esculentum</i>	AW218420		2.00E-35
538	G2784	<i>Solanum tuberosum</i>	BQ115041		2.00E-31
538	G2784	<i>Oryza sativa</i>	OSJN00052		8.00E-31
538	G2784	<i>Zea mays</i>	CC656270		8.00E-29
538	G2784	<i>Pinus taeda</i>	BF516719		6.00E-27
538	G2784	<i>Medicago truncatula</i>	BG589047		2.00E-26
538	G2784	<i>Oryza sativa</i>	gi21740764		4.30E-68
538	G2784	<i>Oryza sativa</i> (japonica cultivar-group)	gi31433498		8.30E-30
538	G2784	<i>Chlamydomonas reinhardtii</i>	gi18137		0.36
538	G2784	<i>Lycopersicon esculentum</i>	gi170408		0.96
538	G2784	<i>Physcomitrella patens</i>	gi11181645		0.98
538	G2784	<i>Nicotiana tabacum</i>	gi237857		1
540	G2790	<i>Brassica oleracea</i>	BH660922		1.00E-35
540	G2790	<i>Medicago truncatula</i>	BQ124408		5.00E-27
540	G2790	<i>Oryza sativa</i> (japonica cultivar-group)	AK072833		6.00E-27
540	G2790	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU895329		9.00E-26
540	G2790	<i>Gossypium</i>	BG440718		1.00E-25

		<i>arboreum</i>			
540	G2790	<i>Glycine max</i>	BG046947		2.00E-25
540	G2790	<i>Solanum tuberosum</i>	BQ514720		4.00E-25
540	G2790	<i>Gossypium hirsutum</i>	CA993210		1.00E-24
540	G2790	<i>Lycopersicon esculentum</i>	AF096263		2.00E-24
540	G2790	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	AI166770		4.00E-24
540	G2790	<i>Oryza sativa</i>	gi14488370		8.00E-28
540	G2790	<i>Brassica napus</i>	gi11045087		3.10E-26
540	G2790	<i>Lycopersicon esculentum</i>	gi5669656		1.00E-25
540	G2790	<i>Oryza sativa</i> (japonica cultivar-group)	gi32480231		2.20E-25
540	G2790	<i>Glycine max</i>	gi3399777		0.0012
540	G2790	<i>Pennisetum glaucum</i>	gi527657		0.002
540	G2790	<i>Tulipa gesneriana</i>	gi5923912		0.004
540	G2790	<i>Zea mays</i>	gi18568238		0.009
540	G2790	<i>Phaseolus vulgaris</i>	gi1142621		0.022
540	G2790	<i>Oryza rufipogon</i>	gi1086538		0.037
542	G2802	<i>Oryza sativa</i> (japonica cultivar-group)	AK106152		1.00E-132
542	G2802	<i>Oryza sativa</i> (indica cultivar-group)	CB630225		1.00E-102
542	G2802	<i>Medicago truncatula</i>	BQ148509		7.00E-98
542	G2802	<i>Pinus pinaster</i>	BX251486		7.00E-84
542	G2802	<i>Hordeum vulgare</i>	BI960052		1.00E-77
542	G2802	<i>Brassica oleracea</i>	BH656772		3.00E-76
542	G2802	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BI129724		3.00E-76
542	G2802	<i>Pinus taeda</i>	BF518231		9.00E-74
542	G2802	<i>Glycine max</i>	BM527360		1.00E-71
542	G2802	<i>Triticum aestivum</i>	BJ315410		6.00E-67
542	G2802	<i>Oryza sativa</i>	gi9049470		2.30E-85
542	G2802	<i>Oryza sativa</i> (japonica cultivar-group)	gi18461166		3.50E-78
542	G2802	<i>Brassica napus</i>	gi12751304		1.20E-49
542	G2802	<i>Petunia</i> x <i>hybrida</i>	gi21105748		3.70E-09
542	G2802	<i>Triticum monococcum</i>	gi6732154		3.10E-08
542	G2802	<i>Solanum tuberosum</i>	gi14485513		1.10E-07
542	G2802	<i>Triticum</i> sp.	gi4218535		3.30E-06
542	G2802	<i>Phaseolus vulgaris</i>	gi15148912		9.00E-06
542	G2802	<i>Lycopersicon esculentum</i>	gi6175246		3.50E-05
542	G2802	<i>Medicago truncatula</i>	gi7716952		4.20E-05
544	G2805	<i>Brassica oleracea</i>	BZ506570		4.00E-27
544	G2805	<i>Gossypium hirsutum</i>	CA992724		6.00E-05

544	G2805	<i>Glycine max</i>	CA802497		3.00E-04
544	G2805	<i>Lycopersicon esculentum</i>	BE460507		0.002
544	G2805	<i>Eschscholzia californica</i>	CD480753		0.005
544	G2805	<i>Oryza sativa (japonica cultivar- group)</i>	AK062955		0.005
544	G2805	<i>Sorghum bicolor</i>	BE363054		0.016
544	G2805	<i>Solanum tuberosum</i>	BM406262		0.016
544	G2805	<i>Gossypium arboreum</i>	BG440924		0.035
544	G2805	<i>Lactuca sativa</i>	BQ850404		0.079
544	G2805	<i>Oryza sativa (japonica cultivar- group)</i>	gi21741263		0.00027
544	G2805	<i>Petunia x hybrida</i>	gi21389179		0.00048
544	G2805	<i>Oryza sativa</i>	gi13129497		0.0027
544	G2805	<i>Glycine max</i>	gi22597158		0.05
544	G2805	<i>Lycopersicon esculentum</i>	gi6175246		0.35
544	G2805	<i>Phaseolus vulgaris</i>	gi15148914		0.54
544	G2805	<i>Medicago truncatula</i>	gi7716952		0.61
544	G2805	<i>Theobroma cacao</i>	gi15487902		0.87
544	G2805	<i>Triticum monococcum</i>	gi6732156		1
544	G2805	<i>Papaver somniferum</i>	gi169002		1
545	G2826	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER166362 1	753	
545	G2826	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER180202 1	754	
545	G2826	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER726571 1	755	
545	G2826	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER74662 1	756	
545	G2826	<i>Glycine max</i>	uC-gmflminsoy032f06b1	757	
545	G2826	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER173260 2	758	
545	G2826	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER200967 1	759	
545	G2826	<i>Oryza sativa</i>	OSC100895.C1.p14.fg	760	
545	G2826	<i>Oryza sativa</i>	OSC22205.C1.p1.fg	1279	
545	G2826	<i>Oryza sativa</i>	OSC23411.C1.p1.fg	761	
545	G2826	<i>Oryza sativa</i>	OSC2409.C1.p2.fg	762	
545	G2826	<i>Oryza sativa</i>	OSC25680.C1.p1.fg	763	
545	G2826	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER436044 1	764	
545	G2826	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER518126 1	765	
545	G2826	<i>Oryza sativa</i>	Os_S106189	1616	
545	G2826	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-54039	1959	
545	G2826	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-54252	1960	
545	G2826	<i>Lycopersicon</i>	SGN-UNIGENE-	1961	

		<i>esculentum</i>	SINGLET-392715		
546	G2826	<i>Brassica oleracea</i>	BH725134		7.00E-79
546	G2826	<i>Oryza sativa</i> (indica cultivar-group)	AAAAA01004859		1.00E-37
546	G2826	<i>Oryza sativa</i>	AP003214		2.00E-37
546	G2826	<i>Lotus japonicus</i>	BU494379		1.00E-36
546	G2826	<i>Glycine max</i>	BI315690		6.00E-35
546	G2826	<i>Lycopersicon esculentum</i>	BG135559		1.00E-33
546	G2826	<i>Medicago truncatula</i>	BF004070		5.00E-32
546	G2826	<i>Beta vulgaris</i>	BQ488216		4.00E-26
546	G2826	<i>Sorghum bicolor</i>	BE358938		1.00E-21
546	G2826	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BU877646		1.00E-20
546	G2826	<i>Oryza sativa</i>	gi15528588		3.00E-35
546	G2826	<i>Sorghum bicolor</i>	gi18390109		8.30E-17
546	G2826	<i>Oryza sativa</i> (japonica cultivar-group)	gi32482926		9.80E-07
546	G2826	<i>Petunia x hybrida</i>	gi14275902		1.50E-05
546	G2826	<i>Pisum sativum</i>	gi7008009		0.00016
546	G2826	<i>Zea mays</i>	gi18674684		0.0002
546	G2826	<i>Silene latifolia</i>	gi1628463		0.00045
546	G2826	<i>Lycopersicon esculentum</i>	gi1345540		0.0006
546	G2826	<i>Nicotiana tabacum</i>	gi14516835		0.0017
546	G2826	<i>Rumex obtusifolius</i>	gi20152613		0.0022
547	G2830	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER16384_5	1280	
548	G2830	<i>Brassica oleracea</i>	BH993354		9.00E-65
548	G2830	<i>Glycine max</i>	BM177052		5.00E-13
548	G2830	<i>Phaseolus coccineus</i>	CA902517		3.00E-08
548	G2830	<i>Lotus japonicus</i>	AP006108		8.00E-07
548	G2830	<i>Zea mays</i>	BZ652013		5.9
548	G2830	<i>Mesembryanthemum crystallinum</i>	BG269090		7.7
548	G2830	<i>Medicago truncatula</i>	AC135797		7.7
548	G2830	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	BI137362		7.7
548	G2830	<i>Zea mays</i> subsp. <i>mays</i>	gi31414978		0.96
548	G2830	<i>Nicotiana tabacum</i>	gi8099397		0.99
550	G2832	<i>Brassica oleracea</i>	BZ004148		4.00E-39
550	G2832	<i>Petunia x hybrida</i>	AB003672		8.00E-36
550	G2832	<i>Limnanthes alba</i>	BV007314		2.00E-20
550	G2832	<i>Medicago truncatula</i>	CB892199		6.00E-10
550	G2832	<i>Oryza sativa</i> (japonica cultivar-group)	AK106924		7.00E-10
550	G2832	<i>Oryza sativa</i> (indica cultivar-group)	AAAAA01002475		7.00E-10

550	G2832	<i>Oryza sativa</i>	AC037426		7.00E-10
550	G2832	<i>Solanum demissum</i>	AC136471		2.00E-08
550	G2832	<i>Lactuca sativa</i>	BU015249		7.00E-08
550	G2832	<i>Zea mays</i>	CC408365		5.00E-06
550	G2832	<i>Petunia x hybrida</i>	gi1786146		9.30E-50
550	G2832	<i>Oryza sativa</i> (japonica cultivar-group)	gi32482980		9.10E-11
550	G2832	<i>Medicago sativa</i>	gi7228329		6.40E-08
550	G2832	<i>Glycine max</i>	gi1763063		7.20E-06
550	G2832	<i>Pisum sativum</i>	gi2129892		4.10E-05
550	G2832	<i>Nicotiana tabacum</i>	gi2981169		8.90E-05
550	G2832	<i>Triticum aestivum</i>	gi485814		0.00041
550	G2832	<i>Oryza sativa</i>	gi12698882		0.00046
550	G2832	<i>Brassica rapa</i>	gi2058504		0.00055
550	G2832	<i>Datisca glomerata</i>	gi4666360		0.0066
552	G2834	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01001233		1.00E-126
552	G2834	<i>Oryza sativa</i> (japonica cultivar-group)	AK072211		1.00E-126
552	G2834	<i>Oryza sativa</i>	AP003235		1.00E-126
552	G2834	<i>Brassica oleracea</i>	BZ014527		1.00E-106
552	G2834	<i>Vitis vinifera</i>	BM436747		1.00E-105
552	G2834	<i>Zea mays</i>	AY106636		1.00E-101
552	G2834	<i>Ipomoea batatas</i>	BM878854		3.00E-95
552	G2834	<i>Glycine max</i>	BQ741681		3.00E-94
552	G2834	<i>Solanum tuberosum</i>	BE343020		3.00E-92
552	G2834	<i>Lycopersicon esculentum</i>	BE459539		1.00E-88
552	G2834	<i>Oryza sativa</i>	gi15408708		2.40E-123
552	G2834	<i>Oryza sativa</i> (japonica cultivar-group)	gi19571114		2.40E-123
552	G2834	<i>Lycopersicon esculentum</i>	gi15984226		3.40E-75
552	G2834	<i>Glycine max</i>	gi18376601		2.30E-29
552	G2834	<i>Solanum tuberosum</i>	gi563623		1.10E-20
552	G2834	<i>Zea mays</i>	gi3170601		1.80E-19
552	G2834	<i>Petunia x hybrida</i>	gi14522848		0.51
552	G2834	<i>Nicotiana tabacum</i>	gi4519673		0.73
552	G2834	<i>Oryza sativa</i> (indica cultivar-group)	gi28195113		0.99
552	G2834	<i>Brassica rapa</i>	gi7209506		1
554	G2837	<i>Brassica oleracea</i>	BZ451120		4.00E-55
554	G2837	<i>Vitis vinifera</i>	CD010326		9.00E-13
554	G2837	<i>Glycine max</i>	AQ842019		3.00E-09
554	G2837	<i>Zea mays</i>	BZ806743		3.00E-06
554	G2837	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01007143		8.00E-06
554	G2837	<i>Oryza sativa</i> (japonica cultivar-group)	AP003988		1.00E-05
554	G2837	<i>Brassica napus</i>	CB686322		4.00E-05
554	G2837	<i>Lotus japonicus</i>	AP004945		9.00E-05
554	G2837	<i>Triticum aestivum</i>	CA708862		2.00E-04

554	G2837	<i>Petunia x hybrida</i>	AB000454		4.00E-04
554	G2837	<i>Petunia x hybrida</i>	gi1786140		2.40E-05
554	G2837	<i>Zea diploperennis</i>	gi1076786		0.00014
554	G2837	<i>Pisum sativum</i>	gi7440062		0.00027
554	G2837	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi22002132		0.0003
554	G2837	<i>Lycopersicon</i> <i>esculentum</i>	gi1345540		0.00045
554	G2837	<i>Nicotiana tabacum</i>	gi395147		0.0013
554	G2837	<i>Brassica oleracea</i>	gi1418351		0.0017
554	G2837	<i>Medicago sativa</i>	gi1279563		0.002
554	G2837	<i>Cicer arietinum</i>	gi21068672		0.0022
554	G2837	<i>Zea mays</i>	gi18568237		0.005
555	G2838	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER166362_1	753	
555	G2838	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER180202_1	754	
555	G2838	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER726571_1	755	
555	G2838	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER74662_1	756	
555	G2838	<i>Glycine max</i>	uC-gmflminsoy032f06b1	757	
555	G2838	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER200967_1	759	
555	G2838	<i>Oryza sativa</i>	OSC100895.C1.p14.fg	760	
555	G2838	<i>Oryza sativa</i>	OSC22205.C1.p1.fg	1279	
555	G2838	<i>Oryza sativa</i>	OSC23411.C1.p1.fg	761	
555	G2838	<i>Oryza sativa</i>	OSC2409.C1.p2.fg	762	
555	G2838	<i>Oryza sativa</i>	OSC25680.C1.p1.fg	763	
555	G2838	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER436044_1	764	
555	G2838	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER518126_1	765	
555	G2838	<i>Lycopersicon</i> <i>esculentum</i>	SGN-UNIGENE-54039	1959	
555	G2838	<i>Lycopersicon</i> <i>esculentum</i>	SGN-UNIGENE-54252	1960	
555	G2838	<i>Lycopersicon</i> <i>esculentum</i>	SGN-UNIGENE- SINGLET-392715	1961	
556	G2838	<i>Vitis vinifera</i>	CD714231		7.00E-27
556	G2838	<i>Gossypium</i> <i>arboreum</i>	BF272143		2.00E-20
556	G2838	<i>Brassica oleracea</i>	BZ444318		5.00E-20
556	G2838	<i>Lycopersicon</i> <i>esculentum</i>	BG643969		2.00E-16
556	G2838	<i>Zea mays</i>	CC712091		1.00E-15
556	G2838	<i>Sorghum bicolor</i>	BE360413		7.00E-14
556	G2838	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01009505		1.00E-12
556	G2838	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK068762		2.00E-12
556	G2838	<i>Medicago</i> <i>truncatula</i>	BE943078		5.00E-12
556	G2838	<i>Glycine max</i>	BG047435		5.00E-12
556	G2838	<i>Sorghum bicolor</i>	gi18390109		1.70E-14

556	G2838	<i>Oryza sativa</i>	gi15528588		5.90E-12
556	G2838	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi29027767		2.20E-08
556	G2838	<i>Petunia x hybrida</i>	gi14275902		8.70E-05
556	G2838	<i>Zea mays</i>	gi18674684		0.02
556	G2838	<i>Medicago sativa</i>	gi7228329		0.024
556	G2838	<i>Pisum sativum</i>	gi2129892		0.06
556	G2838	<i>Glycine max</i>	gi1763063		0.095
556	G2838	<i>Datisca glomerata</i>	gi4666360		0.33
556	G2838	<i>Nicotiana tabacum</i>	gi2981169		0.38
557	G2839	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER32534_1	1281	
557	G2839	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER37260_1	1282	
557	G2839	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER379048_1	1283	
557	G2839	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER172363_1	1284	
557	G2839	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER24561_1	1285	
557	G2839	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER32611_1	1286	
557	G2839	<i>Oryza sativa</i>	OSC100424.C1.p49.fg	1287	
557	G2839	<i>Oryza sativa</i>	OSC20005.C1.p5.fg	1288	
557	G2839	<i>Oryza sativa</i>	OSC20005.C1.p7.fg	1289	
557	G2839	<i>Oryza sativa</i>	OSC234.C1.p1.fg	1290	
557	G2839	<i>Oryza sativa</i>	OSC5483.C1.p4.fg	1291	
557	G2839	<i>Oryza sativa</i>	OSC5499.C1.p15.fg	1292	
557	G2839	<i>Zea mays</i>	LIB3732-060-Q1-K6-F2	1293	
557	G2839	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER226176_1	1294	
557	G2839	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER276871_2	1295	
557	G2839	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER49287_1	1296	
557	G2839	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER5148_1	1297	
557	G2839	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER536916_1	1298	
557	G2839	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER72147_1	1299	
557	G2839	<i>Oryza sativa</i>	Os_S109163	1617	
557	G2839	<i>Glycine max</i>	Gma_S4898433	1675	
557	G2839	<i>Glycine max</i>	Gma_S4973977	1676	
557	G2839	<i>Medicago truncatula</i>	Mtr_S5397852	1713	
557	G2839	<i>Hordeum vulgare</i>	Hv_S207187	1749	
557	G2839	<i>Triticum aestivum</i>	Ta_S111267	1914	
557	G2839	<i>Triticum aestivum</i>	Ta_S200273	1915	
557	G2839	<i>Triticum aestivum</i>	Ta_S296415	1916	
557	G2839	<i>Triticum aestivum</i>	Ta_S379755	1917	
557	G2839	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-56766	2078	
558	G2839	<i>Brassica oleracea</i>	BZ083260		1.00E-51
558	G2839	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BQ790831		6.00E-48

558	G2839	<i>Brassica napus</i>	CD842269		7.00E-48
558	G2839	<i>Brassica rapa</i>	L46574		7.00E-30
558	G2839	<i>Vitis vinifera</i>	CA818230		4.00E-25
558	G2839	<i>Petunia x hybrida</i>	AB006600		9.00E-25
558	G2839	<i>Glycine max</i>	BU577326		2.00E-23
558	G2839	<i>Solanum tuberosum</i>	BQ121105		4.00E-23
558	G2839	<i>Populus tremula x Populus tremuloides</i>	BU867080		8.00E-23
558	G2839	<i>Lycopersicon esculentum</i>	AI898309		1.00E-22
558	G2839	<i>Petunia x hybrida</i>	gi2346976		7.10E-27
558	G2839	<i>Oryza sativa (japonica cultivar-group)</i>	gi29124132		3.90E-21
558	G2839	<i>Oryza sativa</i>	gi15623820		1.30E-20
558	G2839	<i>Glycine max</i>	gi1763063		2.40E-16
558	G2839	<i>Nicotiana tabacum</i>	gi2981169		1.20E-15
558	G2839	<i>Datisca glomerata</i>	gi4666360		3.20E-15
558	G2839	<i>Medicago sativa</i>	gi7228329		2.60E-13
558	G2839	<i>Triticum aestivum</i>	gi485814		3.80E-13
558	G2839	<i>Brassica rapa</i>	gi2058506		4.60E-11
558	G2839	<i>Pisum sativum</i>	gi2129892		3.40E-07
560	G2846	<i>Gossypium hirsutum</i>	CA993210		4.00E-46
560	G2846	<i>Oryza sativa (japonica cultivar-group)</i>	AK069366		2.00E-41
560	G2846	<i>Brassica oleracea</i>	BH484306		5.00E-41
560	G2846	<i>Glycine max</i>	BU764909		8.00E-37
560	G2846	<i>Sorghum bicolor</i>	CB926717		4.00E-34
560	G2846	<i>Triticum aestivum</i>	CA600074		1.00E-31
560	G2846	<i>Populus balsamifera subsp. trichocarpa</i>	AI166770		5.00E-29
560	G2846	<i>Populus tremula x Populus tremuloides</i>	BU894578		7.00E-28
560	G2846	<i>Gossypium arboreum</i>	BG440718		4.00E-27
560	G2846	<i>Solanum tuberosum</i>	BQ514720		2.00E-24
560	G2846	<i>Oryza sativa (japonica cultivar-group)</i>	gi21741062		6.40E-42
560	G2846	<i>Brassica napus</i>	gi11045087		1.60E-24
560	G2846	<i>Oryza sativa</i>	gi21740790		1.80E-23
560	G2846	<i>Lycopersicon esculentum</i>	gi5669656		2.70E-20
560	G2846	<i>Glycine max</i>	gi3399777		3.50E-05
560	G2846	<i>Cucumis melo</i>	gi28558779		0.0011
560	G2846	<i>Mesembryanthemum crystallinum</i>	gi4206118		0.014
560	G2846	<i>Oryza rufipogon</i>	gi1086536		0.028
560	G2846	<i>Phyllostachys acuta</i>	gi527661		0.039
560	G2846	<i>Tulipa gesneriana</i>	gi5923912		0.045
562	G2847	<i>Glycine max</i>	BU084566		8.00E-55
562	G2847	<i>Populus balsamifera subsp.</i>	AI166770		3.00E-50

		<i>trichocarpa</i>			
562	G2847	<i>Brassica napus</i>	CD832456		2.00E-49
562	G2847	<i>Solanum tuberosum</i>	BI175830		1.00E-48
562	G2847	<i>Ipomoea nil</i>	BJ570931		2.00E-46
562	G2847	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK072848		4.00E-45
562	G2847	<i>Gossypium arboreum</i>	BG440718		7.00E-43
562	G2847	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU895329		5.00E-36
562	G2847	<i>Hordeum vulgare</i>	BF620349		6.00E-36
562	G2847	<i>Triticum aestivum</i>	CA642784		5.00E-31
562	G2847	<i>Brassica napus</i>	gi11045087		1.40E-62
562	G2847	<i>Oryza sativa</i>	gi21740790		8.90E-29
562	G2847	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi32480231		8.90E-29
562	G2847	<i>Lycopersicon esculentum</i>	gi5669656		1.20E-24
562	G2847	<i>Mesembryanthemum crystallinum</i>	gi4206118		1.20E-05
562	G2847	<i>Glycine max</i>	gi3399777		0.021
562	G2847	<i>Phyllostachys acuta</i>	gi527661		0.066
562	G2847	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20372895		0.082
562	G2847	<i>Gossypioideis kirkii</i>	gi23476285		0.12
562	G2847	<i>Pennisetum glaucum</i>	gi527657		0.14
564	G2850	<i>Poncirus trifoliata</i>	CD573726		6.00E-68
564	G2850	<i>Lycopersicon esculentum</i>	AI899168		1.00E-45
564	G2850	<i>Medicago truncatula</i>	AL380393		8.00E-41
564	G2850	<i>Brassica napus</i>	CD825720		2.00E-40
564	G2850	<i>Gossypium arboreum</i>	BG440718		4.00E-30
564	G2850	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	AI166770		7.00E-30
564	G2850	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU895329		4.00E-29
564	G2850	<i>Glycine max</i>	BU084566		1.00E-28
564	G2850	<i>Solanum tuberosum</i>	BQ514720		2.00E-27
564	G2850	<i>Gossypium hirsutum</i>	CA993210		4.00E-27
564	G2850	<i>Oryza sativa</i>	gi14488370		3.10E-26
564	G2850	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi21741062		1.60E-25
564	G2850	<i>Brassica napus</i>	gi11045087		5.90E-25
564	G2850	<i>Lycopersicon esculentum</i>	gi5669656		1.00E-18
564	G2850	<i>Pennisetum glaucum</i>	gi527657		2.40E-05
564	G2850	<i>Glycine max</i>	gi3399777		8.00E-05
564	G2850	<i>Phyllostachys acuta</i>	gi527661		0.0061

564	G2850	<i>Oryza australiensis</i>	gi1086526		0.0077
564	G2850	<i>Oryza officinalis</i>	gi1086534		0.0077
564	G2850	<i>Tripsacum australe</i>	gi527663		0.01
566	G2851	<i>Brassica napus</i>	CD832456		7.00E-93
566	G2851	<i>Glycine max</i>	BU084566		5.00E-67
566	G2851	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	AI166770		2.00E-65
566	G2851	<i>Brassica oleracea</i>	BH927065		6.00E-56
566	G2851	<i>Solanum tuberosum</i>	BI175830		1.00E-55
566	G2851	<i>Gossypium arboreum</i>	BG440718		1.00E-51
566	G2851	<i>Ipomoea nil</i>	BJ570931		5.00E-51
566	G2851	<i>Oryza sativa</i> (japonica cultivar-group)	AK072848		2.00E-50
566	G2851	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU895329		3.00E-42
566	G2851	<i>Hordeum vulgare</i>	BF620349		7.00E-39
566	G2851	<i>Brassica napus</i>	gi11045087		1.60E-162
566	G2851	<i>Oryza sativa</i>	gi21740790		1.10E-27
566	G2851	<i>Oryza sativa</i> (japonica cultivar-group)	gi32480231		1.10E-27
566	G2851	<i>Lycopersicon esculentum</i>	gi5669656		4.20E-15
566	G2851	<i>Phyllostachys acuta</i>	gi527661		0.0081
566	G2851	<i>Glycine max</i>	gi3399777		0.012
566	G2851	<i>Pisum sativum</i>	gi13365610		0.018
566	G2851	<i>Pennisetum glaucum</i>	gi527657		0.021
566	G2851	<i>Tulipa gesneriana</i>	gi5923912		0.077
566	G2851	<i>Phaseolus vulgaris</i>	gi1142621		0.09
567	G2854	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER907_3	1300	
567	G2854	<i>Oryza sativa</i>	OSC18775.C1.p1.fg	1301	
567	G2854	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER13712_1	1302	
567	G2854	<i>Oryza sativa</i>	Os_S32676	1618	
567	G2854	<i>Oryza sativa</i>	Os_S75860	1619	
567	G2854	<i>Glycine max</i>	Gma_S4975207	1677	
567	G2854	<i>Hordeum vulgare</i>	Hv_S153237	1750	
567	G2854	<i>Hordeum vulgare</i>	Hv_S63965	1751	
567	G2854	<i>Zea mays</i>	Zm_S11522955	1823	
567	G2854	<i>Zea mays</i>	Zm_S11525357	1824	
567	G2854	<i>Triticum aestivum</i>	Ta_S125786	1918	
567	G2854	<i>Triticum aestivum</i>	Ta_S152820	1919	
567	G2854	<i>Triticum aestivum</i>	Ta_S267457	1920	
567	G2854	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-44207	2079	
567	G2854	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-56600	2080	
567	G2854	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-17539	2081	
567	G2854	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-333119	2082	

567	G2854	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-396174	2083	
567	G2854	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-49629	2084	
568	G2854	<i>Nicotiana plumbaginifolia</i>	NPL292767		1.00E-143
568	G2854	<i>Oryza sativa (japonica cultivar- group)</i>	AK101593		1.00E-130
568	G2854	<i>Zea mays</i>	AY107267		1.00E-128
568	G2854	<i>Beta vulgaris</i>	BVU313097		1.00E-110
568	G2854	<i>Gossypium hirsutum</i>	CA993585		1.00E-109
568	G2854	<i>Nicotiana tabacum</i>	AF029351		1.00E-104
568	G2854	<i>Brassica napus</i>	CD832069		1.00E-104
568	G2854	<i>Triticum aestivum</i>	BT009299		1.00E-100
568	G2854	<i>Medicago truncatula</i>	CB893695		2.00E-97
568	G2854	<i>Prunus persica</i>	BU045049		3.00E-92
568	G2854	<i>Nicotiana plumbaginifolia</i>	gi9663767		7.20E-137
568	G2854	<i>Oryza sativa</i>	gi12583812		6.80E-125
568	G2854	<i>Oryza sativa (japonica cultivar- group)</i>	gi32488785		6.90E-116
568	G2854	<i>Beta vulgaris</i>	gi30524689		6.30E-106
568	G2854	<i>Nicotiana tabacum</i>	gi2708532		1.30E-98
568	G2854	<i>Sorghum bicolor</i>	gi22208507		6.30E-25
568	G2854	<i>Zea mays</i>	gi23928438		4.60E-22
568	G2854	<i>Spinacia oleracea</i>	gi133247		4.60E-19
568	G2854	<i>Oryza sativa (indica cultivar-group)</i>	gi4680340		4.60E-19
568	G2854	<i>Cucumis sativus</i>	gi7528270		5.60E-19
569	G2859	<i>Glycine max</i>	BE347561.1	1303	
569	G2859	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-452318	2085	
570	G2859	<i>Glycine max</i>	BE347561		2.00E-47
570	G2859	<i>Populus tremula x Populus tremuloides</i>	BU811904		3.00E-47
570	G2859	<i>Populus tremula</i>	BU889630		8.00E-32
570	G2859	<i>Hordeum vulgare subsp. vulgare</i>	CA003238		3.00E-30
570	G2859	<i>Sorghum propinquum</i>	BG103016		7.00E-30
570	G2859	<i>Gossypium arboreum</i>	BF273287		1.00E-29
570	G2859	<i>Oryza sativa (japonica cultivar- group)</i>	AK101063		2.00E-29
570	G2859	<i>Sorghum bicolor</i>	BG048756		2.00E-29
570	G2859	<i>Lycopersicon esculentum</i>	AI490119		8.00E-29
570	G2859	<i>Medicago truncatula</i>	CB066613		1.00E-28
570	G2859	<i>Oryza sativa (japonica cultivar- group)</i>	gi20804997		1.40E-30

570	G2859	<i>Tulipa gesneriana</i>	gi5923912		4.70E-30
570	G2859	<i>Oryza sativa</i>	gi11862964		6.30E-29
570	G2859	<i>Pinus taeda</i>	gi6166283		2.40E-11
570	G2859	<i>Brassica napus</i>	gi27650307		2.70E-06
570	G2859	<i>Phyllostachys acuta</i>	gi527661		3.30E-05
570	G2859	<i>Gossypium hirsutum</i>	gi13346182		4.20E-05
570	G2859	<i>Petunia x hybrida</i>	gi10998404		6.00E-05
570	G2859	<i>Mesembryanthemum crystallinum</i>	gi4206118		0.00012
570	G2859	<i>Glycine max</i>	gi3399777		0.00024
571	G2865	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER4111_3	1304	
571	G2865	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER4111_4	1305	
571	G2865	<i>Glycine max</i>	Gma_S5127199	1678	
571	G2865	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-55990	2086	
571	G2865	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-18331	2087	
572	G2865	<i>Brassica oleracea</i>	BH680810		4.00E-39
572	G2865	<i>Glycine max</i>	BE057473		6.00E-24
572	G2865	<i>Brassica rapa subsp. pekinensis</i>	BZ614080		2.00E-17
572	G2865	<i>Medicago truncatula</i>	AL389569		8.00E-14
572	G2865	<i>Lotus corniculatus var. japonicus</i>	CB829442		3.00E-12
572	G2865	<i>Hedyotis centranthoides</i>	CB086514		2.00E-11
572	G2865	<i>Lycopersicon esculentum</i>	AW624871		9.00E-10
572	G2865	<i>Triphysaria versicolor</i>	BM356795		1.00E-09
572	G2865	<i>Beta vulgaris</i>	BQ592169		3.00E-07
572	G2865	<i>Lotus japonicus</i>	AG233200		7.00E-07
572	G2865	<i>Oryza sativa</i>	gi15528806		1.80E-08
572	G2865	<i>Cucumis melo</i>	gi28558779		0.00016
572	G2865	<i>Oryza sativa (japonica cultivar-group)</i>	gi17385671		0.00017
572	G2865	<i>Lycopersicon esculentum</i>	gi6175252		0.091
572	G2865	<i>Cicer arietinum</i>	gi3641870		0.12
572	G2865	<i>Phaseolus vulgaris</i>	gi1142621		0.2
572	G2865	<i>Zea mays</i>	gi4321762		0.27
572	G2865	<i>Prunus dulcis</i>	gi6635842		0.85
572	G2865	<i>Gossypium barbadense</i>	gi1000088		0.95
572	G2865	<i>Brassica napus</i>	gi27650307		0.97
574	G2866	<i>Populus tremula x Populus tremuloides</i>	PTR306827		2.00E-38
574	G2866	<i>Glycine max</i>	BU926504		2.00E-32
574	G2866	<i>Medicago truncatula</i>	BF649039		9.00E-28
574	G2866	<i>Oryza sativa (japonica cultivar-</i>	AK103865		6.00E-25

		group)			
574	G2866	<i>Hordeum vulgare</i>	BG301068		5.00E-20
574	G2866	<i>Triticum aestivum</i>	BJ228821		9.00E-20
574	G2866	<i>Helianthus annuus</i>	BU018212		3.00E-18
574	G2866	<i>Zea mays</i>	BF727992		9.00E-18
574	G2866	<i>Oryza sativa</i>	AU056864		1.00E-17
574	G2866	<i>Cycas rumphii</i>	CB089859		7.00E-17
574	G2866	<i>Populus tremula x</i> <i>Populus tremuloides</i>	gi20269055		8.40E-40
574	G2866	<i>Oryza sativa</i>	gi8096369		4.20E-25
574	G2866	<i>Oryza sativa (indica</i> <i>cultivar-group)</i>	gi30962267		1.40E-19
574	G2866	<i>Cucumis sativus</i>	gi6136832		1.80E-19
574	G2866	<i>Triticum aestivum</i>	gi32400272		2.30E-19
574	G2866	<i>Zinnia elegans</i>	gi20257219		4.70E-19
574	G2866	<i>Vitis vinifera</i>	gi29465672		9.10E-19
574	G2866	<i>Vigna radiata</i>	gi11131105		1.30E-18
574	G2866	<i>Pisum sativum</i>	gi1352057		2.70E-18
574	G2866	<i>Antirrhinum majus</i>	gi18071490		4.50E-18
576	G2869	<i>Oryza sativa</i> <i>(japonica cultivar-</i> <i>group)</i>	AK070026		1.00E-120
576	G2869	<i>Oryza sativa</i>	AB071300		1.00E-104
576	G2869	<i>Mangifera indica</i>	AY255705		7.00E-84
576	G2869	<i>Zea mays</i>	AY107195		1.00E-79
576	G2869	<i>Oryza sativa (indica</i> <i>cultivar-group)</i>	CB631221		3.00E-78
576	G2869	<i>Medicago</i> <i>truncatula</i>	BI308096		2.00E-73
576	G2869	<i>Triticum aestivum</i>	BQ578824		7.00E-70
576	G2869	<i>Pinus pinaster</i>	BX250119		7.00E-65
576	G2869	<i>Poncirus trifoliata</i>	CD575895		1.00E-63
576	G2869	<i>Solanum tuberosum</i>	BG593647		8.00E-63
576	G2869	<i>Oryza sativa</i>	gi19352039		1.90E-124
576	G2869	<i>Oryza sativa</i> <i>(japonica cultivar-</i> <i>group)</i>	gi20805236		1.90E-124
576	G2869	<i>Oryza sativa (indica</i> <i>cultivar-group)</i>	gi26251300		5.50E-120
576	G2869	<i>Mangifera indica</i>	gi30027167		1.90E-116
576	G2869	<i>Prunus persica</i>	gi27450533		2.10E-84
576	G2869	<i>Bruguiera</i> <i>sexangula</i>	gi24371055		1.80E-53
576	G2869	<i>Stevia rebaudiana</i>	gi26324158		1.80E-53
576	G2869	<i>Pisum sativum</i>	gi1235582		2.10E-53
576	G2869	<i>Malus x domestica</i>	gi1732359		2.30E-53
576	G2869	<i>Zea mays</i>	gi7230385		2.30E-53
578	G2884	<i>Oryza sativa</i> <i>(japonica cultivar-</i> <i>group)</i>	AK100530		1.00E-46
578	G2884	<i>Zea mays</i>	AB062095		6.00E-46
578	G2884	<i>Oryza sativa (indica</i> <i>cultivar-group)</i>	CB630542		6.00E-45
578	G2884	<i>Solanum tuberosum</i>	BM407041		4.00E-38
578	G2884	<i>Medicago</i> <i>truncatula</i>	CB891281		1.00E-32

578	G2884	<i>Brassica napus</i>	CD825309		5.00E-32
578	G2884	<i>Vitis vinifera</i>	CD800109		8.00E-32
578	G2884	<i>Sorghum bicolor</i>	CD424269		7.00E-31
578	G2884	<i>Stevia rebaudiana</i>	BG523436		7.00E-30
578	G2884	<i>Lactuca sativa</i>	BQ858556		2.00E-29
578	G2884	<i>Zea mays</i>	gi14189890		2.50E-47
578	G2884	<i>Oryza sativa</i> (japonica cultivar-group)	gi24308616		3.40E-44
578	G2884	<i>Oryza glaberrima</i>	gi31338862		3.90E-35
578	G2884	<i>Oryza sativa</i> (indica cultivar-group)	gi31338860		2.10E-34
578	G2884	<i>Oryza sativa</i>	gi15289981		2.70E-13
578	G2884	<i>Nicotiana tabacum</i>	gi4519671		3.70E-06
578	G2884	<i>Chlamydomonas reinhardtii</i>	gi5916207		1.50E-05
578	G2884	<i>Mesembryanthemum crystallinum</i>	gi6942190		0.00012
578	G2884	<i>Solanum bulbocastanum</i>	gi32470629		0.00013
578	G2884	<i>Dianthus caryophyllus</i>	gi13173408		0.026
579	G2885	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER270810_1	1306	
579	G2885	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-66716	2088	
580	G2885	<i>Oryza sativa</i> (japonica cultivar-group)	AK100530		5.00E-81
580	G2885	<i>Zea mays</i>	AB062095		4.00E-80
580	G2885	<i>Oryza sativa</i> (indica cultivar-group)	CB630542		8.00E-72
580	G2885	<i>Solanum tuberosum</i>	BM407041		3.00E-54
580	G2885	<i>Medicago truncatula</i>	CB891281		1.00E-49
580	G2885	<i>Vitis vinifera</i>	CD800109		7.00E-46
580	G2885	<i>Stevia rebaudiana</i>	BG523436		2.00E-45
580	G2885	<i>Lactuca sativa</i>	BQ858556		2.00E-45
580	G2885	<i>Glycine max</i>	AW596288		2.00E-42
580	G2885	<i>Sorghum bicolor</i>	CD424269		2.00E-42
580	G2885	<i>Zea mays</i>	gi14189890		6.70E-79
580	G2885	<i>Oryza sativa</i> (japonica cultivar-group)	gi24308616		9.40E-72
580	G2885	<i>Oryza sativa</i> (indica cultivar-group)	gi31338860		4.20E-40
580	G2885	<i>Oryza glaberrima</i>	gi31338862		9.30E-40
580	G2885	<i>Oryza sativa</i>	gi15289981		1.80E-18
580	G2885	<i>Nicotiana tabacum</i>	gi4519671		1.60E-09
580	G2885	<i>Solanum bulbocastanum</i>	gi32470629		4.10E-09
580	G2885	<i>Chlamydomonas reinhardtii</i>	gi5916207		4.90E-08
580	G2885	<i>Mesembryanthemum crystallinum</i>	gi6942190		1.20E-07
580	G2885	<i>Brassica napus</i>	gi10041875		0.00086
582	G2887	<i>Brassica napus</i>	CD828428		9.00E-90

582	G2887	<i>Medicago truncatula</i>	AF254124		3.00E-73
582	G2887	<i>Petunia x hybrida</i>	AF509865		2.00E-70
582	G2887	<i>Prunus persica</i>	BU044475		4.00E-70
582	G2887	<i>Oryza sativa</i> (japonica cultivar-group)	AK068153		8.00E-67
582	G2887	<i>Hordeum vulgare</i> subsp. <i>spontaneum</i>	BJ481205		1.00E-63
582	G2887	<i>Oryza sativa</i>	AX654724		2.00E-61
582	G2887	<i>Sorghum propinquum</i>	BG159075		4.00E-61
582	G2887	<i>Brassica oleracea</i>	BH986593		5.00E-61
582	G2887	<i>Solanum tuberosum</i>	BQ118148		6.00E-61
582	G2887	<i>Medicago truncatula</i>	gi7716952		2.20E-71
582	G2887	<i>Petunia x hybrida</i>	gi21105732		3.30E-70
582	G2887	<i>Oryza sativa</i> (japonica cultivar-group)	gi27452910		6.50E-49
582	G2887	<i>Oryza sativa</i>	gi6730946		3.90E-42
582	G2887	<i>Glycine max</i>	gi22597158		1.80E-39
582	G2887	<i>Phaseolus vulgaris</i>	gi15148914		7.80E-37
582	G2887	<i>Brassica napus</i>	gi31322572		7.00E-36
582	G2887	<i>Triticum sp.</i>	gi4218537		1.90E-35
582	G2887	<i>Triticum monococcum</i>	gi6732160		1.90E-35
582	G2887	<i>Solanum tuberosum</i>	gi14485513		2.40E-35
584	G2888	<i>Oryza sativa</i> (japonica cultivar-group)	AK106796		8.00E-76
584	G2888	<i>Brassica oleracea</i>	BH707475		1.00E-72
584	G2888	<i>Zea mays</i>	BZ821684		3.00E-69
584	G2888	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01002232		8.00E-69
584	G2888	<i>Physcomitrella patens</i> subsp. <i>patens</i>	BJ192201		1.00E-67
584	G2888	<i>Glycine max</i>	BI972592		4.00E-67
584	G2888	<i>Medicago truncatula</i>	BI265111		1.00E-64
584	G2888	<i>Triticum aestivum</i>	BQ806659		3.00E-56
584	G2888	<i>Capsicum annuum</i>	BM063853		6.00E-56
584	G2888	<i>Phaseolus coccineus</i>	CA902521		6.00E-56
584	G2888	<i>Oryza sativa</i> (japonica cultivar-group)	gi27357980		2.90E-77
584	G2888	<i>Solanum tuberosum</i>	gi563623		7.60E-55
584	G2888	<i>Zea mays</i>	gi3170601		3.20E-53
584	G2888	<i>Lycopersicon esculentum</i>	gi9858780		1.50E-51
584	G2888	<i>Oryza sativa</i>	gi10934090		1.00E-50
584	G2888	<i>Glycine max</i>	gi18376601		3.30E-11
584	G2888	<i>Cucurbita maxima</i>	gi17221648		0.032
584	G2888	<i>Chlorella vulgaris</i>	gi2224373		0.11
584	G2888	<i>Helianthus annuus</i>	gi349267		0.16

584	G2888	<i>Petunia x hybrida</i>	gi14275902		0.17
586	G2898	<i>Medicago truncatula</i>	AJ501279		2.00E-41
586	G2898	<i>Glycine max</i>	BG651880		2.00E-41
586	G2898	<i>Solanum tuberosum</i>	BQ516260		3.00E-35
586	G2898	<i>Populus tremula</i>	BU816897		8.00E-32
586	G2898	<i>Zinnia elegans</i>	AU292820		4.00E-30
586	G2898	<i>Oryza sativa</i> (japonica cultivar-group)	AK064663		7.00E-30
586	G2898	<i>Zea mays</i>	CD999897		5.00E-29
586	G2898	<i>Triticum aestivum</i>	BM135160		2.00E-28
586	G2898	<i>Gossypium arboreum</i>	BG446904		6.00E-21
586	G2898	<i>Nuphar advena</i>	CD475578		1.00E-19
586	G2898	<i>Vicia faba</i>	gi541981		1.60E-20
586	G2898	<i>Oryza sativa</i> (japonica cultivar-group)	gi20161572		3.90E-19
586	G2898	<i>Ipomoea nil</i>	gi1052956		6.30E-19
586	G2898	<i>Solanum tuberosum</i>	gi2894109		1.00E-18
586	G2898	<i>Pisum sativum</i>	gi436424		1.00E-18
586	G2898	<i>Nicotiana tabacum</i>	gi2196548		2.80E-16
586	G2898	<i>Glycine max</i>	gi123379		5.90E-16
586	G2898	<i>Canavalia gladiata</i>	gi1813329		7.50E-16
586	G2898	<i>Narcissus pseudonarcissus</i>	gi18419623		2.50E-15
586	G2898	<i>Oryza sativa</i> (indica cultivar-group)	gi23345287		2.50E-15
587	G2907	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER30744_2	1307	
587	G2907	<i>Oryza sativa</i>	OSC100568.C1.p1.fg	1308	
587	G2907	<i>Oryza sativa</i>	OSC9760.C1.p1.fg	1309	
587	G2907	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER298_131	1310	
587	G2907	<i>Zea mays</i>	ZEAMA-08NOV01-CLUSTER298_90	1311	
587	G2907	<i>Oryza sativa</i>	Os_S108142	1620	
587	G2907	<i>Oryza sativa</i>	Os_S31898	1621	
587	G2907	<i>Oryza sativa</i>	Os_S33014	1622	
587	G2907	<i>Glycine max</i>	Gma_S5116414	1679	
587	G2907	<i>Hordeum vulgare</i>	Hv_S52718	1752	
587	G2907	<i>Zea mays</i>	Zm_S11441767	1825	
587	G2907	<i>Zea mays</i>	Zm_S11491750	1826	
587	G2907	<i>Lycopersicon esculentum</i>	Les_S5295643	1934	
587	G2907	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-SINGLET-472560	2089	
588	G2907	<i>Oryza sativa</i> (japonica cultivar-group)	AK105116		1.0e-999
588	G2907	<i>Brassica napus</i>	AF491304		1.0e-999
588	G2907	<i>Nicotiana tabacum</i>	AF253511		1.0e-999
588	G2907	<i>Lycopersicon esculentum</i>	AF096260		1.00E-174
588	G2907	<i>Oryza sativa</i> (indica)	AAAA01006749		1.00E-121

		cultivar-group)			
588	G2907	<i>Brassica oleracea</i>	BZ507433		1.00E-113
588	G2907	<i>Oryza sativa</i>	AC079935		1.00E-106
588	G2907	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BM817419		3.00E-70
588	G2907	<i>Zea mays</i>	BZ998506		4.00E-68
588	G2907	<i>Capsicum annuum</i>	BM063122		5.00E-63
588	G2907	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi19920098		2.20E-229
588	G2907	<i>Brassica napus</i>	gi20127124		3.60E-208
588	G2907	<i>Nicotiana tabacum</i>	gi11612392		2.20E-198
588	G2907	<i>Lycopersicon</i> <i>esculentum</i>	gi5669650		4.70E-117
588	G2907	<i>Petroselinum</i> <i>crispum</i>	gi1084392		6.00E-43
588	G2907	<i>Triticum aestivum</i>	gi32400790		4.00E-07
588	G2907	<i>Pennisetum ciliare</i>	gi549986		9.00E-06
588	G2907	<i>Glycine max</i>	gi17645766		8.40E-05
588	G2907	<i>Oryza sativa</i>	gi19070767		0.00016
588	G2907	<i>Chlamydomonas</i> <i>reinhardtii</i>	gi28207761		0.0013
589	G2913	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER38751 1	1312	
589	G2913	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER93389 1	1313	
589	G2913	<i>Oryza sativa</i>	Os S107744	1623	
590	G2913	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK065847		2.00E-57
590	G2913	<i>Glycine max</i>	CD487091		1.00E-52
590	G2913	<i>Solanum tuberosum</i>	BM404700		4.00E-45
590	G2913	<i>Medicago</i> <i>truncatula</i>	BF004903		9.00E-45
590	G2913	<i>Citrus sinensis</i>	BQ623105		1.00E-34
590	G2913	<i>Lycopersicon</i> <i>esculentum</i>	BF051118		1.00E-34
590	G2913	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	CB634137		1.00E-33
590	G2913	<i>Brassica oleracea</i>	BZ021766		4.00E-33
590	G2913	<i>Amborella</i> <i>trichopoda</i>	CD483238		3.00E-31
590	G2913	<i>Populus tremula</i>	BU889297		1.00E-30
590	G2913	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi32490476		2.40E-74
590	G2913	<i>Vicia faba</i>	gi541981		1.30E-08
590	G2913	<i>Solanum tuberosum</i>	gi2894109		1.70E-07
590	G2913	<i>Nicotiana tabacum</i>	gi2196548		7.20E-06
590	G2913	<i>Zea mays</i>	gi8920409		4.70E-05
590	G2913	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	gi21314337		7.90E-05
590	G2913	<i>Daucus carota</i>	gi3551257		0.0002
590	G2913	<i>Canavalia gladiata</i>	gi1813329		0.0011
590	G2913	<i>Narcissus</i> <i>pseudonarcissus</i>	gi18419623		0.0018
590	G2913	<i>Ipomoea nil</i>	gi1085860		0.049

591	G2930	<i>Zea mays</i>	Zm_S11448159	1827	
591	G2930	<i>Lycopersicon esculentum</i>	Les_S5268274	1935	
592	G2930	<i>Triticum aestivum</i>	CD872621		1.00E-12
592	G2930	<i>Lycopersicon esculentum</i>	BI203387		4.00E-09
592	G2930	<i>Populus tremula x Populus tremuloides</i>	BU884102		8.00E-09
592	G2930	<i>Sorghum bicolor</i>	CD428713		2.00E-08
592	G2930	<i>Oryza sativa (indica cultivar-group)</i>	CB624355		7.00E-08
592	G2930	<i>Zinnia elegans</i>	AU288915		1.00E-07
592	G2930	<i>Oryza sativa (japonica cultivar- group)</i>	CB660906		2.00E-07
592	G2930	<i>Oryza sativa</i>	AP003683		6.00E-05
592	G2930	<i>Glycine max</i>	BQ611037		6.00E-05
592	G2930	<i>Medicago truncatula</i>	BG456206		2.00E-04
592	G2930	<i>Oryza sativa</i>	gi15528806		1.40E-09
592	G2930	<i>Oryza sativa (japonica cultivar- group)</i>	gi29788848		0.016
592	G2930	<i>Pennisetum glaucum</i>	gi527655		0.56
592	G2930	<i>Phyllostachys acuta</i>	gi527661		0.61
592	G2930	<i>Zea mays</i>	gi100921		0.7
592	G2930	<i>Sorghum bicolor</i>	gi527667		0.8
592	G2930	<i>Tripsacum australe</i>	gi527663		0.89
592	G2930	<i>Glycine max</i>	gi3399777		0.9
592	G2930	<i>Phaseolus vulgaris</i>	gi1142619		0.97
592	G2930	<i>Catharanthus roseus</i>	gi3954807		1
593	G2933	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER243321_1	1314	
593	G2933	<i>Oryza sativa</i>	OSC7496.C1.p10.fg	1315	
593	G2933	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER88899_1	1316	
593	G2933	<i>Oryza sativa</i>	Os_S39118	1624	
593	G2933	<i>Zea mays</i>	Zm_S11445525	1828	
593	G2933	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-53603	2090	
594	G2933	<i>Brassica oleracea</i>	BH587081		6.00E-59
594	G2933	<i>Populus tremula x Populus tremuloides</i>	BU884102		8.00E-37
594	G2933	<i>Lycopersicon esculentum</i>	BI205905		6.00E-29
594	G2933	<i>Glycine max</i>	BQ611037		4.00E-28
594	G2933	<i>Triticum aestivum</i>	CD872523		4.00E-24
594	G2933	<i>Lupinus albus</i>	CA410291		4.00E-23
594	G2933	<i>Oryza sativa (japonica cultivar- group)</i>	CB660906		5.00E-23
594	G2933	<i>Oryza sativa (indica cultivar-group)</i>	CB624355		1.00E-22
594	G2933	<i>Medicago truncatula</i>	AC125478		6.00E-21

594	G2933	<i>Zinnia elegans</i>	AU288915		9.00E-20
594	G2933	<i>Oryza sativa</i>	gi15528806		3.90E-26
594	G2933	<i>Pennisetum glaucum</i>	gi527657		8.60E-07
594	G2933	<i>Phyllostachys acuta</i>	gi527661		4.10E-05
594	G2933	<i>Sorghum bicolor</i>	gi527667		5.60E-05
594	G2933	<i>Tripsacum australe</i>	gi527663		0.00024
594	G2933	<i>Mesembryanthemum crystallinum</i>	gi4206118		0.00048
594	G2933	<i>Oryza sativa</i> (japonica cultivar-group)	gi20521292		0.0012
594	G2933	<i>Zea mays</i>	gi18542170		0.0014
594	G2933	<i>Oryza australiensis</i>	gi1086526		0.0031
594	G2933	<i>Oryza rufipogon</i>	gi1086538		0.0055
596	G2934	<i>Brassica oleracea</i>	BH680810		3.00E-50
596	G2934	<i>Glycine max</i>	BE057473		1.00E-28
596	G2934	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BZ614080		9.00E-24
596	G2934	<i>Medicago truncatula</i>	AL389569		4.00E-14
596	G2934	<i>Lotus corniculatus</i> var. <i>japonicus</i>	CB829442		5.00E-14
596	G2934	<i>Hedyotis centranthoides</i>	CB086514		2.00E-13
596	G2934	<i>Lycopersicon esculentum</i>	AW624871		7.00E-13
596	G2934	<i>Triphysaria versicolor</i>	BM356795		6.00E-12
596	G2934	<i>Beta vulgaris</i>	BQ592169		2.00E-10
596	G2934	<i>Triticum aestivum</i>	CD452898		2.00E-08
596	G2934	<i>Oryza sativa</i>	gi15528806		8.90E-13
596	G2934	<i>Oryza sativa</i> (japonica cultivar-group)	gi17385671		1.00E-05
596	G2934	<i>Brassica napus</i>	gi27650307		0.0022
596	G2934	<i>Phaseolus vulgaris</i>	gi1142619		0.0024
596	G2934	<i>Cucumis melo</i>	gi28558779		0.0029
596	G2934	<i>Zea mays</i>	gi100874		0.014
596	G2934	<i>Cicer arietinum</i>	gi3641870		0.18
596	G2934	<i>Brassica oleracea</i>	gi12049596		0.26
596	G2934	<i>Pennisetum glaucum</i>	gi527655		0.33
596	G2934	<i>Phyllostachys acuta</i>	gi527661		0.37
598	G2958	<i>Gossypium hirsutum</i>	GHI458442		3.00E-39
598	G2958	<i>Prunus persica</i>	BU041850		1.00E-34
598	G2958	<i>Capsicum annuum</i>	BM063701		3.00E-34
598	G2958	<i>Solanum tuberosum</i>	BG890076		4.00E-34
598	G2958	<i>Vitis vinifera</i>	CB921417		1.00E-33
598	G2958	<i>Poncirus trifoliata</i>	CD576407		1.00E-33
598	G2958	<i>Brassica oleracea</i>	BH695204		2.00E-32
598	G2958	<i>Lactuca sativa</i>	BQ991083		2.00E-32
598	G2958	<i>Medicago truncatula</i>	BF647616		4.00E-29
598	G2958	<i>Cucumis sativus</i>	AB029148		9.00E-29

598	G2958	<i>Gossypium hirsutum</i>	gi22531416		5.20E-40
598	G2958	<i>Oryza sativa</i> (indica cultivar-group)	gi30962267		1.50E-35
598	G2958	<i>Oryza sativa</i>	gi17154533		7.70E-35
598	G2958	<i>Populus tremula</i> x <i>Populus tremuloides</i>	gi20269059		8.40E-34
598	G2958	<i>Pinus taeda</i>	gi32396301		2.50E-32
598	G2958	<i>Triticum aestivum</i>	gi32400272		3.90E-32
598	G2958	<i>Cucumis sativus</i>	gi6136834		4.10E-32
598	G2958	<i>Vigna radiata</i>	gi11131101		1.10E-30
598	G2958	<i>Nicotiana tabacum</i>	gi4887012		6.00E-30
598	G2958	<i>Solanum tuberosum</i>	gi25989504		1.20E-29
600	G2964	<i>Brassica oleracea</i>	BH549078		2.00E-76
600	G2964	<i>Brassica napus</i>	CD822240		4.00E-67
600	G2964	<i>Zea mays</i>	AY104443		4.00E-60
600	G2964	<i>Solanum tuberosum</i>	BQ505464		6.00E-54
600	G2964	<i>Lotus corniculatus</i> var. <i>japonicus</i>	AP006377		2.00E-50
600	G2964	<i>Hordeum vulgare</i>	BI957620		2.00E-49
600	G2964	<i>Gossypium arboreum</i>	BE053739		2.00E-49
600	G2964	<i>Glycine max</i>	AW348431		3.00E-48
600	G2964	<i>Oryza sativa</i> (indica cultivar-group)	CB635890		1.00E-47
600	G2964	<i>Oryza sativa</i> (japonica cultivar-group)	CB660704		1.00E-47
600	G2964	<i>Oryza sativa</i>	gi5441893		3.20E-47
600	G2964	<i>Oryza sativa</i> (japonica cultivar-group)	gi32488659		8.60E-47
600	G2964	<i>Pisum sativum</i>	gi14018368		5.30E-09
600	G2964	<i>Pinus pinaster</i>	gi18129298		9.80E-07
600	G2964	<i>Brassica napus</i>	gi1171040		0.012
600	G2964	<i>Brassica oleracea</i>	gi18266051		0.012
600	G2964	<i>Zea mays</i>	gi459269		0.28
600	G2964	<i>Minulus guttatus</i>	gi127382		0.79
600	G2964	<i>Glycine max</i>	gi532703		0.81
600	G2964	<i>Hordeum vulgare</i>	gi4456620		0.92
602	G2967	<i>Brassica oleracea</i>	BZ064831		2.00E-51
602	G2967	<i>Petunia x hybrida</i>	AB006606		8.00E-06
602	G2967	<i>Medicago truncatula</i>	BG582425		1.00E-05
602	G2967	<i>Brassica napus</i>	CB686322		2.00E-04
602	G2967	<i>Vitis vinifera</i>	CB008696		0.004
602	G2967	<i>Vitis aestivalis</i>	CB074763		0.004
602	G2967	<i>Glycine max</i>	BF324612		0.005
602	G2967	<i>Oryza sativa</i> (japonica cultivar-group)	AY219847		0.006
602	G2967	<i>Lactuca sativa</i>	BQ868010		0.006
602	G2967	<i>Oryza sativa</i>	CNS08CA5		0.006
602	G2967	<i>Petunia x hybrida</i>	gi2346988		4.40E-10
602	G2967	<i>Medicago sativa</i>	gi7228329		0.00039
602	G2967	<i>Pisum sativum</i>	gi2129892		0.00076

602	G2967	<i>Oryza sativa</i> (japonica cultivar-group)	gi28849865		0.001
602	G2967	<i>Brassica rapa</i>	gi2058504		0.0015
602	G2967	<i>Triticum aestivum</i>	gi485814		0.0052
602	G2967	<i>Oryza sativa</i>	gi12698882		0.0094
602	G2967	<i>Datisca glomerata</i>	gi4666360		0.01
602	G2967	<i>Glycine max</i>	gi1763063		0.014
602	G2967	<i>Nicotiana tabacum</i>	gi2981169		0.018
603	G2969	<i>Oryza sativa</i>	OSC100047.C1.p3.fg	1317	
603	G2969	<i>Oryza sativa</i>	Os_S108460	1625	
603	G2969	<i>Glycine max</i>	Gma_S4895054	1680	
603	G2969	<i>Glycine max</i>	Gma_S4932729	1681	
603	G2969	<i>Glycine max</i>	Gma_S4971594	1682	
603	G2969	<i>Lycopersicon esculentum</i>	Les_S5265247	1936	
603	G2969	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-57728	2091	
604	G2969	<i>Brassica oleracea</i>	BH481194		1.00E-107
604	G2969	<i>Medicago truncatula</i>	BI311225		9.00E-76
604	G2969	<i>Lactuca sativa</i>	BQ874458		1.00E-70
604	G2969	<i>Prunus persica</i>	BU040439		3.00E-69
604	G2969	<i>Helianthus annuus</i>	BQ967662		2.00E-65
604	G2969	<i>Populus tremuloides</i>	CA932621		7.00E-65
604	G2969	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01007031		1.00E-62
604	G2969	<i>Oryza sativa</i> (japonica cultivar-group)	AC135205		1.00E-62
604	G2969	<i>Solanum tuberosum</i>	BQ115018		7.00E-62
604	G2969	<i>Glycine max</i>	BE822664		1.00E-61
604	G2969	<i>Oryza sativa</i> (japonica cultivar-group)	gi29893575		2.90E-62
604	G2969	<i>Oryza sativa</i>	gi5777616		3.70E-46
604	G2969	<i>Glycine max</i>	gi28542706		0.083
604	G2969	<i>Chlorella vulgaris</i>	gi2224427		0.13
604	G2969	<i>Chloroplast Chlorella vulgaris</i>	gi7515285		0.13
604	G2969	<i>Petunia x hybrida</i>	gi100396		0.88
604	G2969	<i>Nicotiana tabacum</i>	gi8099397		0.94
604	G2969	<i>Pisum sativum</i>	gi3088648		1
606	G2972	<i>Brassica oleracea</i>	BZ070725		1.00E-13
606	G2972	<i>Oryza sativa</i>	OSJN00040		2.00E-04
606	G2972	<i>Oryza sativa</i> (japonica cultivar-group)	AK108645		2.00E-04
606	G2972	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01000197		6.00E-04
606	G2972	<i>Brassica napus</i>	CD844215		0.002
606	G2972	<i>Petunia x hybrida</i>	AB000454		0.005
606	G2972	<i>Populus tremula x Populus tremuloides</i>	BU813541		0.008
606	G2972	<i>Citrus sinensis</i>	CB293113		0.025
606	G2972	<i>Lotus japonicus</i>	AP004523		0.025

606	G2972	<i>Lotus corniculatus</i> var. <i>japonicus</i>	CB828590		0.025
606	G2972	<i>Glycine max</i>	gi1763063		6.00E-08
606	G2972	<i>Oryza sativa</i>	gi12698882		2.50E-06
606	G2972	<i>Petunia x hybrida</i>	gi439487		4.70E-06
606	G2972	<i>Nicotiana tabacum</i>	gi2981169		4.90E-06
606	G2972	<i>Datisca glomerata</i>	gi4666360		1.20E-05
606	G2972	<i>Medicago sativa</i>	gi7228329		1.30E-05
606	G2972	<i>Triticum aestivum</i>	gi485814		3.50E-05
606	G2972	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi29124140		9.50E-05
606	G2972	<i>Brassica rapa</i>	gi2058506		0.00024
606	G2972	<i>Pisum sativum</i>	gi2129892		0.027
607	G2979	<i>Lycopersicon</i> <i>esculentum</i>	SGN-UNIGENE-49425	2092	
608	G2979	<i>Zea mays</i>	AY107996		2.00E-68
608	G2979	<i>Thellungiella</i> <i>salsuginea</i>	BI698460		1.00E-60
608	G2979	<i>Vitis vinifera</i>	CB920900		4.00E-45
608	G2979	<i>Helianthus annuus</i>	CD853183		2.00E-41
608	G2979	<i>Medicago</i> <i>truncatula</i>	BG450549		3.00E-39
608	G2979	<i>Glycine max</i>	BM524804		8.00E-38
608	G2979	<i>Lycopersicon</i> <i>esculentum</i>	BI924306		8.00E-37
608	G2979	<i>Solanum tuberosum</i>	BE920312		7.00E-32
608	G2979	<i>Eschscholzia</i> <i>californica</i>	CD478692		9.00E-32
608	G2979	<i>Sorghum bicolor</i>	BG273641		5.00E-28
608	G2979	<i>Nicotiana tabacum</i>	gi6328415		4.40E-10
608	G2979	<i>Physcomitrella</i> <i>patens</i>	gi26190147		1.00E-09
608	G2979	<i>Triticum</i> <i>monococcum</i>	gi13619655		3.90E-09
608	G2979	<i>Triticum sp.</i>	gi5763821		3.90E-09
608	G2979	<i>Daucus carota</i>	gi8977833		5.80E-09
608	G2979	<i>Oryza sativa</i>	gi12225043		9.90E-09
608	G2979	<i>Chenopodium</i> <i>rubrum</i>	gi11558192		3.00E-08
608	G2979	<i>Populus alba</i>	gi27802536		3.10E-08
608	G2979	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi32479738		1.10E-07
608	G2979	<i>Thlaspi</i> <i>caerulescens</i>	gi22086272		2.90E-07
609	G2981	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER28852_1	1318	
609	G2981	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER28852_2	1319	
609	G2981	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER28852_4	1320	
609	G2981	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER28852_5	1321	
609	G2981	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER28852_6	1322	
609	G2981	<i>Glycine max</i>	GLYMA-28NOV01-	1323	

			CLUSTER28852_8		
609	G2981	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER28852_9	1324	
609	G2981	<i>Glycine max</i>	LIB3242-344-Q1-J1-G7	1325	
609	G2981	<i>Glycine max</i>	LIB4392-029-R1-K1-C8	1326	
609	G2981	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER89637_1	1327	
609	G2981	<i>Oryza sativa</i>	Os_S104685	1626	
609	G2981	<i>Glycine max</i>	Gma_S4882455	1683	
609	G2981	<i>Zea mays</i>	Zm_S11334447	1829	
609	G2981	<i>Zea mays</i>	Zm_S11524241	1830	
609	G2981	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-50978	2093	
610	G2981	<i>Populus tremula x Populus tremuloides</i>	AY307373		1.00E-123
610	G2981	<i>Oryza sativa (japonica cultivar- group)</i>	AY224589		1.00E-106
610	G2981	<i>Zea mays</i>	AY108383		1.00E-105
610	G2981	<i>Poncirus trifoliata</i>	CD573622		1.00E-96
610	G2981	<i>Glycine max</i>	BU579005		8.00E-85
610	G2981	<i>Solanum tuberosum</i>	BM406319		6.00E-79
610	G2981	<i>Lycopersicon esculentum</i>	BG134590		2.00E-76
610	G2981	<i>Pinus taeda</i>	BG040894		4.00E-74
610	G2981	<i>Marchantia polymorpha</i>	C96290		2.00E-71
610	G2981	<i>Lactuca sativa</i>	BU012590		4.00E-66
610	G2981	<i>Populus tremula x Populus tremuloides</i>	gi32187097		8.20E-119
610	G2981	<i>Oryza sativa (japonica cultivar- group)</i>	gi29371983		2.80E-101
610	G2981	<i>Triticum sp.</i>	gi11877791		4.10E-47
610	G2981	<i>Triticum monococcum</i>	gi13619653		4.10E-47
610	G2981	<i>Populus alba</i>	gi27802536		0.0064
610	G2981	<i>Gnetum gnemon</i>	gi5019435		0.037
610	G2981	<i>Nicotiana tabacum</i>	gi6328415		0.069
610	G2981	<i>Oryza sativa</i>	gi12225043		0.071
610	G2981	<i>Physcomitrella patens</i>	gi26190147		0.099
610	G2981	<i>Chenopodium rubrum</i>	gi11558192		0.15
611	G2982	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER28852_1	1318	
611	G2982	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER28852_2	1319	
611	G2982	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER28852_4	1320	
611	G2982	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER28852_5	1321	
611	G2982	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER28852_6	1322	
611	G2982	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER28852_8	1323	
611	G2982	<i>Glycine max</i>	LIB3242-344-Q1-J1-G7	1325	

611	G2982	<i>Glycine max</i>	LIB4392-029-R1-K1-C8	1326	
611	G2982	<i>Oryza sativa</i>	ORYSA-22JAN02-CLUSTER89637 1	1327	
611	G2982	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-50978	2093	
612	G2982	<i>Brassica napus</i>	CD813391		1.00E-79
612	G2982	<i>Populus tremula x Populus tremuloides</i>	AY307373		2.00E-59
612	G2982	<i>Zea mays</i>	AY108383		6.00E-57
612	G2982	<i>Oryza sativa (japonica cultivar-group)</i>	AY224551		2.00E-54
612	G2982	<i>Glycine max</i>	BU579005		8.00E-52
612	G2982	<i>Pinus taeda</i>	BG040894		3.00E-50
612	G2982	<i>Solanum tuberosum</i>	BM406319		2.00E-47
612	G2982	<i>Marchantia polymorpha</i>	C96290		3.00E-47
612	G2982	<i>Lycopersicon esculentum</i>	BM412584		1.00E-42
612	G2982	<i>Triticum sp.</i>	TSP271917		9.00E-40
612	G2982	<i>Populus tremula x Populus tremuloides</i>	gi32187097		1.20E-58
612	G2982	<i>Oryza sativa (japonica cultivar-group)</i>	gi29367654		6.80E-54
612	G2982	<i>Triticum sp.</i>	gi11877791		2.00E-40
612	G2982	<i>Triticum monococcum</i>	gi13619653		2.00E-40
612	G2982	<i>Daucus carota</i>	gi8977833		0.0044
612	G2982	<i>Nicotiana tabacum</i>	gi6328415		0.057
612	G2982	<i>Physcomitrella patens</i>	gi26190147		0.17
612	G2982	<i>Thlaspi caerulescens</i>	gi22086272		0.21
612	G2982	<i>Oryza sativa</i>	gi12225043		0.24
612	G2982	<i>Chenopodium rubrum</i>	gi11558192		0.25
613	G2983	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER73435 1	1328	
613	G2983	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER73435 2	1329	
613	G2983	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER73435 3	1330	
613	G2983	<i>Oryza sativa</i>	OSC101922.C1.p4.fg	1331	
613	G2983	<i>Oryza sativa</i>	OSC102287.C1.p18.fg	1332	
613	G2983	<i>Oryza sativa</i>	OSC32392.C1.p1.fg	1333	
613	G2983	<i>Oryza sativa</i>	Os_S83060	1627	
613	G2983	<i>Glycine max</i>	Gma_S4865673	1684	
613	G2983	<i>Medicago truncatula</i>	Mtr_S5361396	1714	
613	G2983	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-49230	2094	
614	G2983	<i>Glycine max</i>	AX105305		3.00E-57
614	G2983	<i>Medicago truncatula</i>	BG588588		2.00E-55
614	G2983	<i>Populus tremula x Populus tremuloides</i>	BU828082		8.00E-51

614	G2983	<i>Brassica oleracea</i>	BH250068		9.00E-50
614	G2983	<i>Lycopersicon esculentum</i>	BG134747		2.00E-48
614	G2983	<i>Beta vulgaris</i>	BQ593610		3.00E-47
614	G2983	<i>Lupinus albus</i>	CA410814		3.00E-44
614	G2983	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i> x <i>Populus deltoides</i>	CA826202		9.00E-36
614	G2983	<i>Zea mays</i>	CC347703		1.00E-27
614	G2983	<i>Oryza sativa</i>	OSJN00105		3.00E-27
614	G2983	<i>Oryza sativa</i>	gi10241438		8.10E-35
614	G2983	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi21740884		4.10E-31
614	G2983	<i>Petunia x hybrida</i>	gi22087128		3.60E-22
614	G2983	<i>Lycopersicon esculentum</i>	gi28070968		5.80E-22
614	G2983	<i>Populus tremula</i> x <i>Populus tremuloides</i>	gi3955021		4.50E-10
614	G2983	<i>Narcissus pseudonarcissus</i>	gi18419580		3.90E-05
614	G2983	<i>Ceratopteris richardii</i>	gi3868829		0.025
614	G2983	<i>Physcomitrella patens</i>	gi7415618		0.079
614	G2983	<i>Helianthus annuus</i>	gi349379		0.15
614	G2983	<i>Zinnia elegans</i>	gi24417147		0.3
615	G2990	<i>Oryza sativa</i>	OSC4898.C1.p6.fg	1334	
615	G2990	<i>Zea mays</i>	LIB3279-221-Q6-K6-B2	1335	
615	G2990	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER42733_1	1336	
615	G2990	<i>Oryza sativa</i>	Os_S56831	1628	
615	G2990	<i>Glycine max</i>	Gma_S4897246	1685	
615	G2990	<i>Medicago truncatula</i>	Mtr_S5341529	1715	
615	G2990	<i>Triticum aestivum</i>	Ta_S171947	1921	
615	G2990	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-49426	2095	
615	G2990	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-52525	2096	
616	G2990	<i>Brassica oleracea</i>	BH738007		1.00E-100
616	G2990	<i>Medicago truncatula</i>	AC139600		3.00E-84
616	G2990	<i>Flaveria bidentis</i>	FBI18580		8.00E-81
616	G2990	<i>Glycine max</i>	BF069575		4.00E-59
616	G2990	<i>Solanum tuberosum</i>	BE471989		7.00E-56
616	G2990	<i>Flaveria trinervia</i>	FTR18577		3.00E-51
616	G2990	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	AI166342		5.00E-45
616	G2990	<i>Vitis vinifera</i>	CB970621		7.00E-45
616	G2990	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AP005152		2.00E-43
616	G2990	<i>Zea mays</i>	CC335993		3.00E-42
616	G2990	<i>Flaveria bidentis</i>	gi13277220		1.10E-76

616	G2990	<i>Oryza sativa</i> (japonica cultivar-group)	gi32480091		2.10E-38
616	G2990	<i>Flaveria trinervia</i>	gi13277216		1.60E-29
616	G2990	<i>Oryza sativa</i>	gi5091602		3.00E-28
616	G2990	<i>Lactuca sativa</i>	gi29119890		9.00E-20
616	G2990	<i>Bromheadia finlaysoniana</i>	gi2108256		4.30E-06
616	G2990	<i>Lycopersicon esculentum</i>	gi100214		1.20E-05
616	G2990	<i>Daucus carota</i>	gi224556		1.70E-05
616	G2990	<i>Nicotiana glauca</i>	gi1247388		1.90E-05
616	G2990	<i>Gossypium barbadense</i>	gi451544		3.80E-05
617	G2992	<i>Oryza sativa</i>	Os_S94181	1629	
617	G2992	<i>Zea mays</i>	Zm_S11399262	1831	
618	G2992	<i>Brassica oleracea</i>	BZ087784		3.00E-94
618	G2992	<i>Brassica napus</i>	CD817420		4.00E-65
618	G2992	<i>Medicago truncatula</i>	AC139600		6.00E-51
618	G2992	<i>Flaveria bidentis</i>	FBI18580		6.00E-48
618	G2992	<i>Glycine max</i>	BF069575		1.00E-47
618	G2992	<i>Oryza sativa</i> (japonica cultivar-group)	AP005152		9.00E-44
618	G2992	<i>Vitis vinifera</i>	CB970621		3.00E-43
618	G2992	<i>Flaveria trinervia</i>	FTR18577		2.00E-42
618	G2992	<i>Zea mays</i>	CC335993		4.00E-42
618	G2992	<i>Helianthus annuus</i>	BU022145		8.00E-42
618	G2992	<i>Flaveria bidentis</i>	gi13277220		9.50E-52
618	G2992	<i>Flaveria trinervia</i>	gi13277216		4.40E-43
618	G2992	<i>Oryza sativa</i>	gi5091602		4.40E-40
618	G2992	<i>Oryza sativa</i> (japonica cultivar-group)	gi32480091		4.90E-28
618	G2992	<i>Lactuca sativa</i>	gi29119890		3.50E-18
618	G2992	<i>Sorghum bicolor</i>	gi671656		0.12
618	G2992	<i>Pisum sativum</i>	gi15021756		0.15
618	G2992	<i>Lycopersicon esculentum</i>	gi1345538		0.24
618	G2992	<i>Nicotiana tabacum</i>	gi119714		0.67
618	G2992	<i>Pinus taeda</i>	gi1076237		0.67
620	G2993	<i>Glycine max</i>	CA783548		8.00E-56
620	G2993	<i>Oryza sativa</i> (japonica cultivar-group)	CNS08CD7		2.00E-51
620	G2993	<i>Brassica oleracea</i>	BH972041		1.00E-49
620	G2993	<i>Medicago truncatula</i>	AC139600		4.00E-46
620	G2993	<i>Lotus corniculatus</i> var. japonicus	AP006401		2.00E-45
620	G2993	<i>Flaveria bidentis</i>	FBI18579		4.00E-45
620	G2993	<i>Vitis aestivalis</i>	CB289369		5.00E-44
620	G2993	<i>Lotus japonicus</i>	AP004968		5.00E-44
620	G2993	<i>Zea mays</i>	CC613855		1.00E-43
620	G2993	<i>Oryza sativa (indica)</i>	AAAA01010656		1.00E-42

		cultivar-group)			
620	G2993	<i>Flaveria bidentis</i>	gi13374061		5.60E-43
620	G2993	<i>Oryza sativa</i>	gi5091602		1.20E-40
620	G2993	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi32480091		5.00E-35
620	G2993	<i>Flaveria trinervia</i>	gi13277216		2.50E-32
620	G2993	<i>Lactuca sativa</i>	gi29119890		3.00E-19
620	G2993	<i>Zea mays</i>	gi6016218		0.17
620	G2993	<i>Malus domestica</i>	gi1946218		0.28
620	G2993	<i>Pisum sativum</i>	gi23504755		0.68
620	G2993	<i>Lycopersicon esculentum</i>	gi1418988		0.77
620	G2993	<i>Zea mays</i> subsp. <i>mays</i>	gi21953540		0.82
622	G2996	<i>Brassica napus</i>	CD826370		7.00E-88
622	G2996	<i>Flaveria bidentis</i>	FBI18579		3.00E-57
622	G2996	<i>Brassica oleracea</i>	BZ009581		1.00E-55
622	G2996	<i>Lotus japonicus</i>	AP004968		1.00E-51
622	G2996	<i>Zea mays</i>	CC673594		5.00E-51
622	G2996	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK109528		2.00E-49
622	G2996	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01010656		2.00E-49
622	G2996	<i>Glycine max</i>	AW508242		4.00E-46
622	G2996	<i>Oryza sativa</i>	OSJN00063		7.00E-43
622	G2996	<i>Medicago truncatula</i>	AC139600		1.00E-41
622	G2996	<i>Flaveria bidentis</i>	gi13374061		1.40E-55
622	G2996	<i>Oryza sativa</i>	gi5091602		4.40E-43
622	G2996	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi32480091		1.00E-41
622	G2996	<i>Flaveria trinervia</i>	gi13277216		9.70E-39
622	G2996	<i>Lactuca sativa</i>	gi29119890		8.30E-17
622	G2996	<i>Glycine max</i>	gi347455		9.40E-13
622	G2996	<i>Phaseolus vulgaris</i>	gi81870		5.70E-12
622	G2996	<i>Lycopersicon esculentum</i>	gi100215		7.00E-12
622	G2996	<i>Vigna unguiculata</i>	gi791150		1.20E-11
622	G2996	<i>Solanum tuberosum</i>	gi24745586		1.30E-11
624	G2998	<i>Brassica oleracea</i>	BH543781		1.00E-108
624	G2998	<i>Brassica napus</i>	CD825397		1.00E-105
624	G2998	<i>Gossypium arboreum</i>	BG443964		3.00E-60
624	G2998	<i>Lotus corniculatus</i> var. <i>japonicus</i>	AP006401		2.00E-56
624	G2998	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	CNS08CD7		3.00E-48
624	G2998	<i>Glycine max</i>	CA783548		2.00E-46
624	G2998	<i>Zea mays</i>	CC613855		3.00E-46
624	G2998	<i>Flaveria bidentis</i>	FBI18579		4.00E-46
624	G2998	<i>Lotus japonicus</i>	AP004968		1.00E-43
624	G2998	<i>Oryza sativa</i> (<i>indica</i>	AAAA01000157		9.00E-42

		cultivar-group)			
624	G2998	<i>Oryza sativa</i>	gi5091602		3.10E-43
624	G2998	<i>Oryza sativa</i> (japonica cultivar-group)	gi19387257		6.40E-42
624	G2998	<i>Flaveria bidentis</i>	gi13277218		8.00E-39
624	G2998	<i>Flaveria trinervia</i>	gi13277216		3.40E-38
624	G2998	<i>Lactuca sativa</i>	gi29119890		2.10E-20
624	G2998	<i>Nicotiana glauca</i>	gi1247386		0.0026
624	G2998	<i>Sporobolus vaginatus</i>	gi6478148		0.0038
624	G2998	<i>Cucumis sativus</i>	gi3810890		0.0077
624	G2998	<i>Zea mays</i>	gi15321716		0.0086
624	G2998	<i>Chlamydomonas reinhardtii</i>	gi16209575		0.009
626	G2999	<i>Brassica oleracea</i>	BH686720		4.00E-68
626	G2999	<i>Lotus corniculatus</i> var. japonicus	AP006401		2.00E-55
626	G2999	<i>Gossypium arboreum</i>	BG443964		1.00E-40
626	G2999	<i>Flaveria bidentis</i>	FBI18579		2.00E-39
626	G2999	<i>Glycine max</i>	CA783548		2.00E-39
626	G2999	<i>Lotus japonicus</i>	AP004968		2.00E-38
626	G2999	<i>Oryza sativa</i> (japonica cultivar-group)	AK108246		6.00E-38
626	G2999	<i>Zea mays</i>	CC629064		2.00E-37
626	G2999	<i>Oryza sativa</i> (indica cultivar-group)	AAAA01010656		3.00E-36
626	G2999	<i>Brassica napus</i>	CD835782		4.00E-36
626	G2999	<i>Flaveria bidentis</i>	gi13277220		1.70E-40
626	G2999	<i>Oryza sativa</i> (japonica cultivar-group)	gi19387257		1.10E-34
626	G2999	<i>Oryza sativa</i>	gi5091602		5.10E-33
626	G2999	<i>Flaveria trinervia</i>	gi13277216		3.20E-31
626	G2999	<i>Lactuca sativa</i>	gi29119890		1.10E-16
626	G2999	<i>Asarum europaeum</i>	gi8163936		0.92
626	G2999	<i>Mesembryanthemum crystallinum</i>	gi3342196		0.98
626	G2999	<i>Nicotiana glauca</i>	gi18448717		0.99
626	G2999	<i>Calycanthus floridus</i>	gi8163940		1
628	G3002	<i>Brassica oleracea</i>	BZ508225		5.00E-37
628	G3002	<i>Vitis vinifera</i>	CB347557		3.00E-25
628	G3002	<i>Glycine max</i>	BM886058		4.00E-24
628	G3002	<i>Brassica napus</i>	CD818854		1.00E-23
628	G3002	<i>Zea mays</i>	CC675142		3.00E-21
628	G3002	<i>Sorghum bicolor</i>	AF369906		3.00E-20
628	G3002	<i>Lycopersicon esculentum</i>	AW092295		4.00E-19
628	G3002	<i>Lotus corniculatus</i> var. japonicus	AP006401		6.00E-19
628	G3002	<i>Oryza sativa</i> (japonica cultivar-group)	AK111350		1.00E-18

628	G3002	<i>Oryza sativa</i>	10A19I		1.00E-18
628	G3002	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi28301934		1.30E-25
628	G3002	<i>Oryza sativa</i>	gi5091602		1.90E-23
628	G3002	<i>Flaveria bidentis</i>	gi13277218		2.90E-22
628	G3002	<i>Flaveria trinervia</i>	gi13277216		9.90E-14
628	G3002	<i>Lactuca sativa</i>	gi29119890		7.40E-09
628	G3002	<i>Picea mariana</i>	gi2982264		0.68
628	G3002	<i>Chloroplast</i> <i>Schismus barbatus</i>	gi2735522		0.85
628	G3002	<i>Chloroplast</i> <i>Rytidosperma pumilum</i>	gi2735530		0.95
628	G3002	<i>Lycopersicon esculentum</i>	gi12231300		0.96
628	G3002	<i>Zea mays</i>	gi477226		0.98
630	G3003	<i>Glycine max</i>	GMA311808		8.00E-83
630	G3003	<i>Helianthus annuus</i>	CD849311		7.00E-81
630	G3003	<i>Medicago truncatula</i>	CA921097		1.00E-79
630	G3003	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK071104		2.00E-78
630	G3003	<i>Brassica oleracea</i>	BH986891		8.00E-78
630	G3003	<i>Gossypium arboreum</i>	BQ407338		6.00E-75
630	G3003	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU825617		1.00E-74
630	G3003	<i>Triticum turgidum</i>	BF293596		4.00E-72
630	G3003	<i>Eschscholzia californica</i>	CD476634		8.00E-72
630	G3003	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01004319		2.00E-66
630	G3003	<i>Glycine max</i>	gi18376601		9.80E-78
630	G3003	<i>Oryza sativa</i>	gi15290024		3.50E-73
630	G3003	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi20161636		3.50E-73
630	G3003	<i>Lycopersicon esculentum</i>	gi15984226		2.90E-23
630	G3003	<i>Solanum tuberosum</i>	gi563623		4.80E-16
630	G3003	<i>Zea mays</i>	gi3170601		1.00E-11
630	G3003	<i>Fragaria x ananassa</i>	gi1362039		0.2
630	G3003	<i>Nicotiana tabacum</i>	gi4887016		0.91
630	G3003	<i>Vigna radiata</i>	gi11131101		0.97
630	G3003	<i>Betula pendula</i>	gi30577628		1
632	G3008	<i>Brassica oleracea</i>	BZ501815		1.00E-112
632	G3008	<i>Lotus corniculatus</i> var. <i>japonicus</i>	AP006419		1.00E-104
632	G3008	<i>Medicago truncatula</i>	AC125389		4.00E-97
632	G3008	<i>Vigna radiata</i>	AF467783		2.00E-92
632	G3008	<i>Lotus japonicus</i>	AP004499		3.00E-91
632	G3008	<i>Cucumis melo</i>	AB063192		2.00E-90
632	G3008	<i>Lycopersicon</i>	AF328784		8.00E-90

		<i>esculentum</i>			
632	G3008	<i>Nicotiana tabacum</i>	AB015855		1.00E-88
632	G3008	<i>Zea mays</i>	AX077258		7.00E-86
632	G3008	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01009163		3.00E-85
632	G3008	<i>Cucumis melo</i>	gi15425735		8.50E-96
632	G3008	<i>Vigna radiata</i>	gi18643339		1.20E-94
632	G3008	<i>Nicotiana tabacum</i>	gi30016896		1.80E-93
632	G3008	<i>Lycopersicon esculentum</i>	gi14280042		9.80E-93
632	G3008	<i>Oryza sativa (japonica cultivar-group)</i>	gi17221605		1.30E-90
632	G3008	<i>Dianthus caryophyllus</i>	gi7739795		2.30E-87
632	G3008	<i>Zea mays</i>	gi13121846		2.70E-82
632	G3008	<i>Fagus sylvatica</i>	gi10241607		9.50E-80
632	G3008	<i>Rosa hybrid cultivar</i>	gi20378359		1.00E-59
632	G3008	<i>Cicer arietinum</i>	gi8894550		9.50E-13
634	G3017	<i>Oryza sativa (japonica cultivar-group)</i>	AK109662		1.00E-39
634	G3017	<i>Solanum tuberosum</i>	BQ513392		6.00E-37
634	G3017	<i>Glycine max</i>	AW349686		3.00E-36
634	G3017	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01007394		6.00E-32
634	G3017	<i>Oryza sativa</i>	AP003983		3.00E-30
634	G3017	<i>Triticum aestivum</i>	CA654295		4.00E-29
634	G3017	<i>Brassica oleracea</i>	BZ043983		2.00E-26
634	G3017	<i>Zea mays</i>	BH779475		6.00E-26
634	G3017	<i>Physcomitrella patens subsp. patens</i>	BJ164531		8.00E-18
634	G3017	<i>Hordeum vulgare subsp. vulgare</i>	BU980391		5.00E-14
634	G3017	<i>Oryza sativa</i>	gi13486646		3.90E-35
634	G3017	<i>Oryza sativa (japonica cultivar-group)</i>	gi20160648		2.00E-15
634	G3017	<i>Pinus taeda</i>	gi6166283		3.60E-07
634	G3017	<i>Tulipa gesneriana</i>	gi5923912		4.10E-07
634	G3017	<i>Lycopersicon esculentum</i>	gi5669656		1.60E-06
634	G3017	<i>Antirrhinum majus</i>	gi166428		3.10E-06
634	G3017	<i>Brassica napus</i>	gi11045087		4.10E-06
634	G3017	<i>Petunia x hybrida</i>	gi10998404		7.90E-05
634	G3017	<i>Glycine max</i>	gi3399777		0.00011
634	G3017	<i>Perilla frutescens</i>	gi4519199		0.00035
636	G3021	<i>Brassica napus</i>	CD834815		3.00E-67
636	G3021	<i>Brassica oleracea</i>	BH955481		8.00E-24
636	G3021	<i>Medicago truncatula</i>	AC125475		3.00E-22
636	G3021	<i>Gossypium arboreum</i>	BQ411429		9.00E-12
636	G3021	<i>Glycine max</i>	CD394118		2.00E-11
636	G3021	<i>Gossypium hirsutum</i>	AI727885		2.00E-08

636	G3021	<i>Prunus persica</i>	BU043443		5.00E-08
636	G3021	<i>Solanum tuberosum</i>	BM110947		6.00E-08
636	G3021	<i>Vitis vinifera</i>	CD798414		1.00E-05
636	G3021	<i>Cycas rumphii</i>	CB092407		2.00E-05
636	G3021	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi20160528		0.00013
636	G3021	<i>Oryza sativa</i>	gi15528743		0.0017
636	G3021	<i>Chlamydomonas reinhardtii</i>	gi895614		0.82
636	G3021	<i>Pinus taeda</i>	gi6166283		0.83
636	G3021	<i>Triticum aestivum</i>	gi100802		0.92
636	G3021	<i>Prunus armeniaca</i>	gi2677828		1
636	G3021	<i>Hordeum vulgare</i>	gi4105117		1
638	G3032	<i>Hordeum vulgare</i>	BF256704		6.00E-14
638	G3032	<i>Brassica oleracea</i>	BH466839		1.00E-13
638	G3032	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AP004872		2.00E-13
638	G3032	<i>Chlamydomonas reinhardtii</i>	AF309494		4.00E-13
638	G3032	<i>Gossypium arboreum</i>	AW726892		9.00E-13
638	G3032	<i>Oryza sativa</i>	CA757143		4.00E-12
638	G3032	<i>Sorghum propinquum</i>	BZ694881		4.00E-12
638	G3032	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01004665		1.00E-11
638	G3032	<i>Triticum aestivum</i>	CA743799		2.00E-11
638	G3032	<i>Zea mays</i>	ZMEXTENS		4.00E-11
638	G3032	<i>Chlamydomonas reinhardtii</i>	gi12018147		6.50E-16
638	G3032	<i>Zea mays</i>	gi1076802		8.30E-12
638	G3032	<i>Glycine max</i>	gi99897		1.00E-11
638	G3032	<i>Volvox carteri f. nagariensis</i>	gi6523547		2.60E-11
638	G3032	<i>Santalum album</i>	gi2429362		1.30E-09
638	G3032	<i>Nicotiana tabacum</i>	gi119714		4.70E-09
638	G3032	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi32488576		2.70E-08
638	G3032	<i>Oryza sativa</i>	gi12083527		3.00E-08
638	G3032	<i>Nicotiana glauca</i>	gi2653671		3.40E-08
638	G3032	<i>Zea diploperennis</i>	gi228938		4.70E-08
640	G3044	<i>Lotus corniculatus</i> var. <i>japonicus</i>	CB828026		6.00E-45
640	G3044	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	AK103853		7.00E-44
640	G3044	<i>Avicennia marina</i>	BM497415		3.00E-42
640	G3044	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	CA015610		3.00E-42
640	G3044	<i>Medicago truncatula</i>	BG644829		5.00E-42
640	G3044	<i>Triticum aestivum</i>	BJ267378		1.00E-41
640	G3044	<i>Hordeum vulgare</i>	BE455695		7.00E-41

640	G3044	<i>Glycine max</i>	BU765737		3.00E-40
640	G3044	<i>Triticum monococcum</i>	BF200249		4.00E-40
640	G3044	<i>Solanum tuberosum</i>	BG887287		7.00E-40
640	G3044	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi20804997		4.20E-45
640	G3044	<i>Oryza sativa</i>	gi11862964		1.00E-41
640	G3044	<i>Tulipa gesneriana</i>	gi5923912		2.30E-37
640	G3044	<i>Pinus taeda</i>	gi6166283		1.80E-11
640	G3044	<i>Gossypium hirsutum</i>	gi13346180		4.60E-05
640	G3044	<i>Oryza rufipogon</i>	gi1086538		8.60E-05
640	G3044	<i>Phyllostachys acuta</i>	gi527661		0.00022
640	G3044	<i>Lycopersicon esculentum</i>	gi6175252		0.00027
640	G3044	<i>Glycine max</i>	gi3399777		0.00039
640	G3044	<i>Sorghum bicolor</i>	gi527665		0.00052
642	G3054	<i>Brassica oleracea</i>	BZ041399		3.00E-37
642	G3054	<i>Brassica napus</i>	CD836802		3.00E-36
642	G3054	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	BQ791259		4.00E-36
642	G3054	<i>Oryza sativa</i>	AP004635		9.00E-25
642	G3054	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	AAAA01000844		9.00E-25
642	G3054	<i>Triticum aestivum</i>	CD861617		6.00E-24
642	G3054	<i>Lycopersicon esculentum</i>	AW930486		1.00E-22
642	G3054	<i>Trifolium purpureum</i>	BU576932		1.00E-20
642	G3054	<i>Lotus japonicus</i>	BI417981		2.00E-20
642	G3054	<i>Triticum monococcum</i>	BQ801216		3.00E-20
642	G3054	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi29467558		6.40E-20
642	G3054	<i>Pisum sativum</i>	gi14018368		2.50E-15
642	G3054	<i>Oryza sativa</i>	gi5441893		2.20E-10
642	G3054	<i>Pinus pinaster</i>	gi18129298		3.60E-05
642	G3054	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi3153151		0.63
642	G3054	<i>Hordeum vulgare</i>	gi7443232		0.63
643	G3055	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER35081_1	1337	
643	G3055	<i>Glycine max</i>	GLYMA-28NOV01- CLUSTER35081_2	1338	
643	G3055	<i>Oryza sativa</i>	LIB4831-032-R1-N1-E4	1339	
643	G3055	<i>Oryza sativa</i>	ORYSA-22JAN02- CLUSTER3268_1	1340	
643	G3055	<i>Zea mays</i>	701166667H1	1341	
643	G3055	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER22810_1	1342	
643	G3055	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER22810_2	1343	
643	G3055	<i>Zea mays</i>	ZEAMA-08NOV01- CLUSTER22810_3	1344	
643	G3055	<i>Zea mays</i>	ZEAMA-08NOV01-	1345	

			CLUSTER22810_4		
643	G3055	<i>Glycine max</i>	Gma_S5098126	1686	
643	G3055	<i>Zea mays</i>	Zm_S11417368	1832	
643	G3055	<i>Triticum aestivum</i>	Ta_S159757	1922	
643	G3055	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-330143	2097	
644	G3055	<i>Brassica oleracea</i>	BZ078892		2.00E-95
644	G3055	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01000844		1.00E-80
644	G3055	<i>Oryza sativa</i>	AP004635		1.00E-80
644	G3055	<i>Triticum monococcum</i>	BQ801216		1.00E-71
644	G3055	<i>Brassica napus</i>	CD836802		2.00E-71
644	G3055	<i>Sorghum bicolor</i>	BE593461		2.00E-67
644	G3055	<i>Brassica rapa subsp. pekinensis</i>	BQ791259		8.00E-64
644	G3055	<i>Lycopersicon esculentum</i>	AW930486		3.00E-58
644	G3055	<i>Hordeum vulgare subsp. vulgare</i>	BU971385		1.00E-57
644	G3055	<i>Zea mays</i>	CC372422		3.00E-56
644	G3055	<i>Oryza sativa (japonica cultivar- group)</i>	gi29467558		1.80E-99
644	G3055	<i>Pisum sativum</i>	gi14018368		2.50E-32
644	G3055	<i>Oryza sativa</i>	gi5441893		2.30E-10
644	G3055	<i>Citrus unshiu</i>	gi7024449		1.10E-08
644	G3055	<i>Zea mays</i>	gi22293		1.30E-08
644	G3055	<i>Sorghum bicolor</i>	gi21623		3.70E-08
644	G3055	<i>Cicer arietinum</i>	gi21068672		1.30E-07
644	G3055	<i>Hordeum vulgare</i>	gi1229138		5.70E-07
644	G3055	<i>Lycopersicon esculentum</i>	gi1166450		8.50E-07
644	G3055	<i>Nicotiana tabacum</i>	gi395147		1.50E-06
646	G3059	<i>Vitis vinifera</i>	CB349575		7.00E-59
646	G3059	<i>Brassica oleracea</i>	BH714891		1.00E-55
646	G3059	<i>Oryza sativa (japonica cultivar- group)</i>	AK108658		6.00E-50
646	G3059	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01001811		2.00E-45
646	G3059	<i>Oryza sativa</i>	AC098571		2.00E-45
646	G3059	<i>Zea mays</i>	CC169635		1.00E-38
646	G3059	<i>Hordeum vulgare subsp. vulgare</i>	BI958345		1.00E-36
646	G3059	<i>Populus balsamifera subsp. trichocarpa</i>	AI166416		2.00E-21
646	G3059	<i>Sorghum bicolor</i>	CF073535		6.00E-19
646	G3059	<i>Medicago truncatula</i>	AW329637		1.00E-12
646	G3059	<i>Oryza sativa</i>	gi13603429		8.50E-53
646	G3059	<i>Oryza sativa (japonica cultivar- group)</i>	gi29467558		2.70E-08
646	G3059	<i>Spinacia oleracea</i>	gi2815305		3.40E-06

646	G3059	<i>Pisum sativum</i>	gi31580864		0.00044
646	G3059	<i>Pinus pinaster</i>	gi18129298		0.0015
646	G3059	<i>Petroselinum crispum</i>	gi1169081		0.016
646	G3059	<i>Hordeum vulgare</i>	gi1418972		0.027
646	G3059	<i>Nicotiana tabacum</i>	gi1076624		0.047
646	G3059	<i>Triticum sp.</i>	gi100838		0.074
646	G3059	<i>Triticum aestivum</i>	gi1199790		0.074
648	G3060	<i>Brassica oleracea</i>	BH549078		2.00E-88
648	G3060	<i>Brassica napus</i>	CD822240		2.00E-76
648	G3060	<i>Zea mays</i>	AY104443		2.00E-62
648	G3060	<i>Lotus corniculatus var. japonicus</i>	AP006377		9.00E-60
648	G3060	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01009959		5.00E-53
648	G3060	<i>Oryza sativa</i>	AP000367		5.00E-53
648	G3060	<i>Solanum tuberosum</i>	BQ505464		5.00E-52
648	G3060	<i>Glycine max</i>	AW348431		3.00E-49
648	G3060	<i>Oryza sativa (japonica cultivar- group)</i>	AP003609		3.00E-48
648	G3060	<i>Triticum aestivum</i>	BF472969		2.00E-47
648	G3060	<i>Oryza sativa (japonica cultivar- group)</i>	gi32488659		5.10E-49
648	G3060	<i>Oryza sativa</i>	gi5441893		2.30E-46
648	G3060	<i>Pisum sativum</i>	gi14018368		7.40E-10
648	G3060	<i>Pinus pinaster</i>	gi18129298		2.90E-07
648	G3060	<i>Lycopersicon esculentum</i>	gi1345534		0.00084
648	G3060	<i>Gossypium hirsutum</i>	gi126075		0.11
648	G3060	<i>Zea mays</i>	gi22293		0.11
648	G3060	<i>Petunia x hybrida</i>	gi121627		0.14
648	G3060	<i>Petunia sp.</i>	gi225181		0.14
648	G3060	<i>Phaseolus vulgaris</i>	gi121632		0.28
650	G3061	<i>Oryza sativa (japonica cultivar- group)</i>	AK072128		2.00E-85
650	G3061	<i>Prunus persica</i>	BU039744		4.00E-84
650	G3061	<i>Lycopersicon esculentum</i>	BE459738		8.00E-84
650	G3061	<i>Solanum tuberosum</i>	BG590535		2.00E-82
650	G3061	<i>Zea mays</i>	AX658844		6.00E-82
650	G3061	<i>Triticum aestivum</i>	CD912590		3.00E-81
650	G3061	<i>Robinia pseudoacacia</i>	BI677739		7.00E-81
650	G3061	<i>Capsicum annuum</i>	BM063853		2.00E-79
650	G3061	<i>Brassica oleracea</i>	BZ520039		2.00E-79
650	G3061	<i>Medicago truncatula</i>	BG645203		3.00E-79
650	G3061	<i>Oryza sativa (japonica cultivar- group)</i>	gi21741797		8.90E-80
650	G3061	<i>Solanum tuberosum</i>	gi563623		1.90E-79
650	G3061	<i>Oryza sativa</i>	gi10934090		6.10E-77

650	G3061	<i>Lycopersicon esculentum</i>	gi9858780		1.70E-74
650	G3061	<i>Zea mays</i>	gi3170601		1.20E-71
650	G3061	<i>Glycine max</i>	gi18376601		2.30E-19
650	G3061	<i>Triticum aestivum</i>	gi485814		0.67
650	G3061	<i>Petunia x hybrida</i>	gi2346986		0.95
650	G3061	<i>Tsuga canadensis</i>	gi4530513		1
651	G3067	<i>Medicago truncatula</i>	Mtr_S5406390	1716	
651	G3067	<i>Medicago truncatula</i>	Mtr_S7093057	1717	
651	G3067	<i>Zea mays</i>	Zm_S11388015	1833	
651	G3067	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-56587	2098	
651	G3067	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-360212	2099	
652	G3067	<i>Oryza sativa (japonica cultivar- group)</i>	AK104311		1.00E-127
652	G3067	<i>Oryza sativa</i>	AP003766		1.00E-105
652	G3067	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01011671		1.00E-102
652	G3067	<i>Medicago truncatula</i>	AC144502		2.00E-92
652	G3067	<i>Lactuca sativa</i>	BQ849595		5.00E-86
652	G3067	<i>Zea mays</i>	CC705079		2.00E-78
652	G3067	<i>Glycine max</i>	BG352898		3.00E-76
652	G3067	<i>Brassica oleracea</i>	BZ503751		1.00E-71
652	G3067	<i>Hedyotis centranthoides</i>	CB087520		2.00E-71
652	G3067	<i>Hordeum vulgare subsp. vulgare</i>	CA030376		4.00E-69
652	G3067	<i>Oryza sativa (japonica cultivar- group)</i>	gi20804915		2.70E-122
652	G3067	<i>Oryza sativa</i>	gi5777616		3.60E-56
652	G3067	<i>Nicotiana tabacum</i>	gi27529852		0.55
652	G3067	<i>Petunia x hybrida</i>	gi20563		0.72
652	G3067	<i>Lycopersicon esculentum</i>	gi122003		0.82
652	G3067	<i>Chloroplast Phaseolus vulgaris</i>	gi21309725		1
652	G3067	<i>Glycine max</i>	gi2129831		1
653	G3070	<i>Triticum aestivum</i>	Ta_S122753	1923	
654	G3070	<i>Brassica oleracea</i>	BH986969		2.00E-72
654	G3070	<i>Oryza sativa (japonica cultivar- group)</i>	AK104311		6.00E-50
654	G3070	<i>Hordeum vulgare subsp. vulgare</i>	CA030376		2.00E-42
654	G3070	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01000203		4.00E-42
654	G3070	<i>Oryza sativa</i>	AP003406		4.00E-42
654	G3070	<i>Zea mays</i>	CC705079		1.00E-40
654	G3070	<i>Medicago truncatula</i>	AC144502		9.00E-40
654	G3070	<i>Lactuca sativa</i>	BQ849595		4.00E-38

654	G3070	<i>Hedyotis centranthoides</i>	CB087520		7.00E-37
654	G3070	<i>Glycine max</i>	BG352898		7.00E-35
654	G3070	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi20804915		7.50E-58
654	G3070	<i>Oryza sativa</i>	gi5777616		1.50E-24
654	G3070	<i>Zea mays</i>	gi1504058		0.88
654	G3070	<i>Chlorella vulgaris</i>	gi2224518		0.97
654	G3070	<i>Chloroplast Chlorella vulgaris</i>	gi7520715		0.97
654	G3070	<i>Medicago sativa</i>	gi913595		1
654	G3070	<i>Brassica napus</i>	gi2809204		1
655	G3076	<i>Oryza sativa</i>	Os_S95874	1630	
655	G3076	<i>Lycopersicon esculentum</i>	SGN-UNIGENE-52322	2100	
656	G3076	<i>Brassica oleracea</i>	BH458827		1.00E-59
656	G3076	<i>Lycopersicon esculentum</i>	AI489100		3.00E-52
656	G3076	<i>Theobroma cacao</i>	CA796492		6.00E-31
656	G3076	<i>Nicotiana glauca X Nicotiana langsdorffii</i>	TOBTID3		3.00E-25
656	G3076	<i>Populus tremula x Populus tremuloides</i>	BU866131		3.00E-21
656	G3076	<i>Medicago truncatula</i>	BQ123004		4.00E-20
656	G3076	<i>Zea mays</i>	CC633595		8.00E-18
656	G3076	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	AK106334		1.00E-17
656	G3076	<i>Oryza sativa</i>	AP003567		4.00E-17
656	G3076	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01001312		4.00E-17
656	G3076	<i>Oryza sativa</i>	gi15408613		1.10E-19
656	G3076	<i>Oryza sativa</i> (<i>japonica</i> cultivar- group)	gi21104797		1.10E-19
656	G3076	<i>Lycopersicon esculentum</i>	gi4959970		4.30E-13
656	G3076	<i>Triticum aestivum</i>	gi100809		2.70E-12
656	G3076	<i>Solanum tuberosum</i>	gi13195751		6.90E-12
656	G3076	<i>Zea mays</i>	gi297020		8.80E-12
656	G3076	<i>Nicotiana glauca X Nicotiana langsdorffii</i>	gi688423		1.00E-11
656	G3076	<i>Phaseolus vulgaris</i>	gi15148924		1.40E-10
656	G3076	<i>Nicotiana tabacum</i>	gi12230709		1.10E-09
656	G3076	<i>Glycine max</i>	gi7488719		1.40E-08
657	G3083	<i>Oryza sativa</i>	LIB3434-065-P1-K1-B5	1346	
657	G3083	<i>Oryza sativa</i>	Os_S54214	1631	
657	G3083	<i>Glycine max</i>	Gma_S4880456	1687	
657	G3083	<i>Hordeum vulgare</i>	Hv_S60182	1753	
657	G3083	<i>Triticum aestivum</i>	Ta_S179586	1924	
657	G3083	<i>Lycopersicon esculentum</i>	SGN-UNIGENE- SINGLET-306367	2101	
658	G3083	<i>Medicago</i>	BQ123004		9.00E-65

		<i>truncatula</i>			
658	G3083	<i>Arachis hypogaea</i>	CD038559		3.00E-58
658	G3083	<i>Glycine max</i>	BE657440		7.00E-51
658	G3083	<i>Theobroma cacao</i>	CA794948		2.00E-48
658	G3083	<i>Phaseolus coccineus</i>	CA899019		8.00E-47
658	G3083	<i>Brassica oleracea</i>	BZ028606		3.00E-42
658	G3083	<i>Brassica napus</i>	CD823868		3.00E-42
658	G3083	<i>Populus tremula x Populus tremuloides</i>	BU866131		5.00E-36
658	G3083	<i>Oryza sativa (indica cultivar-group)</i>	AAAA01006352		2.00E-32
658	G3083	<i>Nicotiana glauca X Nicotiana langsдорffii</i>	TOBTID3		1.00E-31
658	G3083	<i>Nicotiana glauca X Nicotiana langsдорffii</i>	gi688423		8.80E-36
658	G3083	<i>Oryza sativa</i>	gi8570052		1.30E-29
658	G3083	<i>Lycopersicon esculentum</i>	gi4959970		3.10E-17
658	G3083	<i>Nicotiana tabacum</i>	gi12230709		7.50E-16
658	G3083	<i>Triticum aestivum</i>	gi100809		1.60E-15
658	G3083	<i>Solanum tuberosum</i>	gi13195751		3.00E-14
658	G3083	<i>Zea mays</i>	gi297020		6.00E-14
658	G3083	<i>Phaseolus vulgaris</i>	gi15148926		1.90E-13
658	G3083	<i>Nicotiana sp.</i>	gi19680		7.30E-13
658	G3083	<i>Glycine max</i>	gi7488719		5.10E-11
660	G3084	<i>Brassica napus</i>	CD819850		8.00E-16
660	G3084	<i>Prunus persica</i>	BU043737		2.00E-15
660	G3084	<i>Oryza sativa</i>	BI118786		4.00E-15
660	G3084	<i>Oryza sativa (japonica cultivar- group)</i>	AK104501		8.00E-15
660	G3084	<i>Hordeum vulgare subsp. vulgare</i>	AV933892		1.00E-14
660	G3084	<i>Oryza minuta</i>	CB214244		2.00E-14
660	G3084	<i>Hordeum vulgare</i>	BI954130		2.00E-14
660	G3084	<i>Beta vulgaris</i>	BQ592350		7.00E-14
660	G3084	<i>Ipomoea nil</i>	BJ566577		2.00E-13
660	G3084	<i>Populus tremula x Populus tremuloides</i>	PTR306828		4.00E-13
660	G3084	<i>Populus tremula x Populus tremuloides</i>	gi20269057		3.10E-14
660	G3084	<i>Glycine max</i>	gi114733		1.30E-13
660	G3084	<i>Vigna radiata</i>	gi287566		1.60E-13
660	G3084	<i>Oryza sativa (indica cultivar-group)</i>	gi30962267		2.10E-13
660	G3084	<i>Oryza sativa</i>	gi17154533		3.30E-13
660	G3084	<i>Pisum sativum</i>	gi1352058		1.10E-12
660	G3084	<i>Gossypium hirsutum</i>	gi22531416		6.20E-12
660	G3084	<i>Pinus pinaster</i>	gi17976835		7.70E-12
660	G3084	<i>Pinus taeda</i>	gi32396295		7.70E-12
660	G3084	<i>Oryza sativa (japonica cultivar- group)</i>	gi31126760		1.30E-11

		group)			
661	G3086	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER427_57	1347	
661	G3086	<i>Glycine max</i>	GLYMA-28NOV01-CLUSTER427_63	1348	
661	G3086	<i>Glycine max</i>	Gma_S4882467	1688	
661	G3086	<i>Glycine max</i>	Gma_S4911216	1689	
662	G3086	<i>Oryza sativa</i> (japonica cultivar-group)	AK100106		2.00E-42
662	G3086	<i>Ipomoea nil</i>	BJ575230		2.00E-39
662	G3086	<i>Medicago truncatula</i>	CA920438		4.00E-38
662	G3086	<i>Glycine max</i>	BU550331		2.00E-37
662	G3086	<i>Lycopersicon esculentum</i>	AW037896		2.00E-36
662	G3086	<i>Brassica oleracea</i>	BH718970		2.00E-36
662	G3086	<i>Solanum tuberosum</i>	BQ113088		2.00E-36
662	G3086	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	CA014136		1.00E-35
662	G3086	<i>Oryza sativa</i> (<i>indica</i> cultivar-group)	CB634806		2.00E-35
662	G3086	<i>Zea mays</i>	CA831862		2.00E-35
662	G3086	<i>Pinus taeda</i>	gi6166283		4.50E-42
662	G3086	<i>Oryza sativa</i>	gi19401700		2.10E-36
662	G3086	<i>Oryza sativa</i> (japonica cultivar-group)	gi20161021		1.60E-29
662	G3086	<i>Tulipa gesneriana</i>	gi5923912		1.80E-10
662	G3086	<i>Mesembryanthemum crystallinum</i>	gi4206118		6.00E-05
662	G3086	<i>Glycine max</i>	gi3399777		0.00017
662	G3086	<i>Brassica napus</i>	gi27650307		0.00025
662	G3086	<i>Gossypium hirsutum</i>	gi13346182		0.00055
662	G3086	<i>Pennisetum glaucum</i>	gi527657		0.0017
662	G3086	<i>Perilla frutescens</i>	gi4519199		0.0029
664	G3091	<i>Gossypium hirsutum</i>	CD486670		2.00E-93
664	G3091	<i>Medicago truncatula</i>	CB894060		8.00E-90
664	G3091	<i>Solanum tuberosum</i>	BM112649		1.00E-85
664	G3091	<i>Lupinus albus</i>	CA411473		1.00E-85
664	G3091	<i>Vitis vinifera</i>	CB004487		2.00E-85
664	G3091	<i>Glycine max</i>	BQ473916		1.00E-83
664	G3091	<i>Prunus persica</i>	BU041659		2.00E-82
664	G3091	<i>Prunus dulcis</i>	BU574304		4.00E-82
664	G3091	<i>Lactuca sativa</i>	BQ871960		5.00E-82
664	G3091	<i>Lycopersicon esculentum</i>	AW220091		7.00E-81
664	G3091	<i>Oryza sativa</i> (japonica cultivar-group)	gi32489345		1.00E-66
664	G3091	<i>Oryza sativa</i>	gi12643058		6.00E-62
664	G3091	<i>Pisum sativum</i>	gi16117799		9.70E-33
666	G3094	<i>Glycine max</i>	BI969147		2.00E-60

666	G3094	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	BQ765415		2.00E-54
666	G3094	<i>Pinus pinaster</i>	BX254443		3.00E-54
666	G3094	<i>Pinus taeda</i>	AW011103		3.00E-50
666	G3094	<i>Pisum sativum</i>	AB045222		7.00E-46
666	G3094	<i>Lactuca sativa</i>	BQ875949		7.00E-46
666	G3094	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU830426		2.00E-45
666	G3094	<i>Triticum aestivum</i>	BJ270124		4.00E-45
666	G3094	<i>Ipomoea nil</i>	BJ563336		2.00E-44
666	G3094	<i>Sorghum</i> <i>propinquum</i>	BF481787		1.00E-43
666	G3094	<i>Pisum sativum</i>	gi16117799		8.40E-49
666	G3094	<i>Oryza sativa</i> (japonica cultivar- group)	gi32489345		2.00E-29
666	G3094	<i>Oryza sativa</i>	gi12643058		1.00E-27
666	G3094	<i>Welwitschia</i> <i>mirabilis</i>	gi17402656		1
666	G3094	<i>Chlorella vulgaris</i>	gi2224452		1
666	G3094	<i>Gnetum africanum</i>	gi29648802		1
666	G3094	<i>Pelargonium</i> <i>mollicomun</i>	gi9621935		1
668	G3095	<i>Populus tremula</i> x <i>Populus tremuloides</i>	BU812421		2.00E-89
668	G3095	<i>Populus tremula</i>	BU889637		2.00E-78
668	G3095	<i>Oryza sativa</i> (japonica cultivar- group)	AK067251		1.00E-64
668	G3095	<i>Vitis vinifera</i>	CA818053		3.00E-62
668	G3095	<i>Populus</i> <i>balsamifera</i> subsp. <i>trichocarpa</i>	BU870747		3.00E-60
668	G3095	<i>Gossypium</i> <i>arboreum</i>	BG443078		3.00E-57
668	G3095	<i>Medicago</i> <i>truncatula</i>	BQ123285		6.00E-57
668	G3095	<i>Cryptomeria</i> <i>japonica</i>	BP176029		7.00E-57
668	G3095	<i>Glycine max</i>	CA800006		2.00E-56
668	G3095	<i>Oryza sativa</i>	AX653892		4.00E-56
668	G3095	<i>Oryza sativa</i> (japonica cultivar- group)	gi32489345		1.60E-57
668	G3095	<i>Oryza sativa</i>	gi12643058		1.10E-50
668	G3095	<i>Pisum sativum</i>	gi16117799		3.70E-30
668	G3095	<i>Picea mariana</i>	gi2996158		0.97
668	G3095	<i>Ipomoea nil</i>	gi1064830		1
670	G3111	<i>Brassica oleracea</i>	BH673411		6.00E-80
670	G3111	<i>Medicago</i> <i>truncatula</i>	AC126786		1.00E-58
670	G3111	<i>Glycine max</i>	BU762572		8.00E-56
670	G3111	<i>Lycopersicon</i> <i>esculentum</i>	AW443687		1.00E-55
670	G3111	<i>Lotus japonicus</i>	BI418846		3.00E-54
670	G3111	<i>Vitis vinifera</i>	CB919606		3.00E-52
670	G3111	<i>Solanum tuberosum</i>	BI175970		1.00E-48

670	G3111	<i>Mesembryanthemum crystallinum</i>	BE033932		2.00E-48
670	G3111	<i>Lupinus albus</i>	CA411115		3.00E-46
670	G3111	<i>Stevia rebaudiana</i>	BG522187		5.00E-42
670	G3111	<i>Oryza sativa</i>	gi12039329		1.40E-35
670	G3111	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	gi31433314		1.40E-35
670	G3111	<i>Hordeum vulgare</i>	gi2894379		7.20E-34
670	G3111	<i>Cucumis melo</i>	gi17016985		7.10E-27
670	G3111	<i>Zea mays</i>	gi18092342		6.30E-19
670	G3111	<i>Nicotiana tabacum</i>	gi12003386		3.60E-16
670	G3111	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	gi20152976		1.40E-14
670	G3111	<i>Medicago sativa</i>	gi23451086		2.00E-14
670	G3111	<i>Glycine max</i>	gi22597166		3.80E-12
670	G3111	<i>Pisum sativum</i>	gi4240031		1.60E-08

Table 8 lists sequences discovered to be paralogous to a number of transcription factors of the present invention. The columns headings include, from left to right, the *Arabidopsis* SEQ ID NO; corresponding *Arabidopsis* Gene ID (GID) numbers; the GID numbers of the paralogs discovered in a database search; and the SEQ ID NOs assigned to the paralogs.

Table 8. *Arabidopsis* Transcription Factor Genes and Paralogs

Arabidopsis Transcription Factor SEQ ID NO	Arabidopsis TF GID No	Paralog GID No	Paralog Nucleotide SEQ ID NO
3	G12	G1379	1441
		G24	1349
7	G30	G1791	1461
		G1792	1463
		G1795	1465
9	G46	G1004	1425
		G1419	1447
		G29	1351
		G43	1355
11	G47	G2133	1495
39	G148	G142	33
43	G153	G152	1365
		G1760	1459
		G860	1419
45	G155	G131	15
		G135	21
79	G355	G1994	1491
83	G370	G1995	1493
		G2826	1531

		G2838	1535
		G361	1383
		G362	1385
97	G438	G1548	1453
		G390	1389
		G391	1391
		G392	1393
105	G485	G1364	1439
		G2345	1501
		G481	1395
		G482	1397
121	G627	G149	1363
125	G651	G1914	1481
		G1973	1485
127	G652	G1335	1435
141	G807	G810	1417
145	G839	G1196	1429
153	G916	G184	1369
		G186	1371
155	G926	G2632	1517
159	G961	G2535	1507
		G957	157
161	G975	G1387	1443
		G2583	1515
163	G1011	G154	1367
171	G1037	G722	1409
181	G1128	G1399	1445
185	G1142	G2659	1521
189	G1206	G1207	1431
199	G1313	G1325	1433
207	G1357	G1452	1451
		G512	1401
215	G1412	G759	1413
		G773	1415
223	G1451	G990	1423
225	G1452	G1357	1437
		G512	1401
233	G1482	G1888	1477
277	G1792	G1791	1461
		G1795	1465
		G30	7
281	G1797	G1798	283

283	G1798	G1797	281
287	G1816	G225	1375
		G226	1377
		G2718	507
		G682	1407
297	G1840	G1749	1457
		G1839	1473
303	G1863	G2334	1499
305	G1893	G1976	1489
		G3062	1555
311	G1928	G2664	1523
333	G1995	G2826	1531
		G2838	555
		G361	1383
		G362	1385
		G370	1387
341	G2041	G2882	1537
371	G2207	G2199	1497
393	G2334	G1863	303
407	G2432	G736	1411
417	G2457	G2459	1505
419	G2459	G2457	417
425	G2505	G2635	1519
431	G2536	G511	1399
435	G2550	G2546	1509
441	G2567	G1017	167
483	G2650	G617	1405
505	G2717	G204	1373
		G2709	1525
507	G2718	G1816	287
		G225	1375
		G226	1377
		G682	1407
511	G2741	G1435	1449
525	G2768	G600	117
529	G2776	G1652	1455
545	G2826	G1995	333
		G2838	555
		G361	1383
		G362	1385
		G370	1387
547	G2830	G2562	1511
		G2563	1513

		G2828	1533
555	G2838	G1995	333
		G2826	545
		G361	1383
		G362	1385
		G370	1387
557	G2839	G1889	1479
		G1974	1487
		G353	1379
		G354	1381
567	G2854	G1940	1483
569	G2859	G2779	533
571	G2865	G2934	595
593	G2933	G2928	1539
		G2932	1541
607	G2979	G2980	1547
609	G2981	G2982	1551
611	G2982	G2981	1549
615	G2990	G2989	1553
651	G3067	G2966	1545

Table 9 lists the gene identification number (GID) and relationships for homologous (found using analyses according to Example IX) and variant sequences for the sequences of the Sequence Listing.

5

Table 9. Similarity relationships found within the Sequence Listing

SEQ ID NO.	GID	DNA or Protein (PRT)	Species from which Sequence is Derived	Relationship
671		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G12
672		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G12
673		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G12
674		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G12
675		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G12
676		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G12
677		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G12
678		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G12
679		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G12
680		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G12
681		PRT	<i>Oryza sativa</i>	Orthologous to G12
682		PRT	<i>Oryza sativa</i>	Orthologous to G12
683		PRT	<i>Oryza sativa</i>	Orthologous to G12
684		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G12
685		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G30, G1792
686		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G30, G1792

687		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G30, G1792
688		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G30, G1792
689		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G30, G1792
690		PRT	<i>Oryza sativa</i>	Orthologous to G30, G1792
691		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G30, G1792
692		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G46
693		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G46
694		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G46
695		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G46
696		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G46
697		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G46
698		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G46
699		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G46
700		PRT	<i>Oryza sativa</i>	Orthologous to G46
701		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G46
702		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G47
703		PRT	<i>Oryza sativa</i>	Orthologous to G47
704		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G148
705		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G148
706		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G148
707		PRT	<i>Oryza sativa</i>	Orthologous to G148
708		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G148
709		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G148
710		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G148
711		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G148
712		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G148
713		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G153
714		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G153
715		PRT	<i>Oryza sativa</i>	Orthologous to G153
716		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G153
717		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G153
718		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G153
719		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G155
720		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G155
721		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G155
722		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G155
723		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G155
724		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G155
725		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G155
726		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G155
727		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G155
728		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G155
729		PRT	<i>Oryza sativa</i>	Orthologous to G155
730		PRT	<i>Oryza sativa</i>	Orthologous to G155
731		PRT	<i>Oryza sativa</i>	Orthologous to G155
732		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G155
733		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G155
734		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G155
735		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G155
736		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G155
737		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G155
738		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G155
739		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G155

740		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G155
741		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G200
742		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G200
743		PRT	<i>Oryza sativa</i>	Orthologous to G200
744		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G200
745		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G200
746		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G200
747		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G355
748		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G355
749		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G355
750		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G355
751		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G355
752		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G355
753		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G370, G1995, G2826, G2838
754		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G370, G1995, G2826, G2838
755		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G370, G1995, G2826, G2838
756		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G370, G1995, G2826, G2838
757		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G370, G1995, G2826, G2838
758		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G370, G2826
759		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G370, G1995, G2826, G2838
760		PRT	<i>Oryza sativa</i>	Orthologous to G370, G1995, G2826, G2838
761		PRT	<i>Oryza sativa</i>	Orthologous to G370, G1995, G2826, G2838
762		PRT	<i>Oryza sativa</i>	Orthologous to G370, G1995, G2826, G2838
763		PRT	<i>Oryza sativa</i>	Orthologous to G370, G1995, G2826, G2838
764		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G370, G1995, G2826, G2838
765		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G370, G1995, G2826, G2838
766		PRT	<i>Oryza sativa</i>	Orthologous to G372
767		PRT	<i>Oryza sativa</i>	Orthologous to G372
768		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G438
769		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G438
770		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G438
771		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G438
772		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G438
773		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G438
774		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G438
775		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G438
776		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G438
777		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G438
778		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G438
779		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G438
780		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G438
781		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G438
782		PRT	<i>Oryza sativa</i>	Orthologous to G438
783		PRT	<i>Oryza sativa</i>	Orthologous to G438
784		PRT	<i>Oryza sativa</i>	Orthologous to G438
785		PRT	<i>Oryza sativa</i>	Orthologous to G438
786		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G438
787		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G438
788		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G438

[illegible]

846		PRT	<i>Oryza sativa</i>	Orthologous to G652
847		PRT	<i>Oryza sativa</i>	Orthologous to G652
848		PRT	<i>Oryza sativa</i>	Orthologous to G652
849		PRT	<i>Oryza sativa</i>	Orthologous to G652
850		PRT	<i>Oryza sativa</i>	Orthologous to G652
851		PRT	<i>Oryza sativa</i>	Orthologous to G652
852		PRT	<i>Oryza sativa</i>	Orthologous to G652
853		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G652
854		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G652
855		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G652
856		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G652
857		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G652
858		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G652
859		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G652
860		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G652
861		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G807
862		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G807
863		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G807
864		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G807
865		PRT	<i>Oryza sativa</i>	Orthologous to G807
866		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G807
867		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G807
868		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G839
869		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G839
870		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G839
871		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G839
872		PRT	<i>Oryza sativa</i>	Orthologous to G839
873		PRT	<i>Oryza sativa</i>	Orthologous to G839
874		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G839
875		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G839
876		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G839
877		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G916
878		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G916
879		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G916
880		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G916
881		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G916
882		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G916
883		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G916
884		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G916
885		PRT	<i>Oryza sativa</i>	Orthologous to G916
886		PRT	<i>Oryza sativa</i>	Orthologous to G916
887		PRT	<i>Oryza sativa</i>	Orthologous to G916
888		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G916
889		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G926
890		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G926
891		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G926
892		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G926
893		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G926
894		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G926
895		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G961
896		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G961
897		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G961
898		PRT	<i>Oryza sativa</i>	Orthologous to G961
899		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G961
900		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G961
901		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G961
902		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G975

903		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G975
904		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G975
905		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G975
906		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G975
907		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G975
908		PRT	<i>Oryza sativa</i>	Orthologous to G975
909		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G975
910		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G975
911		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G975
912		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1011
913		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1011
914		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1011
915		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1011
916		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1011
917		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1011
918		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1011
919		PRT	<i>Oryza sativa</i>	Orthologous to G1011
920		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1011
921		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1011
922		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1011
923		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1011
924		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1011
925		PRT	<i>Oryza sativa</i>	Orthologous to G1013
926		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1037
927		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1037
928		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1037
929		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1037
930		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1037
931		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1037
932		PRT	<i>Oryza sativa</i>	Orthologous to G1037
933		PRT	<i>Oryza sativa</i>	Orthologous to G1037
934		PRT	<i>Oryza sativa</i>	Orthologous to G1037
935		PRT	<i>Oryza sativa</i>	Orthologous to G1037
936		PRT	<i>Oryza sativa</i>	Orthologous to G1037
937		PRT	<i>Oryza sativa</i>	Orthologous to G1037
938		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1037
939		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1037
940		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1037
941		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1037
942		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1128
943		PRT	<i>Oryza sativa</i>	Orthologous to G1128
944		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1142
945		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1142
946		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1142
947		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1142
948		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1206
949		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1206
950		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1206
951		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1206
952		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1206
953		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1206
954		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1206
955		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1206
956		PRT	<i>Oryza sativa</i>	Orthologous to G1206
957		PRT	<i>Oryza sativa</i>	Orthologous to G1206
958		PRT	<i>Oryza sativa</i>	Orthologous to G1206
959		PRT	<i>Oryza sativa</i>	Orthologous to G1206

960		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1206
961		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1206
962		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1206
963		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1206
964		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1206
965		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1206
966		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1206
967		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1206
968		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1274
969		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1274
970		PRT	<i>Oryza sativa</i>	Orthologous to G1274
971		PRT	<i>Oryza sativa</i>	Orthologous to G1274
972		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1274
973		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1274
974		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1274
975		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1274
976		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1313
977		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1313
978		PRT	<i>Oryza sativa</i>	Orthologous to G1313
979		PRT	<i>Oryza sativa</i>	Orthologous to G1313
980		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1313
981		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1313
982		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1357, G1452
983		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1412
984		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1412
985		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1412
986		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1412
987		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1412
988		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1412
989		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1412
990		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1412
991		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1412
992		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1420
993		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1420
994		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1420
995		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1420
996		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1451
997		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1451
998		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1451
999		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1451
1000		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1451
1001		PRT	<i>Oryza sativa</i>	Orthologous to G1451
1002		PRT	<i>Oryza sativa</i>	Orthologous to G1451
1003		PRT	<i>Oryza sativa</i>	Orthologous to G1451
1004		PRT	<i>Oryza sativa</i>	Orthologous to G1451
1005		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1451
1006		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1451
1007		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1451
1008		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1451
1009		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1468
1010		PRT	<i>Oryza sativa</i>	Orthologous to G1468
1011		PRT	<i>Oryza sativa</i>	Orthologous to G1468
1012		PRT	<i>Oryza sativa</i>	Orthologous to G1468
1013		PRT	<i>Oryza sativa</i>	Orthologous to G1476
1014		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1482
1015		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1482

1016		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1482
1017		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1482
1018		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1482
1019		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1482
1020		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1482
1021		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1482
1022		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1482
1023		PRT	<i>Oryza sativa</i>	Orthologous to G1482
1024		PRT	<i>Oryza sativa</i>	Orthologous to G1482
1025		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1482
1026		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1482
1027		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1482
1028		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1482
1029		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1482
1030		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1482
1031		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1510
1032		PRT	<i>Oryza sativa</i>	Orthologous to G1510
1033		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1539
1034		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1539
1035		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1557
1036		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1660
1037		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1660
1038		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1660
1039		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1660
1040		PRT	<i>Oryza sativa</i>	Orthologous to G1660
1041		PRT	<i>Oryza sativa</i>	Orthologous to G1660
1042		PRT	<i>Oryza sativa</i>	Orthologous to G1660
1043		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1660
1044		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1660
1045		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1660
1046		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1660
1047		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1660
1048		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1730
1049		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1753
1050		PRT	<i>Oryza sativa</i>	Orthologous to G1753
1051		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1779
1052		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1779
1053		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1779
1054		PRT	<i>Oryza sativa</i>	Orthologous to G1779
1055		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1779
1056		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1796
1057		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1816, G2718
1058		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1816, G2718
1059		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1816, G2718
1060		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1816, G2718
1061		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1816, G2718
1062		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1816
1063		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1816, G2718
1064		PRT	<i>Oryza sativa</i>	Orthologous to G1816, G2718
1065		PRT	<i>Oryza sativa</i>	Orthologous to G1816, G2718
1066		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1816, G2718

1067		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1816, G2718
1068		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1893
1069		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1893
1070		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1893
1071		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1893
1072		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1893
1073		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1893
1074		PRT	<i>Oryza sativa</i>	Orthologous to G1893
1075		PRT	<i>Oryza sativa</i>	Orthologous to G1893
1076		PRT	<i>Oryza sativa</i>	Orthologous to G1893
1077		PRT	<i>Oryza sativa</i>	Orthologous to G1893
1078		PRT	<i>Oryza sativa</i>	Orthologous to G1893
1079		PRT	<i>Oryza sativa</i>	Orthologous to G1893
1080		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1893
1081		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1893
1082		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1928
1083		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1928
1084		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1928
1085		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1928
1086		PRT	<i>Oryza sativa</i>	Orthologous to G1928
1087		PRT	<i>Oryza sativa</i>	Orthologous to G1928
1088		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1928
1089		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1928
1090		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1968
1091		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1968
1092		PRT	<i>Oryza sativa</i>	Orthologous to G1968
1093		PRT	<i>Oryza sativa</i>	Orthologous to G1968
1094		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1983
1095		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1983
1096		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1983
1097		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1985
1098		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1988
1099		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1988
1100		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1988
1101		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1988
1102		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1988
1103		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1988
1104		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1988
1105		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2041
1106		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2041
1107		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2041
1108		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2085
1109		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2085
1110		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2085
1111		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2085
1112		PRT	<i>Oryza sativa</i>	Orthologous to G2085
1113		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2085
1114		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2109
1115		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2109
1116		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2142
1117		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2142
1118		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2142
1119		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2142
1120		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2142
1121		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2142
1122		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2142

1123		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2142
1124		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2142
1125		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2239
1126		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2239
1127		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2239
1128		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2239
1129		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2239
1130		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2239
1131		PRT	<i>Oryza sativa</i>	Orthologous to G2239
1132		PRT	<i>Oryza sativa</i>	Orthologous to G2239
1133		PRT	<i>Oryza sativa</i>	Orthologous to G2239
1134		PRT	<i>Oryza sativa</i>	Orthologous to G2239
1135		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2239
1136		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2239
1137		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2317
1138		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2317
1139		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2319
1140		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2319
1141		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2319
1142		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2319
1143		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2432
1144		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2432
1145		PRT	<i>Oryza sativa</i>	Orthologous to G2432
1146		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2453
1147		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2457, G2459
1148		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2457, G2459
1149		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2457, G2459
1150		PRT	<i>Oryza sativa</i>	Orthologous to G2457, G2459
1151		PRT	<i>Oryza sativa</i>	Orthologous to G2457, G2459
1152		PRT	<i>Oryza sativa</i>	Orthologous to G2457, G2459
1153		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2457, G2459
1154		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2457
1155		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2457
1156		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2457
1157		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2457
1158		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2459
1159		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2459
1160		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2459
1161		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2505
1162		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2505
1163		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2536
1164		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2536
1165		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2536
1166		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2536
1167		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2536
1168		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2536
1169		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2536
1170		PRT	<i>Oryza sativa</i>	Orthologous to G2536
1171		PRT	<i>Oryza sativa</i>	Orthologous to G2536
1172		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2536
1173		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2550
1174		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2550
1175		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2550

1176		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2567
1177		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2567
1178		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2567
1179		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2567
1180		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2567
1181		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2567
1182		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2567
1183		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2567
1184		PRT	<i>Oryza sativa</i>	Orthologous to G2567
1185		PRT	<i>Oryza sativa</i>	Orthologous to G2567
1186		PRT	<i>Oryza sativa</i>	Orthologous to G2567
1187		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2567
1188		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2567
1189		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2567
1190		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2567
1191		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2567
1192		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2571
1193		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2571
1194		PRT	<i>Oryza sativa</i>	Orthologous to G2571
1195		PRT	<i>Oryza sativa</i>	Orthologous to G2579
1196		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2579
1197		PRT	<i>Oryza sativa</i>	Orthologous to G2585
1198		PRT	<i>Oryza sativa</i>	Orthologous to G2585
1199		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2585
1200		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2617
1201		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2650
1202		PRT	<i>Oryza sativa</i>	Orthologous to G2650
1203		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2650
1204		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2650
1205		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2650
1206		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2650
1207		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2650
1208		PRT	<i>Oryza sativa</i>	Orthologous to G2661
1209		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2717
1210		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2717
1211		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2717
1212		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2717
1213		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2717
1214		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2717
1215		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2717
1216		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2717
1217		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2717
1218		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2717
1219		PRT	<i>Oryza sativa</i>	Orthologous to G2717
1220		PRT	<i>Oryza sativa</i>	Orthologous to G2717
1221		PRT	<i>Oryza sativa</i>	Orthologous to G2717
1222		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2717
1223		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2717
1224		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2717
1225		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2717
1226		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2717
1227		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2717
1228		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2723
1229		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2741
1230		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2741
1231		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2741
1232		PRT	<i>Oryza sativa</i>	Orthologous to G2741

1233		PRT	<i>Oryza sativa</i>	Orthologous to G2741
1234		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2741
1235		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2741
1236		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2741
1237		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2754
1238		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2754
1239		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2754
1240		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2754
1241		PRT	<i>Oryza sativa</i>	Orthologous to G2754
1242		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2754
1243		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2754
1244		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2768
1245		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2768
1246		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2768
1247		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2768
1248		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2768
1249		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2768
1250		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2768
1251		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2768
1252		PRT	<i>Oryza sativa</i>	Orthologous to G2768
1253		PRT	<i>Oryza sativa</i>	Orthologous to G2768
1254		PRT	<i>Oryza sativa</i>	Orthologous to G2768
1255		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2768
1256		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2768
1257		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2768
1258		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2768
1259		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2768
1260		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2768
1261		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2768
1262		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2776
1263		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2776
1264		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2776
1265		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2776
1266		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2776
1267		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2776
1268		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2776
1269		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2776
1270		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2776
1271		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2776
1272		PRT	<i>Oryza sativa</i>	Orthologous to G2776
1273		PRT	<i>Oryza sativa</i>	Orthologous to G2776
1274		PRT	<i>Oryza sativa</i>	Orthologous to G2776
1275		PRT	<i>Oryza sativa</i>	Orthologous to G2776
1276		PRT	<i>Oryza sativa</i>	Orthologous to G2776
1277		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2776
1278		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2776
1279		PRT	<i>Oryza sativa</i>	Orthologous to G2826, G2838
1280		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2830
1281		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2839
1282		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2839
1283		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2839
1284		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2839
1285		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2839
1286		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2839
1287		PRT	<i>Oryza sativa</i>	Orthologous to G2839
1288		PRT	<i>Oryza sativa</i>	Orthologous to G2839
1289		PRT	<i>Oryza sativa</i>	Orthologous to G2839

1290		PRT	<i>Oryza sativa</i>	Orthologous to G2839
1291		PRT	<i>Oryza sativa</i>	Orthologous to G2839
1292		PRT	<i>Oryza sativa</i>	Orthologous to G2839
1293		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2839
1294		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2839
1295		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2839
1296		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2839
1297		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2839
1298		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2839
1299		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2839
1300		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2854
1301		PRT	<i>Oryza sativa</i>	Orthologous to G2854
1302		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2854
1303		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2859
1304		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2865
1305		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2865
1306		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2885
1307		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2907
1308		PRT	<i>Oryza sativa</i>	Orthologous to G2907
1309		PRT	<i>Oryza sativa</i>	Orthologous to G2907
1310		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2907
1311		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2907
1312		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2913
1313		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2913
1314		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2933
1315		PRT	<i>Oryza sativa</i>	Orthologous to G2933
1316		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2933
1317		PRT	<i>Oryza sativa</i>	Orthologous to G2969
1318		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2981, G2982
1319		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2981, G2982
1320		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2981, G2982
1321		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2981, G2982
1322		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2981, G2982
1323		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2981, G2982
1324		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2981
1325		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2981, G2982
1326		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2981, G2982
1327		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2981, G2982
1328		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2983
1329		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2983
1330		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2983
1331		PRT	<i>Oryza sativa</i>	Orthologous to G2983
1332		PRT	<i>Oryza sativa</i>	Orthologous to G2983
1333		PRT	<i>Oryza sativa</i>	Orthologous to G2983
1334		PRT	<i>Oryza sativa</i>	Orthologous to G2990
1335		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2990
1336		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G2990
1337		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G3055
1338		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G3055

1339		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G3055
1340		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G3055
1341		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G3055
1342		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G3055
1343		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G3055
1344		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G3055
1345		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G3055
1346		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G3083
1347		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G3086
1348		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G3086
1349	G24	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G12
1350	G24	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G12
1351	G29	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G46
1352	G29	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G46
1353	G30	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1792
1354	G30	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1792
1355	G43	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G46
1356	G43	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G46
1357	G131	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G155
1358	G131	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G155
1359	G135	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G155
1360	G135	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G155
1361	G142	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G148
1362	G142	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G148
1363	G149	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G627
1364	G149	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G627
1365	G152	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G153
1366	G152	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G153
1367	G154	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1011
1368	G154	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1011
1369	G184	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G916
1370	G184	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G916
1371	G186	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G916
1372	G186	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G916
1373	G204	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2717
1374	G204	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2717
1375	G225	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1816, G2718
1376	G225	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1816, G2718
1377	G226	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1816, G2718
1378	G226	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1816, G2718
1379	G353	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2839
1380	G353	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2839
1381	G354	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2839
1382	G354	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2839
1383	G361	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G370, G1995, G2826, G2838
1384	G361	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G370, G1995, G2826, G2838
1385	G362	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G370, G1995, G2826, G2838
1386	G362	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G370, G1995, G2826, G2838
1387	G370	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1995, G2826, G2838
1388	G370	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1995, G2826, G2838
1389	G390	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G438
1390	G390	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G438

1391	G391	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G438
1392	G391	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G438
1393	G392	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G438
1394	G392	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G438
1395	G481	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G485
1396	G481	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G485
1397	G482	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G485
1398	G482	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G485
1399	G511	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2536
1400	G511	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2536
1401	G512	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1357, G1452
1402	G512	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1357, G1452
1403	G600	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2768
1404	G600	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2768
1405	G617	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2650
1406	G617	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2650
1407	G682	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1816, G2718
1408	G682	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1816, G2718
1409	G722	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1037
1410	G722	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1037
1411	G736	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2432
1412	G736	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2432
1413	G759	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1412
1414	G759	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1412
1415	G773	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1412
1416	G773	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1412
1417	G810	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G807
1418	G810	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G807
1419	G860	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G153
1420	G860	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G153
1421	G957	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G961
1422	G957	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G961
1423	G990	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1451
1424	G990	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1451
1425	G1004	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G46
1426	G1004	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G46
1427	G1017	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2567
1428	G1017	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2567
1429	G1196	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G839
1430	G1196	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G839
1431	G1207	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1206
1432	G1207	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1206
1433	G1325	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1313
1434	G1325	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1313
1435	G1335	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G652
1436	G1335	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G652
1437	G1357	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1452
1438	G1357	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1452
1439	G1364	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G485
1440	G1364	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G485
1441	G1379	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G12
1442	G1379	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G12
1443	G1387	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G975
1444	G1387	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G975
1445	G1399	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1128

1446	G1399	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1128
1447	G1419	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G46
1448	G1419	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G46
1449	G1435	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2741
1450	G1435	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2741
1451	G1452	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1357
1452	G1452	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1357
1453	G1548	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G438
1454	G1548	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G438
1455	G1652	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2776
1456	G1652	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2776
1457	G1749	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1840
1458	G1749	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1840
1459	G1760	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G153
1460	G1760	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G153
1461	G1791	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G30, G1792
1462	G1791	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G30, G1792
1463	G1792	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G30
1464	G1792	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G30
1465	G1795	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G30, G1792
1466	G1795	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G30, G1792
1467	G1797	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1798
1468	G1797	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1798
1469	G1798	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1797
1470	G1798	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1797
1471	G1816	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2718
1472	G1816	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2718
1473	G1839	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1840
1474	G1839	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1840
1475	G1863	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2334
1476	G1863	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2334
1477	G1888	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1482
1478	G1888	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1482
1479	G1889	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2839
1480	G1889	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2839
1481	G1914	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G651
1482	G1914	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G651
1483	G1940	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2854
1484	G1940	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2854
1485	G1973	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G651
1486	G1973	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G651
1487	G1974	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2839
1488	G1974	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2839
1489	G1976	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1893
1490	G1976	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1893
1491	G1994	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G355
1492	G1994	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G355
1493	G1995	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G370, G2826, G2838
1494	G1995	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G370, G2826, G2838
1495	G2133	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G47
1496	G2133	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G47
1497	G2199	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2207
1498	G2199	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2207
1499	G2334	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1863

1500	G2334	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1863
1501	G2345	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G485
1502	G2345	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G485
1503	G2457	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2459
1504	G2457	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2459
1505	G2459	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2457
1506	G2459	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2457
1507	G2535	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G961
1508	G2535	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G961
1509	G2546	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2550
1510	G2546	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2550
1511	G2562	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2830
1512	G2562	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2830
1513	G2563	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2830
1514	G2563	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2830
1515	G2583	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G975
1516	G2583	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G975
1517	G2632	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G926
1518	G2632	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G926
1519	G2635	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2505
1520	G2635	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2505
1521	G2659	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1142
1522	G2659	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1142
1523	G2664	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1928
1524	G2664	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1928
1525	G2709	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2717
1526	G2709	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2717
1527	G2718	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G1816
1528	G2718	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G1816
1529	G2779	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2859
1530	G2779	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2859
1531	G2826	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G370, G1995, G2838
1532	G2826	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G370, G1995, G2838
1533	G2828	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2830
1534	G2828	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2830
1535	G2838	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G370, G1995, G2826
1536	G2838	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G370, G1995, G2826
1537	G2882	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2041
1538	G2882	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2041
1539	G2928	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2933
1540	G2928	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2933
1541	G2932	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2933
1542	G2932	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2933
1543	G2934	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2865
1544	G2934	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2865
1545	G2966	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G3067
1546	G2966	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G3067
1547	G2980	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2979
1548	G2980	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2979
1549	G2981	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2982
1550	G2981	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2982
1551	G2982	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2981
1552	G2982	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2981
1553	G2989	DNA	<i>Arabidopsis thaliana</i>	Predicted polypeptide sequence is paralogous to G2990
1554	G2989	PRT	<i>Arabidopsis thaliana</i>	Paralogous to G2990

[illegible]

1612		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2567
1613		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2650
1614		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2717
1615		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2754
1616		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2826
1617		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2839
1618		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2854
1619		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2854
1620		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2907
1621		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2907
1622		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2907
1623		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2913
1624		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2933
1625		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2969
1626		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2981
1627		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2983
1628		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2990
1629		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2992
1630		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G3076
1631		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G3083
1632		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G12
1633		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G30, G1792
1634		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G153
1635		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G155
1636		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G355
1637		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G370
1638		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G438
1639		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G438
1640		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G438
1641		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G485
1642		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G624
1643		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G652
1644		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G652
1645		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G652
1646		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G839
1647		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G839
1648		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G916
1649		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G916
1650		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G961
1651		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1011
1652		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1037
1653		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1128
1654		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1206
1655		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1206
1656		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1206
1657		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1412
1658		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1451
1659		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1451
1660		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1468
1661		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1468
1662		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1510
1663		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1816, G2718
1664		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1893
1665		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1928
1666		DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G2142

350

[illegible]

[illegible]

353

[illegible]

[illegible]

[illegible]

2059		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2459
2060		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2536
2061		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2536
2062		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2567
2063		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2567
2064		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2567
2065		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2571
2066		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2650
2067		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2650
2068		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2717
2069		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2717
2070		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2741
2071		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2741
2072		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2768
2073		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2768
2074		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2768
2075		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2776
2076		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2776
2077		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2784
2078		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2839
2079		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2854
2080		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2854
2081		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2854
2082		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2854
2083		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2854
2084		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2854
2085		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2859
2086		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2865
2087		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2865
2088		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2885
2089		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2907
2090		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2933
2091		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2969
2092		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2979
2093		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2981, G2982
2094		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2983
2095		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2990
2096		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G2990
2097		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G3055
2098		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G3067
2099		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G3067
2100		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G3076
2101		DNA	<i>Lycopersicon esculentum</i>	Predicted polypeptide sequence is orthologous to G3083
2102	G131 1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P15154 (sequence variant)
2103	G324 1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P3299 (sequence variant)
2104	G386 1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P15647 (sequence variant)
2105	G624 1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P2461.7 (sequence variant)
2106	G651 1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P2812 (sequence variant)
2107	G744 1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P15010 (sequence variant)
2108	G1037 1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P15001 (sequence variant)
2109	G1150 1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P15631 (sequence variant)
2110	G2041 1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P13846 (sequence variant)
2111	G2106 1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P13733 (sequence variant)
2112	G2319 1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P13388 (sequence variant)
2113	G2453 1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P2750 (sequence variant)
2114	G2453 2	DNA	<i>Arabidopsis thaliana</i>	Expression construct P3322 (sequence variant)

2115	G2559	1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P15538 (sequence variant)
2116	G2639	1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P15568 (sequence variant)
2117	G2679	1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P15056 (sequence variant)
2118	G2768	1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P15431 (sequence variant)
2119	G2771	1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P15182 (sequence variant)
2120	G2784	1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P15148 (sequence variant)
2121	G2802	1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P2771 (sequence variant)
2122	G2907	1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P15595 (sequence variant)
2123	G3003	1	DNA	<i>Arabidopsis thaliana</i>	Expression construct P3291 (sequence variant)
2124	G3380		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1795 Member of G1792 clade
2125	G3380		PRT	<i>Oryza sativa</i>	Orthologous to G1795 Member of G1792 clade
2126	G3381		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G30 Member of G1792 clade
2127	G3381		PRT	<i>Oryza sativa</i>	Orthologous to G30 Member of G1792 clade
2128	G3383		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G1792 Member of G1792 clade
2129	G3383		PRT	<i>Oryza sativa</i>	Orthologous to G1792 Member of G1792 clade
2130	G3392		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G682 Member of G1816 and G2718 clade
2131	G3392		PRT	<i>Oryza sativa</i>	Orthologous to G682 Member of G1816 and G2718 clade
2132	G3393		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G682 Member of G1816 and G2718 clade
2133	G3393		PRT	<i>Oryza sativa</i>	Orthologous to G682 Member of G1816 and G2718 clade
2134	G3394		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G485 Member of G485 clade
2135	G3394		PRT	<i>Oryza sativa</i>	Orthologous to G485 Member of G485 clade
2136	G3395		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G485 Member of G485 clade
2137	G3395		PRT	<i>Oryza sativa</i>	Orthologous to G485 Member of G485 clade
2138	G3396		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G485 Member of G485 clade
2139	G3396		PRT	<i>Oryza sativa</i>	Orthologous to G485 Member of G485 clade
2140	G3397		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G485 Member of G485 clade
2141	G3397		PRT	<i>Oryza sativa</i>	Orthologous to G485 Member of G485 clade
2142	G3398		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G485 Member of G485 clade
2143	G3398		PRT	<i>Oryza sativa</i>	Orthologous to G485 Member of G485 clade
2144	G3429		DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G485 Member of G485 clade
2145	G3429		PRT	<i>Oryza sativa</i>	Orthologous to G485 Member of G485 clade
2146	G3431		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G682 Member of G1816 and G2718 clade
2147	G3431		PRT	<i>Zea mays</i>	Orthologous to G682 Member of G1816 and G2718 clade
2148	G3434		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G485 Member of G485 clade
2149	G3434		PRT	<i>Zea mays</i>	Orthologous to G485 Member of G485 clade
2150	G3435		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G482 Member of G485 clade
2151	G3435		PRT	<i>Zea mays</i>	Orthologous to G482 Member of G485 clade
2152	G3436		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G485 Member of G485 clade
2153	G3436		PRT	<i>Zea mays</i>	Orthologous to G485 Member of G485 clade
2154	G3437		DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G485

				Member of G485 clade
2155	G3437	PRT	<i>Zea mays</i>	Orthologous to G485 Member of G485 clade
2156	G3444	DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G682 Member of G1816 and G2718 clade
2157	G3444	PRT	<i>Zea mays</i>	Orthologous to G682 Member of G1816 and G2718 clade
2158	G3445	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G225 Member of G1816 and G2718 clade
2159	G3445	PRT	<i>Glycine max</i>	Orthologous to G225 Member of G1816 and G2718 clade
2160	G3446	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G225 Member of G1816 and G2718 clade
2161	G3446	PRT	<i>Glycine max</i>	Orthologous to G225 Member of G1816 and G2718 clade
2162	G3447	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G225 Member of G1816 and G2718 clade
2163	G3447	PRT	<i>Glycine max</i>	Orthologous to G225 Member of G1816 and G2718 clade
2164	G3448	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G225 Member of G1816 and G2718 clade
2165	G3448	PRT	<i>Glycine max</i>	Orthologous to G225 Member of G1816 and G2718 clade
2166	G3449	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G225 Member of G1816 and G2718 clade
2167	G3449	PRT	<i>Glycine max</i>	Orthologous to G225 Member of G1816 and G2718 clade
2168	G3450	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G682 Member of G1816 and G2718 clade
2169	G3450	PRT	<i>Glycine max</i>	Orthologous to G682 Member of G1816 and G2718 clade
2170	G3470	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G482 Member of G485 clade
2171	G3470	PRT	<i>Glycine max</i>	Orthologous to G482 Member of G485 clade
2172	G3471	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G482 Member of G485 clade
2173	G3471	PRT	<i>Glycine max</i>	Orthologous to G482 Member of G485 clade
2174	G3472	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G485 Member of G485 clade
2175	G3472	PRT	<i>Glycine max</i>	Orthologous to G485 Member of G485 clade
2176	G3473	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G485 Member of G485 clade
2177	G3473	PRT	<i>Glycine max</i>	Orthologous to G485 Member of G485 clade
2178	G3474	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G485 Member of G485 clade
2179	G3474	PRT	<i>Glycine max</i>	Orthologous to G485 Member of G485 clade
2180	G3475	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G485 Member of G485 clade
2181	G3475	PRT	<i>Glycine max</i>	Orthologous to G485 Member of G485 clade
2182	G3476	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G482 Member of G485 clade
2183	G3476	PRT	<i>Glycine max</i>	Orthologous to G485 Member of G482 clade
2184	G3477	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G482 Member of G485 clade
2185	G3477	PRT	<i>Glycine max</i>	Orthologous to G485 Member of G482 clade
2186	G3478	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G485 Member of G485 clade
2187	G3478	PRT	<i>Glycine max</i>	Orthologous to G485 Member of G485 clade
2188	G3479	DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G153 Member of G153 clade

2189	G3479	PRT	<i>Oryza sativa</i>	Orthologous to G153 Member of G153 clade
2190	G3484	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G153 Member of G153 clade
2191	G3484	PRT	<i>Glycine max</i>	Orthologous to G153 Member of G153 clade
2192	G3485	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G153 Member of G153 clade
2193	G3485	PRT	<i>Glycine max</i>	Orthologous to G153 Member of G153 clade
2194	G3487	DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G153 Member of G153 clade
2195	G3487	PRT	<i>Zea mays</i>	Orthologous to G153 Member of G153 clade
2196	G3488	DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G153 Member of G153 clade
2197	G3488	PRT	<i>Zea mays</i>	Orthologous to G153 Member of G153 clade
2198	G3489	DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G153 Member of G153 clade
2199	G3489	PRT	<i>Zea mays</i>	Orthologous to G153 Member of G153 clade
2200	G3491	DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G807 Member of G807 clade
2201	G3491	PRT	<i>Oryza sativa</i>	Orthologous to G807 Member of G807 clade
2202	G3494	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G807 Member of G807 clade
2203	G3494	PRT	<i>Glycine max</i>	Orthologous to G807 Member of G807 clade
2204	G3495	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G807 Member of G807 clade
2205	G3495	PRT	<i>Glycine max</i>	Orthologous to G807 Member of G807 clade
2206	G3512	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G807 Member of G807 clade
2207	G3512	PRT	<i>Glycine max</i>	Orthologous to G807 Member of G807 clade
2208	G3515	DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G30 Member of G1792 clade
2209	G3515	PRT	<i>Oryza sativa</i>	Orthologous to G30 Member of G1792 clade
2210	G3516	DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1792 Member of G1792 clade
2211	G3516	PRT	<i>Zea mays</i>	Orthologous to G1792 Member of G1792 clade
2212	G3517	DNA	<i>Zea mays</i>	Predicted polypeptide sequence is orthologous to G1791 Member of G1792 clade
2213	G3517	PRT	<i>Zea mays</i>	Orthologous to G1791 Member of G1792 clade
2214	G3518	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1792 Member of G1792 clade
2215	G3518	PRT	<i>Glycine max</i>	Orthologous to G1792 Member of G1792 clade
2216	G3519	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1792 Member of G1792 clade
2217	G3519	PRT	<i>Glycine max</i>	Orthologous to G1792 Member of G1792 clade
2218	G3520	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G1792 Member of G1792 clade
2219	G3520	PRT	<i>Glycine max</i>	Orthologous to G1792 Member of G1792 clade
2220	G3527	DNA	<i>Glycine max</i>	
2221	G3527	PRT	<i>Glycine max</i>	
2222	G3528	DNA	<i>Glycine max</i>	
2223	G3528	PRT	<i>Glycine max</i>	
2224	G3643	DNA	<i>Glycine max</i>	Predicted polypeptide sequence is orthologous to G47 Member of G47 and G2133 clade
2225	G3643	PRT	<i>Glycine max</i>	Orthologous to G47 Member of G47 and G2133 clade
2226	G3644	DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G47 Member of G47 and G2133 clade
2227	G3644	PRT	<i>Oryza sativa</i>	Orthologous to G47 Member of G47 and G2133 clade
2228	G3645	DNA	<i>Brassica rapa</i>	Predicted polypeptide sequence is orthologous to G47 Member of G47 and G2133 clade

2229	G3645	PRT	<i>Brassica rapa</i>	Orthologous to G47 Member of G47 and G2133 clade
2230	G3646	DNA	<i>Brassica oleracea</i>	Predicted polypeptide sequence is orthologous to G2133 Member of G47 and G2133 clade
2231	G3646	PRT	<i>Brassica oleracea</i>	Orthologous to G2133 Member of G47 and G2133 clade
2232	G3647	DNA	<i>Zinnia elegans</i>	Predicted polypeptide sequence is orthologous to G47 Member of G47 and G2133 clade
2233	G3647	PRT	<i>Zinnia elegans</i>	Orthologous to G47 Member of G47 and G2133 clade
2234	G3649	DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G47 and G2133 Member of G47 and G2133 clade
2235	G3649	PRT	<i>Oryza sativa</i>	Orthologous to G47 and G2133 Member of G47 and G2133 clade
2236	G3651	DNA	<i>Oryza sativa</i>	Predicted polypeptide sequence is orthologous to G2133 Member of G47 and G2133 clade
2237	G3651	PRT	<i>Oryza sativa</i>	Orthologous to G2133 Member of G47 and G2133 clade

EXAMPLES

The invention, now being generally described, will be more readily understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. It will be recognized by one of skill in the art that a transcription factor that is associated with a particular first trait may also be associated with at least one other, unrelated and inherent second trait which was not predicted by the first trait.

The complete descriptions of the traits associated with each polynucleotide of the invention are fully disclosed in Table 4 and Table 6. The complete description of the transcription factor gene family and identified conserved domains of the polypeptide encoded by the polynucleotide is fully disclosed in Table 5.

Example I: Full Length Gene Identification and Cloning

Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of -4 or -5 or lower, depending on the length of the query sequence. Putative transcription factor sequence hits were then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

Alternatively, *Arabidopsis thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60°C) and labeled with ^{32}P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim Corp. (now Roche Diagnostics Corp., Indianapolis, IN). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M NaPO_4 pH

7.0, 7% SDS, 1% w/v bovine serum albumin) and hybridized overnight at 60°C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSSC, 1% SDS at 60° C.

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the MARATHON cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded cDNA, blunting cDNA ends, followed by ligation of the MARATHON Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA.

Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained, sequenced and cloned. The process can be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

Example II: Construction of Expression Vectors

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20 or pMEN65, which are both derived from pMON316 (Sanders et al. (1987) *Nucleic Acids Res.* 15:1543-1558) and contain the CaMV 35S promoter to express transgenes. To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with SalI and NotI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a QIAQUICK gel extraction kit (Qiagen, Valencia CA). The fragments of interest were ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, Beverly MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma Chemical Co. St. Louis MO). Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini Prep kits (Qiagen).

Example III: Transformation of *Agrobacterium* with the Expression Vector

After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. (1990) *FEMS Microbiol Letts.* 67: 325-328. *Agrobacterium* strain ABI was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance over 1 cm at 600 nm (A_{600}) of 0.5 – 1.0 was reached. Cells were harvested by

centrifugation at 4,000 x g for 15 min at 4° C. Cells were then resuspended in 250 µl chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 µl chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 µl and 750 µl, respectively. Resuspended
5 cells were then distributed into 40 µl aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

Agrobacterium cells were transformed with plasmids prepared as described above following the protocol described by Nagel et al. (*supra*). For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 µl of
10 *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 µF and 200 µF using a Gene Pulser II apparatus (Bio-Rad, Hercules, CA). After electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100 µg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh
15 medium. The presence of the plasmid construct was verified by PCR amplification and sequence analysis.

Example IV: Transformation of *Arabidopsis* Plants with *Agrobacterium tumefaciens* with Expression Vector

20 After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an optical absorbance at 600 nm wavelength over 1 cm (A_{600}) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and
25 resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 µM benzylamino purine (Sigma), 200 µl/l Silwet L-77 (Lehle Seeds) until an A_{600} of 0.8 was reached.

Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with
30 fiberglass mesh (18 mm X 16 mm). Plants were grown under continuous illumination (50-75 µE/m²/sec) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium
35 as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The

immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

Example V: Identification of *Arabidopsis* Primary Transformants

5 Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile water and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (CLOROX; Clorox Corp. Oakland
10 CA) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled water. The seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH), 1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under
15 continuous illumination (50-75 $\mu\text{E}/\text{m}^2/\text{sec}$) at 22-23° C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T1 generation) were visible and obtained. These seedlings were transferred first to fresh selection plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

 Primary transformants were crossed and progeny seeds (T₂) collected; kanamycin resistant
20 seedlings were selected and analyzed. The expression levels of the recombinant polynucleotides in the transformants varies from about a 5% expression level increase to a least a 100% expression level increase. Similar observations are made with respect to polypeptide level expression.

Example VI: Identification of *Arabidopsis* Plants with Transcription Factor Gene Knockouts

25 The screening of insertion mutagenized *Arabidopsis* collections for null mutants in a known target gene was essentially as described in Krysan et al. (1999) *Plant Cell* 11: 2283-2290. Briefly, gene-specific primers, nested by 5-250 base pairs to each other, were designed from the 5' and 3' regions of a known target gene. Similarly, nested sets of primers were also created specific to each of the T-DNA or transposon ends (the "right" and "left" borders). All possible combinations of gene specific and T-
30 DNA/transposon primers were used to detect by PCR an insertion event within or close to the target gene. The amplified DNA fragments were then sequenced which allows the precise determination of the T-DNA/transposon insertion point relative to the target gene. Insertion events within the coding or intervening sequence of the genes were deconvoluted from a pool comprising a plurality of insertion events to a single unique mutant plant for functional characterization. The method is described in more
35 detail in Yu and Adam, US Application Serial No. 09/177,733 filed October 23, 1998.

Example VII: Identification of Modified Phenotypes in Overexpression or Gene Knockout Plants.

Experiments were performed to identify those transformants or knockouts that exhibited modified biochemical characteristics. Among the biochemicals that were assayed were insoluble sugars, such as arabinose, fucose, galactose, mannose, rhamnose or xylose or the like; prenyl lipids, such as lutein, beta-carotene, xanthophyll-1, xanthophyll-2, chlorophylls A or B, or alpha-, delta- or gamma-tocopherol or the like; fatty acids, such as 16:0 (palmitic acid), 16:1 (palmitoleic acid), 18:0 (stearic acid), 18:1 (oleic acid), 18:2 (linoleic acid), 20:0, 18:3 (linolenic acid), 20:1 (eicosenoic acid), 20:2, 22:1 (erucic acid) or the like; waxes, such as by altering the levels of C29, C31, or C33 alkanes; sterols, such as brassicasterol, campesterol, stigmasterol, sitosterol or stigmastanol or the like, glucosinolates, protein or oil levels.

Fatty acids were measured using two methods depending on whether the tissue was from leaves or seeds. For leaves, lipids were extracted and esterified with hot methanolic H_2SO_4 and partitioned into hexane from methanolic brine. For seed fatty acids, seeds were pulverized and extracted in methanol:heptane:toluene:2,2-dimethoxypropane: H_2SO_4 (39:34:20:5:2) for 90 minutes at 80°C. After cooling to room temperature the upper phase, containing the seed fatty acid esters, was subjected to GC analysis. Fatty acid esters from both seed and leaf tissues were analyzed with a SUPELCO SP-2330 column (Supelco, Bellefonte, PA).

Glucosinolates were purified from seeds or leaves by first heating the tissue at 95°C for 10 minutes. Preheated ethanol:water (50:50) is added and after heating at 95°C for a further 10 minutes, the extraction solvent is applied to a DEAE SEPHADEX column (Pharmacia) which had been previously equilibrated with 0.5 M pyridine acetate. Desulfoglucosinolates were eluted with 300 μl water and analyzed by reverse phase HPLC monitoring at 226 nm.

For wax alkanes, samples were extracted using an identical method as fatty acids and extracts were analyzed on a HP 5890 GC coupled with a 5973 MSD. Samples were chromatographically isolated on a J&W DB35 mass spectrometer (J&W Scientific Agilent Technologies, Folsom, CA).

To measure prenyl lipid levels, seeds or leaves were pulverized with 1 to 2% pyrogallol as an antioxidant. For seeds, extracted samples were filtered and a portion removed for tocopherol and carotenoid/chlorophyll analysis by HPLC. The remaining material was saponified for sterol determination. For leaves, an aliquot was removed and diluted with methanol and chlorophyll A, chlorophyll B, and total carotenoids measured by spectrophotometry by determining optical absorbance at 665.2 nm, 652.5 nm, and 470 nm. An aliquot was removed for tocopherol and carotenoid/chlorophyll composition by HPLC using a Waters $\mu\text{Bondapak}$ C18 column (4.6 mm x 150 mm). The remaining methanolic solution was saponified with 10% KOH at 80°C for one hour. The samples were cooled and diluted with a mixture of methanol and water. A solution of 2% methylene chloride in hexane was mixed in and the samples were centrifuged. The aqueous methanol phase was again re-extracted 2% methylene chloride in hexane and, after centrifugation, the two upper phases were combined and evaporated. 2% methylene chloride in hexane was added to the tubes and the samples were then extracted with one ml of

water. The upper phase was removed, dried, and resuspended in 400 μ l of 2% methylene chloride in hexane and analyzed by gas chromatography using a 50 m DB-5ms (0.25 mm ID, 0.25 μ m phase, J&W Scientific).

Insoluble sugar levels were measured by the method essentially described by Reiter et al. (1999),
5 *Plant J.* 12: 335-345. This method analyzes the neutral sugar composition of cell wall polymers found in *Arabidopsis* leaves. Soluble sugars were separated from sugar polymers by extracting leaves with hot 70% ethanol. The remaining residue containing the insoluble polysaccharides was then acid hydrolyzed with allose added as an internal standard. Sugar monomers generated by the hydrolysis were then
10 reduced to the corresponding alditols by treatment with NaBH₄, then were acetylated to generate the volatile alditol acetates which were then analyzed by GC-FID. Identity of the peaks was determined by comparing the retention times of known sugars converted to the corresponding alditol acetates with the retention times of peaks from wild-type plant extracts. Alditol acetates were analyzed on a Supelco SP-2330 capillary column (30 m x 250 μ m x 0.2 μ m) using a temperature program beginning at 180° C for 2 minutes followed by an increase to 220° C in 4 minutes. After holding at 220° C for 10 minutes, the oven
15 temperature is increased to 240° C in 2 minutes and held at this temperature for 10 minutes and brought back to room temperature.

To identify plants with alterations in total seed oil or protein content, 150mg of seeds from T2 progeny plants were subjected to analysis by Near Infrared Reflectance Spectroscopy (NIRS) using a
20 Foss NirSystems Model 6500 with a spinning cup transport system. NIRS is a non-destructive analytical method used to determine seed oil and protein composition. Infrared is the region of the electromagnetic spectrum located after the visible region in the direction of longer wavelengths. 'Near infrared' owns its name for being the infrared region near to the visible region of the electromagnetic spectrum. For practical purposes, near infrared comprises wavelengths between 800 and 2500 nm. NIRS is applied to
25 organic compounds rich in O-H bonds (such as moisture, carbohydrates, and fats), C-H bonds (such as organic compounds and petroleum derivatives), and N-H bonds (such as proteins and amino acids). The NIRS analytical instruments operate by statistically correlating NIRS signals at several wavelengths with the characteristic or property intended to be measured. All biological substances contain thousands of C-H, O-H, and N-H bonds. Therefore, the exposure to near infrared radiation of a biological sample, such as a seed, results in a complex spectrum which contains qualitative and quantitative information about the
30 physical and chemical composition of that sample.

The numerical value of a specific analyte in the sample, such as protein content or oil content, is mediated by a calibration approach known as chemometrics. Chemometrics applies statistical methods such as multiple linear regression (MLR), partial least squares (PLS), and principle component analysis (PCA) to the spectral data and correlates them with a physical property or other factor, that property or
35 factor is directly determined rather than the analyte concentration itself. The method first provides "wet chemistry" data of the samples required to develop the calibration.

Calibration of NIRS response was performed using data obtained by wet chemical analysis of a population of *Arabidopsis* ecotypes that were expected to represent diversity of oil and protein levels.

The exact oil composition of each ecotype used in the calibration experiment was performed using gravimetric analysis of oils extracted from seed samples (0.5 g or 1.0 g) by the accelerated solvent extraction method (ASE; Dionex Corp, Sunnyvale, CA). The extraction method was validated against certified canola samples (Community Bureau of Reference, Belgium). Seed samples from each ecotype (0.5 g or 1g) were subjected to accelerated solvent extraction and the resulting extracted oil weights compared to the weight of oil recovered from canola seed that has been certified for oil content (Community Bureau of Reference). The oil calibration equation was based on 57 samples with a range of oil contents from 27.0 % to 50.8 %. To check the validity of the calibration curve, an additional set of samples was extracted by ASE and predicted using the oil calibration equation. This validation set counted 46 samples, ranging from 27.9 % to 47.5 % oil, and had a predicted standard error of performance of 0.63 %. The wet chemical method for protein was elemental analysis (%N X 6.0) using the average of 3 representative samples of 5 mg each validated against certified ground corn (NIST). The instrumentation was an Elementar Vario-EL III elemental analyzer operated in CNS operating mode (Elementar Analysensysteme GmbH, Hanau, Germany).

The protein calibration equation was based on a library of 63 samples with a range of protein contents from 17.4 % to 31.2 %. An additional set of samples was analyzed for protein by elemental analysis (n = 57) and scanned by NIRS in order to validate the protein prediction equation. The protein range of the validation set was from 16.8 % to 31.2 % and the standard error of prediction was 0.468 %.

NIRS analysis of *Arabidopsis* seed was carried out on between 40-300 mg experimental sample. The oil and protein contents were predicted using the respective calibration equations.

Data obtained from NIRS analysis was analyzed statistically using a nearest-neighbor (N-N) analysis. The N-N analysis allows removal of within-block spatial variability in a fairly flexible fashion, which does not require prior knowledge of the pattern of variability in the chamber. Ideally, all hybrids are grown under identical experimental conditions within a block (rep). In reality, even in many block designs, significant within-block variability exists. Nearest-neighbor procedures are based on assumption that environmental effect of a plot is closely related to that of its neighbors. Nearest-neighbor methods use information from adjacent plots to adjust for within-block heterogeneity and so provide more precise estimates of treatment means and differences. If there is within-plot heterogeneity on a spatial scale that is larger than a single plot and smaller than the entire block, then yields from adjacent plots will be positively correlated. Information from neighboring plots can be used to reduce or remove the unwanted effect of the spatial heterogeneity, and hence improve the estimate of the treatment effect. Data from neighboring plots can also be used to reduce the influence of competition between adjacent plots. The Papadakis N-N analysis can be used with designs to remove within-block variability that would not be removed with the standard split plot analysis ((Papadakis (1973) *Inst. d'Amelior. Plantes Thessaloniki (Greece) Bull. Scientif.* No. 23; Papadakis (1984) *Proc. Acad. Athens* 59: 326-342).

Experiments were performed to identify those transformants or knockouts that exhibited modified sugar sensing. For such studies, seeds from transformants were germinated on media containing 5% glucose or 9.4% sucrose which normally partially restrict hypocotyl elongation. Plants with altered sugar sensing may have either longer or shorter hypocotyls than normal plants when grown on this media. Additionally, other plant traits may be varied such as root mass.

Experiments may be performed to identify those transformants or knockouts that exhibited an improved pathogen tolerance. For such studies, the transformants are exposed to biotrophic fungal pathogens, such as *Erysiphe orontii*, and necrotrophic fungal pathogens, such as *Fusarium oxysporum*. *Fusarium oxysporum* isolates cause vascular wilts and damping off of various annual vegetables, perennials and weeds (Mauch-Mani and Slusarenko (1994) *Molec Plant-Microbe Interact.* 7: 378-383). For *Fusarium oxysporum* experiments, plants are grown on Petri dishes and sprayed with a fresh spore suspension of *F. oxysporum*. The spore suspension is prepared as follows: A plug of fungal hyphae from a plate culture is placed on a fresh potato dextrose agar plate and allowed to spread for one week. Five ml sterile water is then added to the plate, swirled, and pipetted into 50 ml Armstrong *Fusarium* medium. Spores are grown overnight in *Fusarium* medium and then sprayed onto plants using a Preval paint sprayer. Plant tissue is harvested and frozen in liquid nitrogen 48 hours post-infection.

Erysiphe orontii is a causal agent of powdery mildew. For *Erysiphe orontii* experiments, plants are grown approximately 4 weeks in a greenhouse under 12 hour light (20°C, ~30% relative humidity (rh)). Individual leaves are infected with *E. orontii* spores from infected plants using a camel's hair brush, and the plants are transferred to a Percival growth chamber (20°C, 80% rh.). Plant tissue is harvested and frozen in liquid nitrogen 7 days post-infection.

Botrytis cinerea is a necrotrophic pathogen. *Botrytis cinerea* is grown on potato dextrose agar under 12 hour light (20°C, ~30% relative humidity (rh)). A spore culture is made by spreading 10 ml of sterile water on the fungus plate, swirling and transferring spores to 10 ml of sterile water. The spore inoculum (approx. 105 spores/ml) is then used to spray 10 day-old seedlings grown under sterile conditions on MS (minus sucrose) media. Symptoms are evaluated every day up to approximately 1 week.

Sclerotinia sclerotiorum hyphal cultures are grown in potato dextrose broth. One gram of hyphae is ground, filtered, spun down and resuspended in sterile water. A 1:10 dilution is used to spray 10 day-old seedlings grown aseptically under a 12 hour light/dark regime on MS (minus sucrose) media. Symptoms are evaluated every day up to approximately 1 week.

Pseudomonas syringae pv *maculicola* (Psm) strain 4326 and pv *maculicola* strain 4326 was inoculated by hand at two doses. Two inoculation doses allows the differentiation between plants with enhanced susceptibility and plants with enhanced resistance to the pathogen. Plants are grown for 3 weeks in the greenhouse, then transferred to the growth chamber for the remainder of their growth. Psm ES4326 may be hand inoculated with 1 ml syringe on 3 fully-expanded leaves per plant (4 1/2 wk old), using at least 9 plants per overexpressing line at two inoculation doses, OD=0.005 and OD=0.0005.

Disease scoring is performed at day 3 post-inoculation with pictures of the plants and leaves taken in parallel.

In some instances, expression patterns of the pathogen-induced genes (such as defense genes) may be monitored by microarray experiments. In these experiments, cDNAs are generated by PCR and resuspended at a final concentration of ~ 100 ng/ul in 3X SSC or 150mM Na-phosphate (Eisen and Brown (1999) *Methods Enzymol.* 303: 179-205). The cDNAs are spotted on microscope glass slides coated with polylysine. The prepared cDNAs are aliquoted into 384 well plates and spotted on the slides using, for example, an x-y-z gantry (OmniGrid) which may be purchased from GeneMachines (Menlo Park, CA) outfitted with quill type pins which may be purchased from Telechem International (Sunnyvale, CA). After spotting, the arrays are cured for a minimum of one week at room temperature, rehydrated and blocked following the protocol recommended by Eisen and Brown (1999; *supra*).

Sample total RNA (10 µg) samples are labeled using fluorescent Cy3 and Cy5 dyes. Labeled samples are resuspended in 4X SSC/0.03% SDS/4 µg salmon sperm DNA/2 µg tRNA/ 50mM Na-pyrophosphate, heated for 95°C for 2.5 minutes, spun down and placed on the array. The array is then covered with a glass coverslip and placed in a sealed chamber. The chamber is then kept in a water bath at 62°C overnight. The arrays are washed as described in Eisen and Brown (1999, *supra*) and scanned on a General Scanning 3000 laser scanner. The resulting files are subsequently quantified using IMAGEGENE, software (BioDiscovery, Los Angeles CA).

RT-PCR experiments may be performed to identify those genes induced after exposure to biotrophic fungal pathogens, such as *Erysiphe orontii*, necrotrophic fungal pathogens, such as *Fusarium oxysporum*, bacteria, viruses and salicylic acid, the latter being involved in a nonspecific resistance response in *Arabidopsis thaliana*. Generally, the gene expression patterns from ground plant leaf tissue is examined.

Reverse transcriptase PCR was conducted using gene specific primers within the coding region for each sequence identified. The primers were designed near the 3' region of each DNA binding sequence initially identified.

Total RNA from these ground leaf tissues was isolated using the CTAB extraction protocol. Once extracted total RNA was normalized in concentration across all the tissue types to ensure that the PCR reaction for each tissue received the same amount of cDNA template using the 28S band as reference. Poly(A+) RNA was purified using a modified protocol from the Qiagen OLIGOTEX purification kit batch protocol. cDNA was synthesized using standard protocols. After the first strand cDNA synthesis, primers for Actin 2 were used to normalize the concentration of cDNA across the tissue types. Actin 2 is found to be constitutively expressed in fairly equal levels across the tissue types we are investigating.

For RT PCR, cDNA template was mixed with corresponding primers and Taq DNA polymerase. Each reaction consisted of 0.2 µl cDNA template, 2 µl 10X Tricine buffer, 2 µl 10X Tricine buffer and 16.8 µl water, 0.05 µl Primer 1, 0.05 µl, Primer 2, 0.3 µl Taq DNA polymerase and 8.6 µl water.

The 96 well plate is covered with microfilm and set in the thermocycler to start the reaction cycle. By way of illustration, the reaction cycle may comprise the following steps:

Step 1: 93° C for 3 min;

Step 2: 93° C for 30 sec;

5 Step 3: 65° C for 1 min;

Step 4: 72° C for 2 min;

Steps 2, 3 and 4 are repeated for 28 cycles;

Step 5: 72° C for 5 min; and

STEP 6 4° C.

10 To amplify more products, for example, to identify genes that have very low expression, additional steps may be performed: The following method illustrates a method that may be used in this regard. The PCR plate is placed back in the thermocycler for 8 more cycles of steps 2-4.

Step 2 93° C for 30 sec;

Step 3 65° C for 1 min;

15 Step 4 72° C for 2 min, repeated for 8 cycles; and

Step 5 4° C.

Eight microliters of PCR product and 1.5 µl of loading dye are loaded on a 1.2% agarose gel for analysis after 28 cycles and 36 cycles. Expression levels of specific transcripts are considered low if they were only detectable after 36 cycles of PCR. Expression levels are considered medium or high depending on the levels of transcript compared with observed transcript levels for an internal control such as actin2. Transcript levels are determined in repeat experiments and compared to transcript levels in control (e.g., non-transformed) plants.

Experiments were performed to identify those transformants or knockouts that exhibited an improved environmental stress tolerance. For such studies, the transformants were exposed to a variety of environmental stresses. Plants were exposed to chilling stress (6 hour exposure to 4-8° C), heat stress (6 hour exposure to 32-37° C), high salt stress (6 hour exposure to 200 mM NaCl), drought stress (168 hours after removing water from trays), osmotic stress (6 hour exposure to 3 M mannitol), or nutrient limitation (nitrogen, phosphate, and potassium) (nitrogen: all components of MS medium remained constant except N was reduced to 20 mg/l of NH₄NO₃; phosphate: all components of MS medium except KH₂PO₄, which was replaced by K₂SO₄; potassium: all components of MS medium except removal of KNO₃ and KH₂PO₄, which were replaced by NaH₄PO₄).

Experiments were performed to identify those transformants or knockouts that exhibited a modified structure and development characteristics. For such studies, the transformants were observed by eye to identify novel structural or developmental characteristics associated with the ectopic expression of the polynucleotides or polypeptides of the invention.

Flowering time was measured by the number of rosette leaves present when a visible inflorescence of approximately 3 cm is apparent. Rosette and total leaf number on the progeny stem are

tightly correlated with the timing of flowering (Koornneef et al. (1991) *Mol. Gen. Genet.* 229: 57-66). The vernalization response was also measured. For vernalization treatments, seeds were sown to MS agar plates, sealed with micropore tape, and placed in a 4°C cold room with low light levels for 6-8 weeks. The plates were then transferred to the growth rooms alongside plates containing freshly sown non-vernalized controls. Rosette leaves were counted when a visible inflorescence of approximately 3 cm was apparent.

Modified phenotypes observed for particular overexpressor or knockout plants are provided in Table 4. For a particular overexpressor that shows a less beneficial characteristic, it may be more useful to select a plant with a decreased expression of the particular transcription factor. For a particular knockout that shows a less beneficial characteristic, it may be more useful to select a plant with an increased expression of the particular transcription factor.

The sequences of the Sequence Listing or those in Tables 4 - 9, or those disclosed here, can be used to prepare transgenic plants and plants with altered traits. The specific transgenic plants listed below are produced from the sequences of the Sequence Listing, as noted. Tables 4 and 6 provide exemplary polynucleotide and polypeptide sequences of the invention.

Example VIII: Examples of Genes that Confer Significant Improvements to Plants

Examples of genes and homologs that confer significant improvements to knockout or overexpressing plants are noted below. Experimental observations made by us with regard to specific genes whose expression has been modified in overexpressing or knock-out plants, and potential applications based on these observations, are also presented.

This example provides experimental evidence for increased biomass and abiotic stress tolerance controlled by the transcription factor polypeptides and polypeptides of the invention.

Salt stress assays are intended to find genes that confer better germination, seedling vigor or growth in high salt. Evaporation from the soil surface causes upward water movement and salt accumulation in the upper soil layer where the seeds are placed. Thus, germination normally takes place at a salt concentration much higher than the mean salt concentration of in the whole soil profile. Plants differ in their tolerance to NaCl depending on their stage of development, therefore seed germination, seedling vigor, and plant growth responses are evaluated.

Osmotic stress assays (including NaCl and mannitol assays) are intended to determine if an osmotic stress phenotype is NaCl-specific or if it is a general osmotic stress related phenotype. Plants tolerant to osmotic stress could also have more tolerance to drought and/or freezing.

Drought assays are intended to find genes that mediate better plant survival after short-term, severe water deprivation. Ion leakage will be measured if needed. Osmotic stress tolerance would also support a drought tolerant phenotype.

Temperature stress assays are intended to find genes that confer better germination, seedling vigor or plant growth under temperature stress (cold, freezing and heat).

Sugar sensing assays are intended to find genes involved in sugar sensing by germinating seeds on high concentrations of sucrose and glucose and looking for degrees of hypocotyl elongation. The germination assay on mannitol controls for responses related to osmotic stress. Sugars are key regulatory molecules that affect diverse processes in higher plants including germination, growth, flowering, senescence, sugar metabolism and photosynthesis. Sucrose is the major transport form of photosynthate and its flux through cells has been shown to affect gene expression and alter storage compound accumulation in seeds (source-sink relationships). Glucose-specific hexose-sensing has also been described in plants and is implicated in cell division and repression of "famine" genes (photosynthetic or glyoxylate cycles).

Germination assays followed modifications of the same basic protocol. Sterile seeds were sown on the conditional media listed below. Plates were incubated at 22° C under 24-hour light (120-130 $\mu\text{Ein}/\text{m}^2/\text{s}$) in a growth chamber. Evaluation of germination and seedling vigor was conducted 3 to 15 days after planting. The basal media was 80% Murashige-Skoog medium (MS) + vitamins.

For salt and osmotic stress germination experiments, the medium was supplemented with 150 mM NaCl or 300 mM mannitol. Growth regulator sensitivity assays were performed in MS₂ media, vitamins, and either 0.3 μM ABA, 9.4% sucrose, or 5% glucose.

Temperature stress cold germination experiments were carried out at 8 °C. Heat stress germination experiments were conducted at 32 °C to 37° C for 6 hours of exposure.

For stress experiments conducted with more mature plants, seeds were germinated and grown for seven days on MS + vitamins + 1% sucrose at 22 °C and then transferred to chilling and heat stress conditions. The plants were either exposed to chilling stress (6 hour exposure to 4-8° C), or heat stress (32° C was applied for five days, after which the plants were transferred back 22 °C for recovery and evaluated after 5 days relative to controls not exposed to the depressed or elevated temperature).

Results:

G12 (SEQ ID NO: 3)

Published Information

G12 (At4g36900) is on chromosome 4, contig fragment No. 86, GenBank accession number AL161590 (nid=7270623). The gene has been described as RAP2.10 by Okamuro et al., (1997) *Proc Natl Acad Sci* 94, 7076-7081.

Experimental Observations

G12 was determined to be ubiquitously expressed in plants. The function of G12 was studied using a line homozygous for a T-DNA insertion in the gene. G12 knockout mutant seedlings germinated in the dark on ACC-containing media (an ethylene insensitivity assay) were more severely stunted than the wild-type controls. These results indicate that G12 is involved in the ethylene signal transduction or response pathway, a process in which other proteins of the AP2/EREBP family are implicated. G12 KO

mutant plants were wild-type in morphology and development, and in all other physiological and biochemical analyses that were performed.

In addition to the knockout mutant, the function of the gene was analyzed using transgenic plants in which the cDNA clone for G12 was expressed under the control of the 35S promoter. Overexpression of G12 caused seedlings to develop black necrotic tissue patches on cotyledons and seedlings died before the formation of true leaves. Some 35S::G12 overexpressing seedlings exhibited a weaker phenotype characterized by smaller necrotic patches on leaf margins. However, those plants arrested growth and died before flowering. No seed was obtained from any of the G12 overexpressing lines.

Utilities

The overexpression and knockout phenotypes indicate that G12 can have a role in regulating programmed cell death. Such a function could have various applications. The gene, its equivalents, or its targets could be used to induce cell death in a controlled manner in specific tissues or in response to pathogen attack. For example, if the gene was specifically active in gametes or reproductive organs, it might be used to achieve male or female sterility. Alternatively, in the latter scenario, it might restrict the spread of a pathogen infection through a plant.

G30 (SEQ ID NO: 7)

Published Information

G30 (At1g04370) is part of the BAC clone F19P19, GenBank accession number AC000104 (mid=2341023).

Experimental Observations

Initial experiments were performed with G30 knockout mutant plants. However, these experiments did not uncover the functions of the gene.

In order to characterize the gene further, 35S::G30 overexpressing lines were generated. Morphological analysis of the transgenic plants indicated that G30 could be involved in light regulation: the seedlings had long hypocotyls and elongated cotyledon petioles. In addition, some of the seedlings also had longer roots compared to control plants. At later stages, the plants became darker green, and had glossy leaves, perhaps indicating elevated levels of epidermal wax. The phenotype for G30 overexpression resembled those produced by related AP2 genes.

Utilities

Based on the appearance of 35S::G30 leaves, the gene could be used to engineer changes in the composition and amount of leaf surface components (most likely wax). The ability to manipulate wax composition, amount, or distribution could modify plant tolerance to drought and low humidity, or resistance to insects or pathogens. Additionally, in some species, wax is a valuable commodity and altering its accumulation and/or composition could enhance yield.

The phenotypes of 35S::G30 seedlings indicate that the gene may also be used to manipulate light-regulated developmental processes like shade avoidance. Eliminating shading responses might allow increased planting densities with subsequent yield enhancement.

Additionally, if the dark coloration of 35S::G30 lines reflects an increase in biochemical composition, the gene might be used to improve the nutraceutical value of foodstuffs, or increase photosynthetic capacity to improve yield.

G46 (SEQ ID NO: 9)

Published Information

G46 was first identified in the sequence of P1 clone MBK20 (GenBank accession number AB010070, gene MBK20.1). No information is available about the function(s) of G46.

Experimental Observations

RT-PCR experiments revealed that G46 was ubiquitously expressed, but was potentially induced by stress conditions such as auxin, heat, salt and *Erysiphe*.

The function of G46 was studied using a line homozygous for a T-DNA insertion in the gene. G46 knockout mutant plants were indistinguishable from wild-type in all assays performed.

The function of G46 was also analyzed using transgenic plants in which a cDNA clone of the gene was expressed under the control of the 35S promoter. A number of lines were larger than wild-type plants, developed more rapidly, and yielded an increased quantity of seed compared to wild-type controls.

In the physiological analysis, all three 35S::G46 lines (number 32, 35, and 36) tested showed more resistance to severe water deprivation stress. Seedlings were generally larger and greener than the control plants exposed to the same conditions.

35S::G46 plants were also significantly larger and greener in a soil-based drought assay than wild-type control plants.

Utilities

The reduced sensitivity of 35S::G46 lines in the dehydration stress assay indicated that the gene or its equivalents might be used to engineer crops with increased tolerance to drought, salt, freezing and/or chilling stress, or increased water use efficiency.

Additionally, the increased size and growth rate seen in some of the lines indicated that the gene or its equivalents can be used to increase crop productivity.

G47 (SEQ ID NO: 11)

Published Information

G47 corresponds to gene T22J18.2 (AAC25505). No information is available about the function(s) of G47.

Experimental Observations

The function of G47 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G47 resulted in a variety of morphological and physiological phenotypic alterations.

5 35S::G47 plants showed enhanced tolerance to osmotic stress. In a root growth assay on PEG containing media, G47 overexpressing transgenic seedlings were larger and had more root growth compared to the wild-type controls (Figure 3A). Interestingly, G47 expression levels might be altered by environmental conditions, in particular reduced by salt and osmotic stresses. In addition to the phenotype observed in the osmotic stress assay, germination efficiency for the seeds from G47 overexpressors was
10 low.

35S::G47 plants were also significantly larger and greener in a soil-based drought assay than wild-type controls plants.

Overexpression of G47 also produced a substantial delay in flowering time and caused a marked change in shoot architecture. 35S::G47 transformants were small at early stages and switched to
15 flowering more than a week later than wild-type controls (continuous light conditions). Interestingly, the inflorescences from these plants appeared thick and fleshy, had reduced apical dominance, and exhibited reduced internode elongation leading to a short compact stature (Figure 3B). The branching pattern of the stems also appeared abnormal, with the primary shoot becoming 'kinked' at each coflorescence node. Additionally, the plants showed slightly reduced fertility and formed rather small siliques that were borne
20 on short pedicels and held vertically, close against the stem.

Additional alterations were detected in the inflorescence stems of 35S::G47 plants. Stem sections from T2-21 and T2-24 plants were of wider diameter, and had large irregular vascular bundles containing a much greater number of xylem vessels than wild type. Furthermore some of the xylem vessels within the bundles appeared narrow and were possibly more lignified than were those of controls.

25 G47 was expressed at higher levels in rosette leaves, and transcripts can be detected in other tissues (flower, embryo, silique, and germinating seedling), but apparently not in roots.

Utilities

G47 or its equivalents could potentially be used to manipulate flowering time, to modify plant architecture and stem structure, including development of vascular tissues and lignin content, and to
30 improve plant performance under drought and osmotic stress conditions.

The use of G47 or its equivalents from tree species could offer the potential for modulating lignin content. This might allow the quality of wood used for furniture or construction to be improved.

G148 (SEQ ID NO: 39)

Published Information

35 G148 corresponds to AGAMOUS-LIKE 13 (AGL13), and was originally identified based on its conserved MADS domain (Purugganan et al. (1995) *Genetics* 140: 345-356.; Rounsley et al. (1995).

Plant Cell 7: 1259-1269). No functional information about G148 is available in the public domain. However, its expression pattern indicated that the gene has a role in ovule development; AGL13 transcript was present in ovules at the time of integument development, but fell following fertilization. Additionally, lower levels of expression were found in anther filaments and style tissue (Rounsley et al. (1995) *supra*).

Experimental Observations

Homozygotes were analyzed for a transposon insertion (SLAT collection) within G148; these plants showed no obvious macroscopic changes in morphology and exhibited a similar response to wild type in all of the physiological assays performed.

The effects of G148 overexpression were studied by generating transgenic lines in which a G148 genomic clone was expressed from the 35S CaMV promoter. 35S::G148 transformants displayed a range of morphological changes including a severe reduction in overall plant size, leaf curling, accelerated flowering, and terminal flower formation. Such changes indicate that G148 influences the genetic networks controlling various aspects of development including flowering time and meristem determinacy.

Utilities

The morphological changes seen in the overexpression lines demonstrate that G148 could be used to manipulate various aspects of plant development.

The appearance of terminal flowers in 35S::G148 transformants indicated that the gene or its orthologs can modify inflorescence architecture and confer a determinate habit in species where the shoots otherwise show an indeterminate growth pattern. Such changes completely alter the overall plant form, and may, for example, facilitate mechanical harvesting (as already exemplified by the SELF-PRUNING gene, which controls shoot determinacy in tomato, Pnueli L et al. (1998). *Development* 125: 1979-1989).

Additionally, the accelerated switch to reproductive growth seen in 35S::G148 plants, indicated that the gene can be used to manipulate flowering time in commercial species. Specifically, the gene can accelerate flowering or eliminate any requirement for vernalization. In some instances, a faster cycling time might allow additional harvests of a crop to be made within a given growing season. Shortening generation times can also help speed-up breeding programs, particularly in species such as trees, which grow for many years before flowering.

G151 (SEQ ID NO: 41)

Published Information

G151 corresponds to AGL15, a gene isolated by virtue of its conserved MADS box sequence (Rounsley et al. (1995). *Plant Cell* 7: 1259-1269) and by its preferential expression in young *Brassica napus* embryos (Heck et al. (1995) *Plant Cell* 7:1271-1282). On the basis of AGL15 expression patterns,

it has been suggested that this gene might be involved in embryogenesis (Heck et al., 1995; *supra*, Perry et al. (1996) *Plant Cell* 8:1977-1989; Perry et al. (1999) *Plant Physiol.* 120:121-130). In addition, overexpression of AGL15 has been shown to inhibit perianth organ senescence and abscission (Fernandez et al. (2000) *Plant Cell* 12:183-198). However, G151/AGL15 still remains poorly characterized, and the gene likely has multiple roles.

G151 is expressed preferentially during embryogenesis and accumulates during early seed development (Perry et al., 1996, *supra*). AGL15-specific antibodies were used to demonstrate that AGL15 accumulates before fertilization in the cytoplasm of cells of the egg apparatus and moves into the nucleus during early stages of development in the suspensor, embryo, and endosperm (Perry et al., 1996; 1999, *supra*). Relatively high levels of AGL15 are present in the nuclei during embryo morphogenesis and until the seeds start to dry in *Brassica*, maize, and *Arabidopsis*. It has also been shown that AGL15 is associated with the chromosomes during mitosis, and gel mobility shift assays were used to demonstrate that the protein binds DNA in a sequence-specific manner (Perry et al., 1996, *supra*).

AGL15 expression, however, is not restricted to embryonic tissues. It has been found that the AGL15 protein accumulates transiently in the shoot apices of young *Arabidopsis* and *Brassica* seedlings, and that promoter activity is associated with the shoot apex and the base of leaf petioles throughout the vegetative phase (Fernandez et al. (2000) *supra*). In addition, during the reproductive phase, AGL15 accumulates transiently in floral buds (Fernandez et al. (2000) *supra*). When AGL15 was expressed in *Arabidopsis* under the control of a strong constitutive promoter, delayed abscission of perianth organs in the flowers was noted, changes in leaf shape occurred, and some age-dependent developmental processes (including the transition to flowering and fruit maturation) were delayed (Fernandez et al. (2000) *supra*).

Experimental Observations

The function of G151 was analyzed using a line that was homozygous for a T-DNA insertion within the gene. However, these plants displayed no consistent differences to wild type in any of the assays performed. We surmised that this could be due to potential redundancy between G151 and a highly related gene, G858 (AGL18). (G858 and G151 from a monophyletic clade within the *Arabidopsis* MADS box gene family (Alvarez-Buylla et al. (2000) *Plant J.* 24:457-466).

RT-PCR experiments also indicated that G151 is expressed ubiquitously, with the highest levels occurring in embryo and silique tissues. These results confirmed and expanded previously published observations describing that AGL15/G151 is preferentially expressed in the developing embryo, and also in germinating seedlings and leaf tissue (Rounsley et al. (1995) *supra*; Heck et al., (1995) *supra*; Perry et al., (1996, 1999) *supra*). In addition, G151 expression appeared to be induced by auxin.

35S::G151 overexpressing lines displayed a wild-type response in all of the physiological assays. Furthermore, although our lines expressed the transgene (determined by RT-PCR), for unknown reasons, we failed to recapitulate the effects on petal and sepal abscission, leaf shape, and flowering time that had been obtained by Fernandez et al. (2000) *supra*. It is noteworthy that Fernandez et al. attained much more pronounced results, and detected much higher levels of AGL15 protein, in 35S::AGL15 lines that

harbored a genomic clone of the gene, rather than a cDNA clone. All of the 35S::G151 lines we created contained a cDNA clone; it is possible that the transcript from this transgene was less stable than those in the 'genomic lines' of Fernandez et al. (2000). The discrepancy in results might also derive from differences in the lengths of 5' UTR included in the overexpression construct, or differences in the strengths of different versions of the 35S promoters that were used.

Interestingly, however, in a small number of lines we noted an effect, which was not explicitly mentioned by Fernandez et al. (2000); the seeds were larger than were those of wild type. It is not clear, though, whether this could have been related to delayed seed ripening, which Fernandez et al. documented, or whether it was due to some other aspect of the G151 role in seed or embryo development.

Utilities

Based on the publicly available data, G151 or its equivalents could likely be used to manipulate age related developmental processes such as flowering time, seed maturation and floral organ retention. The latter trait might be of particular interest to the ornamental plant industry and might allow the 'campaign life' of flowers to be extended.

This gene or its equivalents may also be used to increase seed size and yield. The promoter of G151 might be useful for engineering auxin-inducible expression.

G153 (SEQ ID NO: 43)

Published Information

G153 corresponds to the *Arabidopsis* ANR1 gene. This locus was identified by Zhang and Forde (1998) as a MADS box gene that is rapidly induced in the roots of nitrogen starved seedlings, following exposure to a nitrate source. Additionally, it was shown that transgenic lines in which an antisense clone of ANR1 is overexpressed show altered sensitivity to nitrate and, unlike wild-type plants, do not exhibit lateral root proliferation in response to nitrate treatments. From these data, it was concluded that ANR1 is a key regulator of nutrient-induced changes in root architecture (Zhang and Forde (1998) *Science* 279: 407-409).

However, Wang et al. ((2000) *Plant Cell* 12, 1491-1509) have data that contradicts the results of Zhang and Forde (1998). These authors found that ANR1 is actually repressed, rather than induced, following treatment of nitrogen starved seedlings (grown on 10 mM ammonium succinate as the sole nitrogen source) with 5 mM nitrate.

A phylogenetic analysis of the *Arabidopsis* MADS box gene family situated ANR1 in same clade as three other MADS box genes: AGL16 (G860), AGL17 (G152) and AGL21 (G1760) (Alvarez-Buylla et al. (2000) *Proc Natl Acad Sci U. S. A.* 97: 5328-5333). Two of the genes, AGL17 and AGL21 were recently shown to be expressed in specific zones of the root, indicating that different members of the ANR1 clade may play distinct regulatory roles during root development (Burgeff et al. (2002) *Planta* 214: 365-372).

The ANR1 sequence (GenBank accession AX507709) has also been included in a patent publication (WO0216655A) by Harper et al. (2002).

Experimental Observations

RT-PCR experiments revealed that G153 is up-regulated in leaves in response to heat and *Fusarium* treatments. Lower levels of induction were also observed following auxin, ABA, and cold treatments, indicating that G153 might have a role in a variety of stress responses.

To further assess the function of the gene, 35S::G153 overexpressing lines were generated and subjected to a suite of assays. Around a third of the lines showed a marked acceleration in the onset of flowering, indicating that the gene might impinge on genetic pathways that regulate flowering time.

In addition to the effects on flowering, 35S::G153 lines displayed an enhanced performance in an assay intended to reveal alterations in C/N sensing. 35S::G153 seedlings contained less anthocyanin and in a number of cases were larger than wild-type controls grown on high sucrose/N- plates. Seedlings were also larger and greener on high sucrose/N- plates that had been supplemented with glutamine. Together, these data indicated that overexpression of G153 may alter the ability to modulate carbon and/or nitrogen uptake and utilization.

It should be noted that a closely related gene, G1760, prior to the C/N sensing assay being implemented. Like 35S::G153 transformants, 35S::G1760 lines also exhibited early flowering, and RT-PCR studies showed G1760 to be predominantly expressed in roots and to be stress responsive. Thus, G1760 and G153 could have similar and/or overlapping functions.

Utilities

The response of G153 expression to different physiological treatments indicates that the gene or its equivalents could be used to improve resistance to a variety of different stresses. In particular, the enhanced performance of 35S::G153 lines under low nitrogen conditions indicated that G153 might be used to engineer crops that could thrive in environments with reduced nitrogen availability.

The finding that 35S::G153 lines make less anthocyanin on high sucrose media containing glutamine indicated that G153 or its equivalents might be used to modify carbon and nitrogen status, and hence alter assimilate partitioning.

Given the early flowering seen amongst the 35S::G153 transformants, the gene or its equivalents might also be applied to manipulate the flowering time of commercial species. In particular, G153 could be used to accelerate flowering, or eliminate any requirement for vernalization.

G155 (SEQ ID NO: 45)

Published Information

G155 corresponds to AGAMOUS-LIKE 8 (AGL8), and was originally identified based on its conserved MADS domain (Mandel et al. (1995) *Plant Cell* 7: 1763-1771). The gene behaves as an early marker of the switch to reproductive growth; AGL8 RNA is not present during vegetative growth, but accumulates to high levels in the inflorescence apical meristem, as well as in the inflorescence stem and

cauline leaves (Mandel et al. *supra*; Hempel et al. (1997) *Development* 124: 3845-3853). Additionally, AGL8 RNA is excluded from the young flower primordia that arise on the flanks of the inflorescence meristem (Mandel et al. *supra*). Such expression patterns indicate that AGL8 could have a role in maintaining the separation between inflorescence and floral meristem identity. Later, AGL8 RNA also accumulates in the walls of the developing carpels (Gu et al. (1998) *Development* 125: 1509-1517), indicating that it functions in fruit development. This has been confirmed through the study of mutants; the gene was found to have a major role in fruit valve differentiation. Loss of function mutants form siliques that lack coordinated growth, often fail to dehisce, show premature rupture of the carpel valves, and become overcrowded with seeds (Gu et al. (1998) *supra*). Based on this phenotype, the gene was renamed FRUITFUL (FUL). Overexpression lines for FUL also show abnormalities in silique shattering and it has been shown that the gene acts as an inhibitor of the SHATTERPROOF (SHP1, SHP2; GIDs G136, G140) genes (Ferrandiz et al. (2000) *Science* 289: 436-438).

Experimental Observations

To determine whether G155 has functions additional to its known roles in fruit development, overexpression lines were generated and subjected to a battery of assays. 35S::G155 transformants exhibited early flowering and a number of lines also developed terminal flowers, giving a phenotype very similar to that exhibited by the terminal flower 1 mutant (Shannon et al. (1991) *Plant Cell* 3: 877-892.; Bradley et al. (1997) *Science* 275: 80-83. Alterations in silique development in the transformed lines were not detected. However, given that such effects are thought to occur through inhibition of the SHP genes, it is possible that the G155 expression levels in the 35S::G155 lines were not sufficiently high enough to elicit such effects, compared to the 35S::FUL lines reported by Ferrandiz et al. (2000), *supra*.

In addition to the changes in morphology, when subjected to physiological assays, 35S::G155 transformants showed increased sensitivity to osmotic stress in germination assays on either glucose or mannitol plates.

Utilities

Based on its published function, G155 can manipulate flower and fruit traits in commercial species. The overexpression data o demonstrated that G155 or its orthologs could be used to manipulate various other aspects of plant development.

The appearance of terminal flowers in 35S::G155 transformants indicated that the gene can modify inflorescence architecture and confer a determinate habit in species where the shoots show an indeterminate growth pattern. Such changes can completely alter the overall plant form, and can facilitate mechanical harvesting (as exemplified by the SELF-PRUNING gene, which controls shoot determinacy in tomato, Pnueli et al. (1998), *supra*).

Additionally, the rapid switch to reproductive growth seen in 35S::G155 plants, indicated that the gene can manipulate flowering time in commercial species. The gene could be used to accelerate flowering or eliminate any requirement for vernalization. In some instances, a faster cycling time might allow additional harvests of a crop to be made within a given growing season. Shortening generation

times could also help speed-up breeding programs, particularly in species such as trees, which grow for many years before flowering.

The results of physiological assays on 35S::G155 plants indicate that the transcription factor can be used to manipulate abiotic stress responses or to modify source/sink relationships or other sugar regulated processes.

G200 (SEQ ID NO: 53)

Published Information

G200 corresponds to gene AT1g08810, and has been described as MYB60 (Kranz et al. (1998) *Plant J.* 16: 263-276). Expression analysis by reverse Northern blot indicates that G200 is slightly induced only in silique tissue and by IAA, cold and UV treatments (Kranz et al., 1998). No information is available about the function(s) of G200.

Experimental Observations

Analysis of a G200 knockout demonstrated that homozygous G200 knockout plants were phenotypically wild-type. G200 was determined to be ubiquitously expressed in *Arabidopsis*, contradicting the report by Kranz et al., *supra*.

Overexpression of G200 produced pleiotropic effects on plant development, causing alterations in overall plant size, coloration, flowering time, leaf shape, flower structure and fertility.

Relatively few 35S::G200 overexpressing lines were obtained; only 10 T1 plants were recovered from 4 separate 300 mg aliquots of T0 seed (a 300 mg aliquot typically yields 15-120 T1 plants), indicating that G200 can be lethal in plants that highly overexpress the gene.

The 35S::G200 lines that were isolated were generally very small, slightly pale in coloration, had rather pointed and/or contorted leaves, and abnormal phyllotaxy. A number of the lines also produced flower buds slightly earlier than wild type. Additionally, the flowers of overexpressing G200 plants were typically smaller and gaped open more widely than those of controls. Interestingly, in an assay intended to determine whether the transgene expression could alter C:N sensing, 35S::G200 seedlings contained less anthocyanins, and in some cases were greener, than wild-type controls grown on high sucrose/N deficient plates. This indicates that some of the growth defects observed in these lines were related to the carbon or nutrient availability in different growth substrates. Seedlings were also greener on high sucrose/ nitrogen deficient/glutamine-supplemented plates. These data together indicate that overexpression of G200 may alter a plant's ability to modulate carbon and/or nitrogen uptake and utilization.

Utilities

The enhanced performance of G200 overexpression lines under low nitrogen conditions indicate that the gene could be used to engineer crops that could thrive under conditions of reduced nitrogen availability. Such a trait would afford the following benefits: (1) cost savings to the farmer by reducing

the amount of fertilizer needed (2) environmental benefits of reduced fertilizer run-off into watersheds (3) improved yield and stress tolerance.

That 35S::G200 lines make less anthocyanin on high sucrose plus glutamine, indicates G200 might be used to modify carbon and nitrogen status, and hence assimilate partitioning.

5

G319 (SEQ ID NO: 71)

Published Information

G319 (At1g05290) was identified in the sequence of YAC yUP8H12, GenBank accession number AC000098, released by the *Arabidopsis* Genome Initiative based on its sequence similarity within the conserved domain to other CONSTANS-like related proteins in *Arabidopsis*. There is no published or public information about G319.

Experimental Observations

Low levels of G319 expression were detected only in embryo and siliques. No expression of G319 was detected by RT-PCR in any other tissues or conditions tested. The function of G319 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G319 produced plants with short broad leaves and delayed flowering. 35S::G319 plants were wild-type in physiological analyses that were performed.

Utilities

G319 could be used to alter flowering time or produce plants with altered leaf morphology. The delayed flowering displayed by 35S::G319 transformants indicates that the gene might be used to manipulate the flowering time of commercial species. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases. In some species (for example sugar beet), where the vegetative parts of the plant constitute the crop, it would be advantageous to delay or suppress flowering in order to prevent resources being diverted into reproductive development. Additionally, delaying flowering beyond the normal time of harvest could alleviate the risk of transgenic pollen escape from such crops.

Given the effects of G319 overexpression, it is likely that the activity of the gene (or its orthologs) could be modified to accelerate flowering, or eliminate any requirement for vernalization.

30 G354 (SEQ ID NO: 1381)

Published Information

G354 was identified in the sequence of BAC clone F12M12, GenBank accession number AL355775, released by the *Arabidopsis* Genome Initiative. G354 corresponds to ZAT7 (Meissner and Michael (1997) *Plant Mol. Biol.* 33: 615-624).

35 Experimental Observations

The highest level of expression of G354 was observed in rosette leaves, embryos, and siliques. Some expression of G354 was also observed in flowers.

The function of this gene was analyzed using transgenic plants in which G353 was expressed under the control of the 35S promoter. 35S::G354 plants had a reduction in flower pedicel length, and downward pointing siliques. This phenotype was very similar to that described for the brevipedicellus (bp) mutant (Koornneef et al. (1983) *J. Hered.* 74: 265-272) and in overexpression of a related gene G353. Other morphological changes in shoots were also observed in 35S::G354 plants. Many 35S::G354 seedlings had abnormal cotyledons, elongated, thickened hypocotyls, and short roots. The majority of T1 plants had a very extreme phenotype, were tiny, and arrested development without forming inflorescences. T1 plants showing more moderate effects had poor seed yield.

Overexpression of G354 in *Arabidopsis* resulted in seedlings with an altered response to light. In a germination assay conducted in darkness, G354 seedlings failed to show an etiolation response, as can be seen in Figure 4 which shows G354 overexpressing and wild-type seedlings germinated on MS plates in the dark. In some cases the phenotype was severe; overexpression of the transgene resulted in reduced open and greenish cotyledons.

G354 overexpressors were also shown to be tolerant to water deprivation in a soil-based drought assay. Closely related paralogs of this gene, G353 and G2839, also showed an osmotic stress tolerance phenotype in a germination assay on media containing high sucrose; one line of 35S::G353 seedlings and several lines of 35S::G2839 were greener and had higher germination rates than controls. Thus, G354 and its paralogs G353 and G2839 appear to influence osmotic stress responses.

Utilities

G354 could be used to alter inflorescence structure, which may have value in production of novel ornamental plants.

G355 (SEQ ID NO: 79)

Published Information

G355 was identified in the sequence of BAC F3G5 (GenBank accession number AC005896; gene At2g37430), released by the *Arabidopsis* Genome Initiative. G355 is also known as ZAT11 (Meissner and Michael (1997) *Plant Mol. Biol.* 33 :615-624). No information has been published about the function of this gene.

Experimental Observations.

G355 expression was found to be weakly induced in rosette leaves by ABA treatment, drought stress, osmotic stress and infection by *Erysiphe*. An attempt to determine the function of G355 was analyzed using transgenic plants in which the expression of this gene was knocked out using a T-DNA insertion. However, these plants appeared wild-type in all morphological, physiological and biochemical assays performed.

The function of G355 was then studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. G355 overexpressing lines show more tolerance to salt stress and enhanced growth under limiting phosphate in root growth assays. Seedlings in both assays were larger,

greener and had more root growth. 35S::G355 plants were wild-type in morphological analyses that were performed.

Utilities

Based on the increased salt tolerance exhibited by the 35S::G355 lines in physiology assays, this gene might be used to engineer salt tolerant crops and trees that can flourish in saline soils, or under drought conditions. The trait is of particular importance early in the life cycle, since evaporation from the soil surface causes upward water movement, and salt accumulates in the upper soil layer where the seeds are placed. Thus, germination normally takes place at a salt concentration much higher than the mean salt level in the whole soil profile. Increased salt tolerance during the germination stage of a crop plant would therefore enhance survivability and yield.

The response of 35S::G355 seedlings to low phosphate conditions indicates that the gene could be used to manipulate nutrient uptake, or the ability to grow in poor nutrient soils. Phosphorus is a limiting nutrient in plant growth and is often added to soil as fertilizer. Young plants have a rapid intake of phosphate and sufficient phosphate is important for yield of root crops such as carrot, potato and parsnip. Phosphate costs represent a relatively small but significant portion of farmers' operating costs (3-4% of total costs to a corn farmer in the US, higher to a vegetable grower). Plants that are tolerant to phosphate deficiency could represent a cost saving for farmers, especially in areas where soils are very poor. They could also provide environmental benefits by reducing pollution from field runoff.

G370 (SEQ ID NO: 83)

Published Information

G370 was initially described as ZFP8, one of a set of C2H2 zinc finger proteins (Tague and Goodman (1995) *Plant Mol. Biol.* 28: 267-279). No functional information is available about ZFP8.

Experimental Observations

G370 was shown to be expressed throughout the aerial portions of the plant, but showed no detectable expression in roots. It was not induced by any condition tested. A knockout line homozygous for a T-DNA insertion in G370 was initially used to determine the function of this gene and showed more sensitivity to osmotic stress in a germination assay. Thus, when selectively regulated, the gene could have utility in creating plants with enhanced tolerance to dehydration stresses.

The function of G370 was also studied using overexpressing transgenic plants in which the gene was expressed under the control of the 35S promoter. All 35S::G370 primary transformants were small. Flowers showed a striking increase in trichome density on sepals, and carried ectopic trichomes on petals, anthers, and carpels. The changes in morphology produced by overexpression of G370 are indicative of heterochronic shifts (i.e. cells in various lineages and tissues adopt fates that are normally associated with cells from other developmental stages). For example, trichomes are normally associated with vegetative rather than reproductive organs. Additionally, aerial rosettes occur when a secondary inflorescence

meristem develops in a manner comparable to a primary shoot meristem during the vegetative phase of growth.

Utilities

5 G370 is expressed throughout the aerial portions of the plant, but shows no detectable expression in roots. It was not induced by any condition tested. A line homozygous for a T-DNA insertion in G370 was initially used to determine the function of this gene and showed more sensitivity to osmotic stress in a germination assay and displayed defects in leaf and inflorescence development.

10 The function of G370 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. All 35S::G370 primary transformants were small and stunted. Flowers showed a striking increase in trichome density on sepals, and carried ectopic trichomes on petals, anthers, and carpels. Because insufficient seed was produced by 35S::G370 plants, no physiological analyses were performed.

15 G370 is closely related to five other Z-C2H2 genes: G2826, G1995, G361, G362, and G2838, which produced broadly similar phenotypes when overexpressed, such as ectopic trichomes on flowers, aerial rosettes, and various other morphological defects. The changes in morphology produced by overexpression of genes in this clade are suggestive of heterochronic shifts (i.e. cells in various lineages and tissues adopt fates that are normally associated with cells from other developmental stages). For example, trichomes are normally associated with vegetative rather than reproductive organs. Additionally, aerial rosettes occur when a secondary inflorescence meristem develops in a manner comparable to a primary shoot meristem during the vegetative phase of growth.

20

G372 (SEQ ID NO: 85)

Published Information

25 G372 was identified in the sequence of BAC clone T6D20, GenBank accession number U90439, released by the *Arabidopsis* Genome Initiative. There is no other published or public information about the function of G372.

Experimental Observations

30 As determined by RT-PCR, G372 is highly expressed under all environmental conditions tested. The function of G372 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G372 in *Arabidopsis* delayed the onset of flowering resulted in plants with increased leaf size and plant biomass compared to control plants. Leaf size was twice that of the controls in many cases

Utilities

35 Given the effects of G372 overexpression, the gene or its orthologs could be used to modify leaf size and flowering time. Increasing leaf size in crop plants through the activity of G372 could result in the direct increase in yield in situations where the vegetative tissues are the harvested products. In

addition, the increases in leaf surface area attributed to G372 activity could also result in yield increases in fruit bearing or seed bearing crops due to the increase in the photosynthetic capacity of larger leaves. In species such as sugarbeet where the vegetative parts of the plants constitute the crop and the reproductive tissues are discarded, it would be advantageous to delay or prevent flowering. Extending vegetative development can bring about large increases in yields. Additionally, a major concern is the escape of transgenic pollen from GMOs to wild species or so-called organic crops. Systems that prevent or delay vegetative transgenic crops from flowering could be used to mitigate this concern.

G438 (SEQ ID NO: 97)

10 Published Information

G438 was identified as a homeobox gene (MUP 24.4) within P1 clone MUP 24 (GenBank accession number AB005246). We have also identified G438 as the *Arabidopsis* REVOLUTA (REV) gene (Ratcliffe et al., (2000) *Plant Cell* 12: 315-317). Based on its mutant phenotype, REV had previously been identified as having a key role in regulating the relative growth of apical versus non-apical (cambial) meristems (Alvarez, J. (1994). The SPITZEN gene. In Arabidopsis: An atlas of morphology and development, ed., J. Bowman). pp. 188-189. New York: Springer-Verlag); Talbert et al. (1995) *Development* 121: 2723-2735). The revoluta phenotype is highly pleiotropic but is characterized by a failure in development of all types of apical meristem: lateral shoot meristems in the axils of cauline and rosette leaves are often completely absent, or replaced by a solitary leaf. These effects are most evident in higher order shoots, but in some cases, the primary shoot meristem also fails and terminates growth in a cluster of filamentous structures. Rev floral meristems often fail to complete normal development and form incomplete or abortive filamentous structures. In contrast to apical meristems, structures formed by non-apical meristems, such as leaves, stems and floral organs often become abnormally large and contorted in the rev mutant.

The features of rev mutants are similar to those of the interfascicular fiberless1 (ifl1) mutant. Ifl1 was isolated during screens for mutants lacking normal stem fiber differentiation (Zhong et al. (1997) *Plant Cell* 9, 2159-2170). Wild-type *Arabidopsis* plants form interfascicular fibers which become lignified and add support to the inflorescence stem (Aloni et al. (1987) *Annu. Rev. Plant Physiol.* 38: 179-204; Zhong et al. (1997) *supra*; Zhong et al. (1999) *Plant Cell* 11: 2139-2152. In the ifl1 mutant, normal interfascicular fibers are absent and the differentiation of both xylary fibers and vessel elements is disrupted. In additions to these internal features, ifl1 mutants have secondary morphological features very similar to those of rev. Recently the IFL1 gene was cloned by Zhong et al. (1999) *supra*. We have found that the IFL1 sequence and map position are identical to those of the REV gene cloned by us, demonstrating that REV and IFL1 are in fact, the same gene (Ratcliffe et al. (2000) *supra*).

It has been suggested that REV promotes the growth of apical meristems (including floral meristems) at the expense of non-apical meristems (Talbert et al. (1995) *supra*). It is not yet clear, however, whether expression data support such a role: strong expression of REV has been detected in

interfascicular regions and developing vascular tissue, but in-situ expression analysis of apical meristems has not yet been reported (Zhong et al. (1999) *supra*). REV is a group III HD-ZIP protein and shares high sequence similarity (and organization) with the proteins encoded by three other *Arabidopsis* genes:

Athb8, Athb9, and Athb14 (Sessa et al. (1998) *Plant Mol. Biol.* 38: 609-622). It is possible, therefore,

5 that these genes act together in the same developmental process.

Closely Related Genes from Other Species

Blast searches reveal that the *Physcomitrella patens* homeobox protein PpHB10 has a relatively high degree of sequence identity to REV. The function of PpHB10 has not been published but it contains 465 conserved amino acid identities to REV across its 880 amino acid sequence. The existence of this
10 similar protein in such a distantly related species suggests that potential orthologs from dicots or monocots would be expected to have a much greater degree of identity to REV over their sequences.

Experimental Observations

G438 was initially identified as MUP24.4, a novel putative homeobox gene within P1 clone MUP24 (GenBank Accession AB005246). Annotation was confirmed by isolation of the G438 cDNA:
15 the cDNA had an in-frame stop codon immediately 5' to the predicted start codon and comprised 18 exons that had been predicted within the genomic sequence.

Plants homozygous for a T-DNA insertion in the G438 sequence were obtained by PCR based screening of DNA pools from the Jack Collection of insertional mutants (Campisi et al. (1999) *Plant Journal* 17, 699-707). The T-DNA insertion was located 466 bp downstream of the putative start codon,
20 and was predicted to create a null mutation. The mutation was recessive and produced a *revoluta* phenotype. The most prominent characteristic was a failure in the development of all types of apical meristem: lateral shoot meristems in the axils of cauline and rosette leaves were often completely absent, or replaced by a solitary leaf. These effects were most evident in higher order shoots, but in some cases, the primary shoot meristem also failed and terminated growth in a cluster of filamentous structures.
25 Overall, the mutant had a dramatic reduction in branching at maturity compared to wild-type plants. The T-DNA insertion mutant also showed delayed senescence, had enlarged revolute leaves, long pendent stems, and exhibited floral meristem defects whereby flowers had enlarged organs, altered organ numbers, or sporadically failed to develop and were replaced by filamentous structures.

The similarity between the phenotype of KOG438 and that described for *revoluta* raised the
30 possibility that the two genes were allelic. This possibility was strengthened by the fact that the *rev* mutation mapped to a region of chromosome 5 close to MUP 24 (Talbert et al. (1995) *supra*). To examine this, we obtained mutants homozygous for the *rev-1* and *rev-1011* alleles (kindly supplied by E. Meyerowitz) and compared their phenotype to the KOG438 mutant. The features of these mutants were very similar to those of KOG438. The most prominent characteristic of these mutants was a reduction in
35 branching in the inflorescence. Populations of *rev-1*, KOG438, *rev-1011*, and wild type (Col) plants were grown under continuous light conditions and the inflorescences examined at approximately 5 weeks after sowing. The structures present in axils of the cauline leaves on the primary shoot and the cauline leaves

on secondary shoots (i.e. paraclades borne by the primary shoot) were noted (Table 10). Cauline leaf axils either contained a leaf, a shoot or were empty. The total number of visible shoots on the entire plant was also recorded.

5 TABLE 10. Structures present in axils of the cauline leaves on the primary shoot and the cauline leaves on secondary shoot of G438 overexpressors

Wild type Columbia (12 plants scored at approx. 5 weeks from sowing)

primary cauline (26 on 12 plants)

100% contained shoots

0% contained leaves

0% empty

secondary cauline (60 on 12 plants):

95% contained shoots

0% contained leaves

5% empty

Mean total number of visible shoots = 45 +/- 8

rev-1 (14 plants scored at approx. 5 weeks from sowing)

primary cauline (32 on 14 plants)

25% contained shoots

3% contained leaves

72% empty

secondary cauline (24 on 14 plants):

0% contained shoots

0% contained leaves

100% empty

10

Mean total number of visible shoots = 3.5 +/- 0.8

rev-1011 (6 plants scored at approx. 5 weeks from sowing)

primary cauline (10 on 6 plants)

10% contained shoots

20% contained leaves

70% empty

secondary cauline (2 on 6 plants):

0% contained shoots

0% contained leaves

100% empty

15

Mean total number of visible shoots = 2.2 +/- 1.2

KO438 (27 plants scored at approx. 5 weeks from sowing)

primary cauline (38 on 27 plants)

71% contained shoots

3% contained leaves

26% empty

secondary cauline (55 on 27 plants):

4% contained shoots

4% contained leaves

92% empty

20 Mean total number of visible shoots = 3.4 +/- 0.6

We concluded that *rev-1*, *rev-1011*, and KO438 plants all exhibited a severe reduction in the development of secondary and higher order shoots compared to wild type at this flowering stage. *Rev-1* and *rev-1011* had a slightly stronger phenotype than KO438 based on the number of cauline leaves bearing shoots. The *rev-1* and *rev-1011* alleles had been isolated in a Nossen background. A batch of *rev-1* were therefore grown alongside wild-type Nossen in continuous light conditions. The wild-type Nossen plants were noted to develop a similar architecture to the wild type Columbia plants in the previous experiment. The plants were examined at approximately 10 weeks after sowing in this second experiment. At this time *rev-1* plants had 9.7 +/- 1.6 and Nossen wild type had 55 +/- 5 visible shoots.

The additional shoots on the *rev-1* plants at 10 weeks compared to 5 weeks were mainly axillary shoots that had grown out from the basal rosette. Only 2/61 of these rosette inflorescences had any side shoots.

To check whether G438 was the *REV* gene we isolated the G438 sequence from *rev-1*, *rev-1011*, wild type Columbia and wild type Nossen. The G438 sequence from *rev-1* and *rev-1011* were found to be identical, indicating that both were the same allele! These sequences exhibited eight single-base changes compared to that from wild type Nossen (and 9 differences compared to wild type Columbia, due to a single base polymorphism between Nossen and Columbia in the 5th intron). Of these eight changes, one was upstream of the putative start codon, four were present in putative introns, and two were present in the 3' UTR. The final change was a G to A substitution predicted to disrupt the splice site at the junction between the eleventh intron and the twelfth exon. To confirm the intron-exon boundaries, the G438 cDNA sequence was isolated by PCR from cDNA derived from a mixture of tissues. The gene consisted of 18 exons, which were predicted to encode an 842 amino acid homeodomain leucine-zipper protein. The splice-site mutation in G438 from *rev-1* was expected to prevent removal of the eleventh intron, resulting in an aberrant transcript.

The above result strongly suggested that G438 was *REV* gene. We therefore performed a genetic complementation test and crossed homozygotes for the KOG438 with *rev-1* and *rev-1011* homozygotes, and wild type plants. All 20 F1 plants from the cross to wild type had a wild-type phenotype. Twenty F1 plants from the KOG438 x *rev-1* population and 20 F1 plants from the KOG438 x *rev-1011* population all exhibited a *revoluta* phenotype. These data confirmed that G438 was the *REV* gene.

The T-DNA collection from which KOG438 was derived contained a GUS reporter gene construct. We stained heterozygous KOG438 plants with GUS to see whether a tissue specific expression pattern for G438 would be revealed. GUS staining was not noted in wild type controls at any stage. In seedlings containing KOG438, no staining was seen before 3 days after sowing. From 5-8 days after sowing, strong staining was visible in the axils of rosette leaves in positions where secondary shoots were developing. Strong expression was not noted in the primary apex. These expression patterns correlate well with the enhanced deficiencies in axillary shoot development (compared to the primary shoot) in the *rev* mutant. It is possible that there is an increased requirement for *REV* in axillary shoots (compared to the primary) to ensure their proper initiation and outgrowth. GUS staining was also noted in the vascular tissue, roots (but not root tips), and in the stigmata and pedicels of flowers. (To verify that GUS staining was due to the T-DNA inserted in G438 and not some other background T-DNA, selfed seed was collected from F1 plants in the KOG438 x wt population. In the F2 population, 48 plants were resistant and 17 were sensitive to kanamycin. This 3:1 segregation suggested that the T-DNA was inserted at a single locus, i.e. within G438).

Shortly after we isolated the *REV* gene, the cloning of *INTERFASCICULAR FIBERLESS1 (IFL1)* was reported (Zhong et al. (1999) *supra*). *IFL1* was found to be the same gene as *REV*, but had been studied independently and under a different name (Ratcliffe et al. (2000) *supra*). The salient feature of the *ifl1* mutant was an absence of lignified interfascicular fiber cells in the stem (although it was noted to

have features such as enlarged curled leaves). In wild type, these cells can be visualized by phloroglucinol staining, but are absent from the mutant (Zhong et al. (1997) *supra*). To examine whether these cells were absent, stem sections were cut from *revoluta* plants (F1 from the KOG438 x *rev-1* and KOG438 x *rev-1011* crosses) and wild type plants and stained with phloroglucinol. Lignified interfascicular fiber cells could be seen stained purple in the wild type but were absent from the *revoluta* mutants, confirming that *rev* has an *ifl1* phenotype.

The finding that *IFL1* is *REVOLUTA* might help explain the deficiencies in fiber differentiation in the mutant. Lignified fiber cells are essential in providing support for the plant stem, and are thought to develop in response to the polar auxin flow which originates at the shoot tips (Aloni (1987) *supra*; Zhong (1999) *supra*). *IFL1* was proposed to act either by regulating polar auxin flow or by regulating the genes involved in the transduction of hormonal signals that trigger fiber differentiation. *REVOLUTA* is considered to be essential for apical meristem development. Since the auxin stream that induces fiber differentiation derives from shoots, it seems reasonable to suggest that defects in shoot meristem development would alter the polar auxin flow, and as a consequence, influence fiber differentiation. Thus, the interfascicular fiber-less phenotype of the *rev* mutant may be an indirect effect of the apical meristem deficiencies.

The precise role of *REV* still remains elusive. It has been suggested that *REV* promotes the growth of apical meristems (including floral meristems) at the expense of non-apical (cambial) meristems (Talbert et al. (1995) *supra*). It is not yet clear, however, whether expression data supports such a role: strong expression of *REV* has been detected in interfascicular regions and developing vascular tissue, but detailed in-situ expression analysis of apical meristems has not yet been reported (Zhong et al. (1999) *supra*). *REV* is a group III HD-ZIP protein and shares high sequence similarity (and organization) with the proteins encoded by three other *Arabidopsis* genes being studied: G392 (*Athb8*), G390 (*Athb9*), and G391 (*Athb14*) (Sessa et al. (1998) *supra*). It is possible, therefore, that these genes act together in the same developmental process. Supporting this suggestion, *Athb8* has a similar expression pattern to *REV* and is transcribed in the procambial regions of vascular bundles (Baima et al. (1995) *supra*). Thus, to gain a full understanding of *REV* function and its contribution to plant architecture, it will be necessary to study the gene in conjunction with the other homologs. To further this aim we are now studying G438 alongside G392. A homozygous population of KOG392 plants has recently been obtained. The KOG392 plants display a wild-type morphology and exhibit a wild-type staining pattern with phloroglucinol. Crosses are now being made to obtain the KOG438;KOG392 double mutant. We are also in the process of producing overexpressors for G438 and G392. It is hoped that these studies will provide a greater understanding of the function of G438 and thereby allow us to engineer plants with a modified stem lignin content or altered patterns of branching.

RT-PCR analyses detected G438 expression at medium to high levels in all tissues and conditions tested. Further expression analysis was possible, however, since the T-DNA insertion contained an enhancer trap construct (Campisi et al. (1999) *supra*). GUS staining could therefore be used

to reveal the expression pattern of genes within which insertions occurred. GUS staining of seedlings homozygous and heterozygous for the G438 T-DNA insertion revealed very strong expression within axillary shoots. This expression data has not yet been confirmed by other methods, but correlates with the marked effects of the rev mutation on outgrowth of higher order shoots.

5 Utilities

The mutant phenotypes indicate that REV/IFL1 has an important role in determining overall plant architecture and the distribution of lignified fiber cells within the stem. A number of utilities can be envisaged based upon these functions.

(1) Modification of lignin composition

10 Modifying the activity of REVOLUTA orthologs from tree species could offer the potential for modulating lignin content. This might allow the quality of wood used for furniture or construction to be improved.

(2) Modification of plant architecture

In *Arabidopsis*, reduced REV activity results in a reduction of higher-order shoot development.
15 Reducing activity of REV orthologs might generate trees that lack side branches, and have fewer knots in the wood.

G485 (SEQ ID NO: 105)

Published Information

20 G485 is a member of the Hap3-like subfamily of CCAAT-box binding transcription factors. G485 corresponds to gene At4g14540, annotated by the *Arabidopsis* Genome Initiative. The gene corresponds to sequence 1042 from Patent Application WO0216655 on stress-regulated genes, transgenic plants and methods of use, in which G485 was reported to be cold responsive in a microarray analysis (Harper et al. (2002) Patent Application WO0216655). No information is available about the function(s)
25 of G485.

Experimental Observations

RT-PCR analyses of the endogenous levels of G485 indicated that this gene is expressed in all tissues and under all conditions tested. Homozygotes for a T-DNA insertion allele of G485 flowered several days later than control plants. G485 was then overexpressed, and gain of function and loss of
30 function studies on G485 revealed opposite effects on flowering time. Under conditions of continuous light, approximately half of the 35S::G485 primary transformants flowered distinctly up to a week earlier than wild-type controls. These effects were observed in each of two independent T1 plantings derived from separate transformation dates. These studies indicate that G485 acts as a floral activator and is also necessary in that role within the plant.

35

Utilities

Based on the loss of function and gain of function phenotypes, G485 or its orthologs could be used to modify flowering time.

5 The delayed flowering displayed by G485 knockouts indicated that the gene or its orthologs might be used to manipulate the flowering time of commercial species. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases.

The early flowering effects seen in the G485 overexpressors could be applied to accelerate flowering, or eliminate any requirement for vernalization.

10 **G581 (SEQ ID NO: 115)**Published Information

G581 was first identified as *Atmyc1* by Urao et al. (1996) *Plant Mol. Biol.* 32: 571-576. It has been shown that its transcripts were more abundant in developing seeds than in stems and leaves. G581 contains a Sph box (CATGCATG) in its promoter region that is known as a cis-regulatory element
15 conferring seed-specific expression. No other information regarding G581 function is available in the literature.

Experimental Observations

Using an RT-PCR-based approach, it was determined that G581 was uniformly expressed in all tissues tested, and the expression level was unchanged by all of the environmental conditions or
20 pathogens infections tested.

The function of G581 was first studied by knockout analysis. Homozygous plants containing a T-DNA insertion within the first half of the G581 coding region displayed wild-type morphology at all developmental stages. Furthermore, G581 knockout mutant plants behaved similarly to wild type in all physiological and biochemical assays performed.

25 The function of G581 was also assessed by analysis of transgenic *Arabidopsis* lines in which the cDNA was constitutively expressed from the 35S CaMV promoter. Overexpression of G581 resulted in plants with alterations in seed coloration, and a mild delay in the onset of flowering. Seeds from 35S::G581 transgenic lines were pale and larger compared to wild-type controls. In addition, G581 overexpressing lines germinated better on plates containing low nitrogen or plates with low nitrogen
30 supplemented with glutamine. Under such conditions, seedlings also had less measurable anthocyanin accumulation when compared to wild-type controls.

Utilities

The enhanced growth of G581 overexpression lines under low nitrogen conditions indicate that the gene could be used to engineer crops that could thrive under conditions of reduced nitrogen
35 availability.

G581 could be used to alter anthocyanin production or accumulation. This could enhance the health benefits of foodstuffs, could be used to alter pigment production for horticultural purposes, or possibly increase resistance to a variety of stresses.

5 Additionally, the delayed flowering displayed by 35S::G581 transformants indicates that the gene might be used to manipulate the flowering time of commercial species. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases.

Given the effects of G581 overexpression, it is likely that the activity of the gene (or its orthologs) could also be modified to accelerate flowering, or eliminate any requirement for vernalization.

10 Finally, the changes in size and coloration shown by 35S::G581 seeds indicate that the gene might be used to enhance seed traits or yield.

G624 (SEQ ID NO: 119 and SEQ ID NO: 2105)

Published Information

15 G624 was identified in the sequence of BAC F18E5, GenBank accession number AL022603, released by the *Arabidopsis* Genome Initiative.

Experimental Observations

20 Overexpression of G624 produced a moderate delay in the onset of flowering (approximately one week under continuous light conditions). A number of the late flowering 35S::G624 transformants also displayed a marked increase in vegetative biomass compared to controls. No altered phenotypes were detected in any of the physiological assays.

Intriguingly, overexpression lines containing a truncated form of the cDNA (SEQ ID NO: 2105) exhibited wild-type morphology but displayed enhanced tolerance to both high sodium chloride and low phosphate growth conditions. It is possible that this effect represents a dominant negative phenotype.

Utilities

25 The delayed flowering displayed by 35S::G624 transformants indicated that the gene or its equivalents might be used to manipulate the flowering time of commercial species. In particular, an extension of vegetative growth or an increase in leaf size can significantly increase biomass and result in substantial yield increases.

30 Based on the increased salt tolerance exhibited by the 35S::G624 lines in physiology assays, this gene or its equivalents might be used to engineer salt tolerant crops and trees that can flourish in salinified soils, or under drought conditions.

The response of 35S::G624 seedlings to low phosphate conditions indicated that the gene or its equivalents could be used to manipulate nutrient uptake or the ability to grow in poor nutrient soils.

35

G627 (SEQ ID NO: 121)Published Information

G627 corresponds to AGAMOUS-LIKE 19 (AGL19) which was isolated by Alvarez-Buylla et al. (2000) *Plant J.* 24: 457-466. No genetic characterization of AGL19 has been reported, but it was
5 found to be specifically expressed in the outer layers of the root meristem (lateral root cap and epidermis) and in the central cylinder cells of mature roots (Alvarez-Buylla et al. (2000), *supra*).

Experimental Observations

RT-PCR expression studies failed to detect G627 in any of the tissue types analyzed. This result partially agrees with the data of Alvarez-Buylla et al. (2000), *supra*, who found that the gene is
10 expressed only in specific regions of the root. It is possible that such regions were not sufficiently represented, for G627 transcript to be detected in the whole root samples analyzed in expression studies. In later experiments, however, a G627 clone was isolated by high cycle PCR from a cDNA sample derived from mixed tissues, and transgenic lines were generated in which this clone was expressed from a 35S promoter.

15 A substantial proportion of the 35S::G627 lines flowered markedly earlier than control plants. Such effects were observed in both the T1 and T2 generations and indicate that the gene plays a role in the regulation of flowering time.

Utilities

Given the early flowering seen amongst the 35S::G627 transformants, the gene or its orthologs
20 may be used to manipulate the flowering time of commercial species. In particular, G627 could be used to accelerate flowering, or eliminate any requirement for vernalization.

G651 (SEQ ID NO: 125 and SEQ ID NO: 2106)Published Information

25 G651 was identified in the sequence of BAC T7I23, GenBank accession number U89959, released by the *Arabidopsis* Genome Initiative. There is no other published or public information about G651.

Experimental Observations

The function of G651 was studied using transgenic plants in which the gene was expressed under
30 the control of the 35S promoter. Two clones were used to determine the function of G651. One clone, P15159, contained no errors compared with the publicly annotated sequence. Another clone, P2812, lacked a glutamic acid residue at position 203 and was 3' truncated, lacking the final 8 amino acids (SEQ ID NO: 2106). The conserved domains were present in both clones.

Equivalent morphological effects were observed in 35S::G651 lines containing either of the
35 different overexpression constructs. Overexpression of G651 produced a number of alterations in *Arabidopsis* growth and development, including changes in leaf morphology, overall size, growth rate,

and fertility. Leaves of 35S::G651 plants had a dark grayish appearance, were often contorted and had an abnormal undulated surface texture. It is possible that such features could reflect changes in leaf cuticle composition/deposition or alterations in the histology of the epidermis. 35S::G651 lines were generally small, slow developing, displayed retarded inflorescence outgrowth, and often had poorly developed flowers with multiple non-specific abnormalities.

G651 (P15159) overexpressing lines behave similarly to the wild-type controls in all physiological assays performed. However, in general, overexpression of G651 caused deleterious effects on plant growth. G651 seedlings were small and vitrified. One line also accumulated anthocyanins. G651 (P2812, comprising SEQ ID NO: 2106) overexpressing lines showed an additional effect and exhibited increased sensitivity to cold stress in a germination assay. Furthermore, 35S::G651 lines harboring P2812 displayed little or no secondary root growth.

Utilities

Depending on the basis of the color change seen in 35S::G651 lines, a number of applications could be envisaged. If the phenotype is due to loosening of epidermal cell layers, the gene or its equivalents might be used to produce fruits, vegetables, and other plant products that can be more easily peeled. If the effects are due to changes in wax composition/accumulation, G651 or its equivalents might be used to afford protection against pests or abiotic stresses such as drought. If, however, the phenotype is due to changes in pigment levels within the leaf, the gene or its equivalents might be applied to alter photosynthetic capacity and yield.

The changes in root development seen in 35S::G651 lines indicated that the gene or its equivalents could be used to manipulate root growth and thereby influence the uptake of water and nutrients.

The altered response to cold germination assays indicated that the gene or its equivalents might be applied to modify abiotic stress responses.

G652 (SEQ ID NO: 127)

Published Information

G652 (At1g14580) was identified in the sequence of BAC T5E21, GenBank accession number AC010657, released by the *Arabidopsis* Genome Initiative based on its sequence similarity within the conserved domain to other Zinc CLDSH related proteins in *Arabidopsis*.

G652 was described in the literature as atGRP2 (de Oliveira et al. (1990) *Plant Cell* 2: 427-436). The authors describe atGRP2 as being rich in glycine and not induced by ethylene, abscisic acid, salicylic acid, water stress or drought. Kingsley and Palis (1994) *Plant Cell* 6: 1522-1523) noted that atGRP2 contains a cold shock domain and two zinc fingers.

Closely Related Genes from Other Species

G652 is glycine rich and shares homology with other GRP proteins found in plants in addition to the cold shock domain and zinc finger domain.

Experimental Observations

G652 appears to be constitutively expressed at medium levels in all tissues and environmental conditions tested as determined by RT-PCR analysis. Expression of G652 was not detected in other tissues. A line homozygous for a T-DNA insertion in G652 was used to determine the function of this gene. The T-DNA insertion of G652 is approximately 75% into the coding sequence of the gene and therefore is likely to result in a null mutation. Plants homozygous for a T-DNA insertions within G652 displayed a spectrum of developmental abnormalities, particularly at the early seedling stage. These phenotypes were variable within the population suggesting that other factors might be influencing the penetrance of the phenotype. For example, seedlings were small and filled with anthocyanins. Almost all the seedlings had defects in cotyledons ranging from unusual shape to fusions. Many seedlings did not survive. Those that did grew slowly. Fertility was reduced compared to controls, senescence delayed, and siliques were often rather short. The reason for this poor fertility was unclear. Many flowers had a reduced number of stamens (4-5 of these organs rather than 6). Interestingly, the absent stamen(s) were usually one or both of the shorter pair. Seeds produced by knockouts of G652 plants were somewhat wrinkled and misshapen.

The G652 knockout line had a reproducible increase in the leaf glucosinolate M39480. It also showed a reproducible increase in seed alpha-tocopherol. A decrease in seed oil as measured by NIR was also observed, but the values were slightly above the cutoff value for statistical significance.

The function of G652 was also studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G652 resulted in plants that were small and slow developing. Many plants died at an early stage of growth. The two lines that were morphologically examined in the T2 generation were small and showed premature senescence of rosette leaves.

Utilities

G652 could be used to manipulate seed tocopherol composition and seed structure and to alter glucosinolate composition in leaves. Tocopherols have anti-oxidant and vitamin E activity. Increases or decreases in specific glucosinolates or total glucosinolate content might be desirable depending upon the particular application. For example: (1) Glucosinolates are undesirable components of the oilseeds used in animal feed, since they produce toxic effects. Low-glucosinolate varieties of canola have been developed to combat this problem. (2) Some glucosinolates have anti-cancer activity; thus, increasing the levels or composition of these compounds might be of interest from a nutraceutical standpoint. (3) Glucosinolates form part of a plants natural defense against insects. Modification of glucosinolate composition or quantity could therefore afford increased protection from predators. Furthermore, in edible crops, tissue specific promoters might be used to ensure that these compounds accumulate specifically in tissues, such as the epidermis, which are not taken for consumption.

Based on the overexpression data, G652 could be used to manipulate plant growth and development. In particular, the accelerated senescence of the 35S::G652 lines indicates that the gene could be used to modify disease responses, or alter the rate of senescence in crops.

5 **G807 (SEQ ID NO: 141)**

Published Information

The heat shock transcription factor G807 is referred to in the public literature as the *Arabidopsis* HSF3, a class-A HSF characterized by an extended HR-A/B oligomerization domain (Nover et al. (1996) *Cell Stress* 1:215-223). G807 is found in the sequence of the chromosome 5 BAC clone F5E19
10 (GenBank accession number AL391147.1; nid=9755718), released by the *Arabidopsis* Genome Initiative. The translation start and stop codons were incorrectly predicted in the BAC annotation. Overexpression of the *Arabidopsis* HSF3 or HSF3-GUS fusion protein results in the constitutive expression of the heat shock proteins and in an increase in the basal thermotolerance in transgenic plants (Prandl et al. (1998) *Mol. Gen. Genet.* 258: 269-278).

15 Experimental Observations

RT-PCR analysis of the endogenous level of G807 transcripts revealed a moderate but constitutive level in all tissue examined. G807 transcript level increased moderately upon heat shock and auxin treatment, but decreased below detectable level following salt treatment. Analysis of a G807 null
20 mutant reveals no apparent morphological, physiological or biochemical changes when compared to control plants.

The function of G807 was analyzed through its ectopic overexpression in *Arabidopsis*. A number of beneficial phenotypes were observed in the transgenic 35S::G807 overexpressor lines that have not been previously reported in the scientific literature. The seedling vigor was generally improved in primary T1 transformants and in the T2 progenies. Seedlings germinated on agar-MS plate under 12 hr
25 light were reproducibly larger and showed longer hypocotyl than control plants. This phenotype was highly penetrant. The long petiole effect was observed in the primary transformants but was not apparent in any of the T2 progenies characterized.

Physiological analysis of 35S::G807 overexpressor lines revealed increased seedling vigor in a cold germination assay (MS-agar, 8° C, 3-15 days). Germinated seedlings were generally larger and
30 accumulated less anthocyanin than control plants treated under the same conditions. This phenotype was observed in a primary screen using a mixed line population, as well as in repeated treatment with individual lines.

Utilities

Based on published data, G807 might be used to improve heat tolerance.
35 From the experimental studies performed by us, a number of other potential applications are apparent:

- (1) G807 could be used to confer chilling tolerance

The growth of many crops is very sensitive to cool temperatures. A gene that enhances growth under chilling conditions could result in enhanced yields. For example, chilling may lead to yield losses and lower product quality through the delayed ripening of maize. Photoinhibition of photosynthesis (disruption of photosynthesis due to high light intensities) often occurs under clear atmospheric conditions subsequent to cold late summer/autumn nights. Another consequence of poor growth is the rather poor ground cover of maize fields in spring, often resulting in soil erosion, increased occurrence of weeds, and reduced uptake of nutrients. A retarded uptake of mineral nitrogen could lead to increased losses of nitrate into the ground water. Enhanced chilling tolerance could also extend the effective growth range of chilling sensitive crop species by allowing earlier planting or later harvest.

Chilling tolerance could also serve as a model for understanding how plants adapt to water deficit. Both chilling and water stress share similar signal transduction pathways and tolerance/adaptation mechanisms. For example, acclimation to chilling temperatures can be induced by water stress or treatment with abscisic acid. Genes induced by low temperature include dehydrins (or LEA proteins). Dehydrins are also induced by salinity, abscisic acid, water stress and during the late stages of embryogenesis.

Another large impact of chilling occurs during post-harvest storage. For example, some fruits and vegetables do not store well at low temperatures (for example, bananas, avocados, melons, and tomatoes). The normal ripening process of the tomato is impaired if it is exposed to cool temperatures. Genes conferring resistance to chilling temperatures may enhance tolerance during post-harvest storage.

(2) G807 could be used to accelerate seedling growth, and thereby allow a crop to become established faster. This would minimize exposure to stress conditions at early stages of growth, when the plants are most sensitive. Additionally, it might allow a crop to become grow faster than competing weed species.

(3) G807 might be used to manipulate light responses such as shade avoidance.

G839 (SEQ ID NO: 145)

Published Information

G839 was identified by amino acid sequence similarity to plant and mammalian ankyrin-repeat proteins. G839 is found in the sequence of the chromosome 5, TAC clone: K17O22 (GenBank accession number AB019224.1, nid=3869063), released by the *Arabidopsis* Genome Initiative. G839 has no other distinctive feature besides the presence of a 33-AA repeated ankyrin element known for protein-protein interaction, in the C-terminus of the predicted protein.

The G839 product is closely related to NPR1, a gene that controls the onset of systemic acquired resistance in plant (Cao et al. (1997) *Cell* 88:57-63; Cao et al. (1998) *Proc. Natl. Acad. Sci.* 95: 6531-6536). However, no information related to the functional characterization of G839 is currently available from the public literature.

Experimental Observations

RT-PCR studies revealed that G839 is expressed throughout the plant, with the lowest levels in germinating seedlings.

The function of G839 was analyzed through its ectopic overexpression in *Arabidopsis*;
5 35S::G839 lines displayed a delay in the onset of flowering (1-7 days), but were otherwise morphologically similar to wild-type control plants. In addition, 35S::G839 lines showed increased vigor and had more secondary root growth than controls when grown on plates containing low nitrogen.

Utilities

Nitrogen is the major nutrient affecting plant growth and development that ultimately impacts
10 yield and stress tolerance. Plants of the G839 overexpressing lines grown under low nitrogen conditions were larger, showed enhanced primary and secondary root growth, and less chlorosis compared to the control plants. In some cases, twice as much root and shoot biomass was observed in the G839 transgenics plants when compared to a comparable wild-type plant, indicating that the gene or its orthologs could be used to engineer crops that could thrive under conditions of reduced nitrogen
15 availability.

The delayed flowering in 35S::G839 lines indicated that the gene or its orthologs can manipulate flowering time. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases.

20 **G916 (SEQ ID NO: 153)**

Published Information

G916 corresponds to gene At4g04450, and it has also been described as WRKY42. No information is available about the function(s) of G916.

Experimental Observations

25 The complete cDNA sequence of G916 was experimentally determined. G916 appears to be expressed at low levels in a range of tissues, and was not significantly induced by any of the conditions tested.

A T-DNA insertion mutant for G916, displayed wild-type morphology. Overexpression of G916 produced a wide spectrum of developmental abnormalities in *Arabidopsis*. Many of the 35S::G916
30 seedlings were extremely tiny and showed an apparent lack of shoot organization. Such plants arrested growth and died at very early stages. Other individuals were small and displayed disproportionately long hypocotyls and narrow cotyledons. At later stages, the majority of surviving lines were markedly smaller than wild type, and formed rather weedy inflorescence stems that yielded very few flowers. Additionally, flowers often had poorly developed organs.

35 In addition, G916 overexpressing lines were larger than control wild-type seedlings in several germination assays. Larger seedlings were observed under conditions of high sucrose. In addition, 35S::G916 seedlings were larger and appeared to have less anthocyanin on high sucrose plates that were

nitrogen deficient, with or without glutamine supplementation. The assays monitor the effect of C on N signaling through anthocyanin production. That 35S::G916 seedlings perform better under conditions of high sucrose alone makes it more difficult to interpret the better seedling performance under conditions of low nitrogen. Tissue specific or inducible expression of this gene could aid in sorting out the complex phenotypes caused by the constitutive overexpression of this gene.

G916 is related to two other WRKY genes, G184 and G186. Members of this clade could have redundant function in *Arabidopsis*. Overexpression of G184 caused a variety of morphological alterations, similar to those of the 35S::G916 seedlings. Similar to the G916 KO mutant, G186 single knockout mutant plants did not show phenotypic alterations in the analyses performed.

10 Utilities

The enhanced performance of G916 overexpression lines under low nitrogen conditions indicate that the gene could be used to engineer crops that could thrive under conditions of reduced nitrogen availability.

That 35S::G916 lines make less anthocyanin on high sucrose plus glutamine, indicates G916 might be used to modify carbon and nitrogen status, and hence assimilate partitioning.

The results of physiological assays indicate that G916 could be used to alter the sugar signaling in plants. In addition to their important role as an energy source and structural component of the plant cell, sugars are central regulatory molecules that control several aspects of plant physiology, metabolism and development. It is thought that this control is achieved by regulating gene expression and, in higher plants, sugars have been shown to repress or activate plant genes involved in many essential processes such as photosynthesis, glyoxylate metabolism, respiration, starch and sucrose synthesis and degradation, pathogen response, wounding response, cell cycle regulation, pigmentation, flowering and senescence. The mechanisms by which sugars control gene expression are not understood.

Because sugars are important signaling molecules, the ability to control either the concentration of a signaling sugar or how the plant perceives or responds to a signaling sugar could be used to control plant development, physiology or metabolism. For example, the flux of sucrose (a sugar used for systemically transporting carbon and energy in most plants) has been shown to affect gene expression and alter storage compound accumulation in seeds. Manipulation of the sucrose signaling pathway in seeds may therefore cause seeds to have more protein, oil or carbohydrate, depending on the type of manipulation. Similarly, in tubers, sucrose is converted to starch that is used as an energy store. It is thought that sugar-signaling pathways may partially determine the levels of starch synthesized in the tubers. The manipulation of sugar signaling in tubers could lead to tubers with higher starch content.

Thus, manipulating the sugar signal transduction pathway may lead to altered gene expression to produce plants with desirable traits. In particular, manipulation of sugar signal transduction pathways could be used to alter source-sink relationships in seeds, tubers, roots and other storage organs leading to increase in yield.

Additionally, the morphological phenotypes shown by 35S::G916 seedlings indicate that the gene might be used to manipulate light responses such as shade avoidance.

G926 (SEQ ID NO: 155)

5 Published Information

G926 is equivalent to Hap2a (Y13720), a member of the CCAAT-box binding transcription factor family. The gene was identified by Edwards et al. ((1998) *Plant Physiol.* 117: 1015-1022). They showed that G926 or AtHap2a was able to functionally complement a Hap2 deficient mutant of yeast indicating that there is functional conservation between these proteins from diverse organisms. In addition, the AtHap2a gene was shown to be ubiquitously expressed in *Arabidopsis*. No functional information, however, was published for this gene.

Closely Related Genes from Other Species

G926 is most closely related to a *Brassica napus* protein (AAC49265). Similarity between the two proteins extends beyond the signature motif of the family to a level that would indicate the genes are orthologous. No functional information is available for the *Brassica napus* protein.

Experimental Observations

Consistent with the published expression pattern (Edwards et al. (1998) *supra*), G926 was determined to be ubiquitously expressed and transcript levels appeared to be unaltered by any environmental stress-related condition tested. A line homozygous for a T-DNA insertion in G926 was used to determine the function of this gene.

The G926 knockout mutant line was morphologically wild-type. Physiological analysis revealed that in the presumed absence of G926 function, the plants became more tolerant to high osmotic conditions during germination. This osmotic stress tolerance could be related to the plant's apparent insensitivity to the growth hormone ABA. This was the second instance where a member of a CCAAT-box protein complex altered the plants osmotic stress response and ABA sensitivity during germination. G926 and G1820 may function as part of the same complex or as part of the same or parallel signal transduction pathways.

G926 overexpressing plants were significantly greener and larger than wild-type control plants in a soil-based drought assay.

ABA plays an important regulatory role in the initiation and maintenance of seed dormancy. Lopez-Molina, L. et al. ((2001)) *Proc. Natl. Acad. Sci. U. S. A.* 98:4782-4787) described a bZIP transcription factor, ABI5, that is involved in maintaining seeds in a quiescent state, preventing germination under adverse conditions such as drought stress. It is possible G926 also functions as part of this checkpoint for the germinating seeds and loss of G926 function promotes germination regardless of the osmotic status of the environment.

Utilities

G926 or its equivalents could be used to improve plant tolerance to drought and salt stress.

G961 (SEQ ID NO: 159)Published Information

G961 was first identified in the sequence of the BAC clone F19D11, GenBank accession number
5 AC005310, released by the *Arabidopsis* Genome Initiative.

Closely Related Genes from Other Species

A rice gene, GenBank accession number BAA84803, appears to be a gene that is related to
10 G961.

Experimental Observations, knockout plants

The function of this gene was analyzed by knockout analysis. Homozygotes for a T-DNA
insertion within G961 exhibited comparable morphology to wild type controls. However, these plants
had altered seed oil content.

15

Experimental Observations, overexpressors

Gene expression profiling by RT-PCR shows that G961 is primarily expressed in shoots,
embryos and siliques at medium levels, and at low levels in flowers. RT-PCR data also indicates an
induction of G961 transcript accumulation upon heat treatment.

20

35S::G961 *Arabidopsis* lines were generated, with which it was determined that overexpression
of G961 produced marked changes in fertility and seed morphology. 35S::G961 transformants appeared
wild-type at early stages of development, but following the switch to flowering, the majority of lines
exhibited very poor fertility. Seeds from these plants frequently aborted and failed to mature. As a result
of such deficiencies, the majority of the lines yielded very few seeds. The seeds that were obtained
25 exhibited some striking differences in morphology compared to wild type controls; seed coloration was
dark and white patches were visible on the seed coat, particularly at the tip near the micropyle. In some
instances, it appeared as though the seeds might be germinating precociously. Aside from the poor
germination efficiency observed for one of the G961 transgenic lines, no consistent differences were
observed between G961 transgenics and the controls in the physiology assays.

30

Utilities

Based on the knock-out and overexpression phenotypes, G961 or its equivalents might be used to
manipulate oil and protein content of seeds. In particular, the changes in morphology and coloration
shown by 35S::G961 seeds indicated that the gene or its equivalents might be used to enhance seed traits
35 or yield.

G975 (SEQ ID NO: 161)

Published Information

After its discovery by us, G975 has appeared in the sequences released by the *Arabidopsis* Genome Initiative (BAC F9L1, GenBank accession number AC007591).

Closely Related Genes from Other Species

The non-*Arabidopsis* gene most highly related to G975 (as detected in BLAST searches, 11-5-99) is represented by L46408 BNAF1258 Mustard flower buds *Brassica rapa* cDNA clone F1258. The similarity between G975 and the *Brassica rapa* gene represented by EST L46408 extends beyond the conserved AP2 domain that characterizes the AP2/EREBP family. In fact, this *Brassica rapa* gene appears to be more closely related to G975 than *Arabidopsis* G1387, indicating that EST L46408 may represent a true G975 ortholog. The similarity between G975 and *Arabidopsis* G1387 also extends beyond the conserved AP2 domain.

Experimental Observations

G975 was discovered by us and is a new member of the AP2/EREBP family (EREBP subfamily) of transcription factors. G975 is expressed in flowers and, at lower levels, in shoots, leaves, and siliques. GC-FID and GC-MS analyses of leaves from G975 overexpressing plants have shown that the levels of C29, C31, and C33 alkanes were substantially increased (up to 10-fold) compared to control plants. A number of additional compounds of similar molecular weight, presumably also wax components, also accumulated to significantly higher levels in G975 overexpressing plants. Although total amounts of wax in G975 overexpressing plants have not yet been measured, C29 alkanes constitute close to 50% of the wax content in wild-type plants (Millar et al. (1998) *Plant Cell* 11: 1889-1902), indicating that a major increase in total wax content occurs in these transgenic plants. However, the transgenic plants had an almost normal phenotype (small morphological differences are detected in leaf appearance), indicating that overexpression of G975 is not deleterious to the plant. It is noteworthy that overexpression of G975 did not cause the dramatic alterations in plant morphology that have been reported for *Arabidopsis* plants in which the FATTY ACID ELONGATION1 gene was overexpressed (Millar et al. (1998) *supra*). G975 could specifically regulate the expression of some of the genes involved in wax metabolism. One *Arabidopsis* AP2 gene was found that is significantly more closely related to G975 than the rest of the members of the AP2/EREBP family. This other gene, G1387, may have a function, and therefore a utility, related to that of G975.

Plants overexpressing G975 were significantly larger and greener than wild-type control plants in a soil-based drought assay.

Utilities

G975 or its equivalents could be used to improve a plant's tolerance to drought or low water conditions.

G975 or its equivalents could be used to manipulate wax composition, amount, or distribution, which in turn could modify plant tolerance to drought and/or low humidity or resistance to insects, as well as plant appearance (shiny leaves). A possible application for this gene or its equivalents might be in reducing the wax coating on sunflower seeds (the wax fouls the oil extraction system during sunflower seed processing for oil). For this purpose, antisense or co-suppression of the gene in a tissue specific manner might be useful.

G975 could also be used to specifically alter wax composition, amount, or distribution in those plants and crops from which wax is a valuable product.

G1011 (SEQ ID NO: 163)

Published Information

G1011 was identified in the sequence of P1 clone MTG10 (gene MTG10.20, GenBank accession number BAB10179.1). No information is available about the function(s) of G1011.

Experimental Observations

The complete cDNA sequence of G1011 was determined, and the initial BAC annotation in GenBank was found to be incorrect. The G1011 cDNA sequence has now been confirmed by a number of full-length cDNA sequences, which have recently been deposited in GenBank.

G1011 function was examined via analysis of a T-DNA insertion mutant for the gene. However, plants that were homozygous for this insertion displayed a wild-type phenotype in all assays performed. Additionally, RT-PCR studies on wild-type plants revealed G1011 expression to be ubiquitously expressed at low levels in a range of tissues.

We have now assessed the role of G1011 by analysis of transgenic *Arabidopsis* lines in which the gene was overexpressed. 35S::G1011 transformants appeared wild-type in the physiology assays, but did display a number of interesting developmental changes during the morphological assays. First, around half of the lines were markedly early flowering. Such effects were observed under either inductive (24-hour light) or non-inductive (12-hour light) photoperiodic conditions, indicating that G1011 might have a central role in determining the timing of the floral transition. Interestingly, under 12-hour light conditions, the lines also developed shorter, more rounded leaves than wild type, but this was not seen under continuous light.

As well as the effects on flowering time, many of the 35S::G1011 lines displayed alterations in flower morphology; floral organs often had alterations in shape or number and petals were rather narrow and green. In particular, it was noted that floral organ abscission was somewhat delayed compared to wild-type flowers, with stamens, petals, and sepals persisting following pollination. It is noteworthy that

Ferrandiz et al. ((2000) *Plant Cell* 12, 183-198) reported similar phenotypes as a result of overexpression of another MADS gene, AGL15.

Utilities

Based on the phenotypes observed in morphological assays, G1011 could have a number of applications.

Given its effects on the floral transition, G1011 might be used to manipulate the flowering time of commercial species. In particular, the gene could be use to accelerate flowering or to eliminate any requirement for vernalization.

The effects on flower morphology are also of commercial interest. G1011 might be used to modify flower development, in order to change form of flowers and fruits. This could create attractive new varieties or be used to influence pollination efficiency. The persistence of outer whorl organs following pollination is also of interest; such a trait could be applied to ornamental plants to prolong the life of blooms.

G1013 (SEQ ID NO: 165)

Published Information

G1013 (At5g43290) is a novel member of the WRKY family of transcription factors. No information is available about the function(s) of G1013.

Experimental Observations

RT-PCR analysis was used to look at the endogenous expression of G1013. Expression of the gene was only detected in floral tissues. It does not appear to be induced by any of the conditions tested.

Homozygous plants were analyzed for a T-DNA insertion within G1013 and found that they showed wild-type morphology at all developmental stages.

The effects of G1013 overexpression were studied. In an assay intended to determine whether the transgene expression could alter C:N sensing, 35S::G1013 seedlings contained less anthocyanins than wild-type controls grown on high sucrose/N- plates. Seedlings were also greener than the wild-type controls on high sucrose/N-/Gln plates. These data together indicate that overexpression of G1013 alters a plant's ability to modulate carbon and/or nitrogen uptake and utilization.

G1013 overexpression also had an effect on plant morphology. 35S::G1013 lines exhibited narrow downward curled leaves, which were sometimes held in a more upright orientation than those of wild type at early stages of growth. Plants from the two T2 lines grown under continuous light also flowered late. In addition to the effects on leaf shape, many lines were slightly smaller than controls, and a few showed sporadic defects in flower development.

Utilities

On the basis of the available analytical data, there are several potential applications for G1013:

(1) the gene or its orthologs could be used to alter plant leaf morphology;

(2) the observation that 35S::G1013 lines make less anthocyanin on high sucrose plus glutamine, indicated G1013 or its orthologs might be used to modify carbon and nitrogen status, and hence assimilate partitioning. The enhanced performance of G1013 overexpression lines under low nitrogen conditions indicate that the gene could be used to engineer crops that could thrive under conditions of reduced nitrogen availability.

(3) the promoter of G1013 could be used to drive floral specific expression *in planta*.

G1037 (SEQ ID NO: 171 and SEQ ID NO: 2108)

Published Information

G1037 was identified in the sequence of BAC MUJ8, GenBank accession number AB028621, released by the *Arabidopsis* Genome Initiative. G1037 has been named ARR12 (Hwang et al. (2002) *Plant Physiol.* 129: 500-515). G1037 was identified in the sequence of BAC F13D4, GenBank accession number AL031369, released by the *Arabidopsis* Genome Initiative. This BAC has since been removed from GenBank, and currently the genomic sequence is not present. G1037 corresponds to the TAIR locus AT2G25180. It is cited in the patent publication WO0216655 concerning stress-regulated genes (Harper et al. (2002)).

Closely Related Genes from Other Species

Several genes with strong similarity to G1037 are present in other species. The most closely related are a putative response regulator from maize (AB062095) and a *Brassica oleracea* gene represented by genomic clone BH007675. No further information is available about these genes.

Experimental Observations

G1037 is a member of the response regulator class of GARP proteins. G1037 was found to be expressed throughout the plant, with highest expression in roots. It may be induced by auxin, ABA, heat, salt, and salicylic acid treatments.

A line homozygous for a T-DNA insertion in G1037 was used to determine the function of this gene. The T-DNA insertion of G1037 was determined to be approximately one third of the way into the coding sequence of the gene, within the conserved GARP domain, and therefore was likely to result in a null mutation. Plants homozygous for the T-DNA insertion showed somewhat inconsistent changes in flowering time. In one experiment, two different populations of G1037 knockout plants were markedly early flowering. However, in a second experiment, only a proportion of the plants showed early flowering, and this phenotype was marginal. It is possible that the effects of a G1037 mutation on

flowering time are dependent on environmental conditions. No altered phenotypes of G1037 knockout plants were detected in any of the physiological or biochemical assays.

The function of this gene has also been analyzed using transgenic plants in which G1037 was expressed under the control of the 35S promoter. It should be noted that the clone contained sequence differences (SEQ ID NO: 2108) from the public BAC sequence (SEQ ID NO: 171). Two 35S::G1037 lines showed more tolerance to salt stress in a germination assay. All 35S::G1037 lines showed wild-type morphology.

Because several members of the response regulator class of GARP genes have been implicated in cytokinin signaling, it is possible that the improved seedling growth noted on salt results from changes in hormone response pathways.

Utilities

G1037 or its equivalents may be useful for alteration of flowering time in crop plants.

G1037 or its equivalents may be useful for engineering salt tolerance. The salt tolerance of G1037 seedlings may also indicate a general increase in tolerance to osmotic stress, indicating a potential use for G1037 or its equivalents in engineering drought tolerance.

G1128 (SEQ ID NO: 181)

Published Information

The sequence of G1128 was obtained from the *Arabidopsis* genome sequencing project, GenBank accession number AB018109, based on its sequence similarity within the conserved domain to other AT-Hook related proteins in *Arabidopsis*.

Experimental Observations

Gene expression profiling using RT/PCR shows that G1128 is predominantly expressed in roots and flowers. Its expression appears to be not induced by any treatments tested.

Previously, the function of this gene was studied by knockout analysis. Plants homozygous for a T-DNA insertion in G1128 were wild type for all assays performed. It should be pointed out that the functional knockout analysis for AT-Hook proteins has not provided useful information so far, as was the case for G280 and G1945. One of reasons could be that there is functional redundancy among some of AT-Hook proteins. In fact, G1128 protein shares a significant homology to one other AT-Hook protein G1399.

The function of G1128 was also studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1128 in *Arabidopsis* produced a wide range of morphological changes including stunted growth, and alterations in leaf and flower development. Analysis of G1128 overexpressors reveals no apparent physiological changes when compared to wild-type control plants.

Utilities

Based on the effects of G1128 overexpression, the gene could be used to manipulate plant growth and development. In particular, the accelerated senescence of the 35S::G1128 lines indicates that the gene could be used to modify disease responses, or alter the rate of senescence in crops. Additionally, if the dark coloration of 35S::G1128 lines reflects an increase in biochemical composition, the gene might be used to improve the nutraceutical value of foodstuffs, or increase photosynthetic capacity to improve yield.

10 G1142 (SEQ ID NO: 185)

Published Information

The sequence of G1142 was obtained from the *Arabidopsis* genome sequencing project (within clone T3K9, GenBank accession number AC004261), based on its sequence similarity within the conserved domain to other bHLH related proteins in *Arabidopsis*.

15

Experimental Observations

RT-PCR analysis indicated that G1142 is ubiquitously expressed. The function of this gene was first studied by knockout analysis. Homozygous plants carrying a T-DNA insertion in G1142 flowered slightly earlier than wild-type controls under continuous conditions light. This phenotype was observed in two independently grown populations of KO.G1142 plants. G1142 knock-out plants were otherwise identical to their wild-type counterparts in all physiological and biochemical assays.

20

The function of G1142 has now been assessed by analysis of transgenic *Arabidopsis* lines in which the cDNA was constitutively expressed from the 35S CaMV promoter. Under continuous light, 35S::G1142 transformants displayed narrow leaves and flowered approximately 5-7 days later than wild-type controls. However, G1142 overexpressing lines behaved similarly to the wild-type controls in all physiological assays performed.

25

Utilities

Based on the analysis of G1142 knock-out plants as well as 35S::G1142 transgenic lines, G1142 or its orthologs can be used to manipulate flowering time in commercial species.

30

The delayed flowering displayed by 35S::G1142 transformants indicated that the gene or its orthologs might be used to manipulate the flowering time of commercial species. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases.

35

Given the early flowering seen in the G1142 null mutant, it is likely that the activity of G1142 or its orthologs can accelerate flowering or eliminate any requirement for vernalization.

The changes in leaf shape in 35S::G1142 lines also indicate that the gene or its orthologs can be used to modify plant architecture.

G1206 (SEQ ID NO: 189)

5 Published Information

G1206 was identified by amino acid sequence similarity to the pea early nodulin gene-binding protein 1 (ENBP1), which binds to an AT-rich sequence motif within the promoter of the early nodulin gene ENOD12 (Christiansen et al., (1996) *Plant Mol. Biol.* 32:809-821). G1206 is in chromosome 1, BAC F24O1 (GenBank accession AC003113.2 GI:7658296), released by the *Arabidopsis* Genome Initiative. The translational start and stop codons were correctly predicted. No public information related to the functional characterization of G1206 has been published or made available.

Experimental Observations

15 An analysis of the endogenous levels of G1206 transcripts by RT-PCR revealed a constitutive expression in all tissues tested. No change in G1206 expression was observed in the biotic and abiotic treatments examined. A line homozygous for a T-DNA insertion in G1206 was used to determine the function of this gene. The characterization of the G1206 null mutant showed no apparent morphological, physiological or biochemical changes when compared to control plants.

The function of G1206 was also analyzed through its ectopic overexpression in plants. 20 Physiological analysis of 35S::G1206 overexpressor lines revealed increased seedling vigor under drought conditions. Seedlings were generally larger and greener than the control plants treated with the same conditions.

Utilities

25 The reduced sensitivity of 35S::G1206 lines in the dehydration stress assay indicates that the gene might be used to engineer crops with increased tolerance to drought, salt, freezing and chilling stress, or increased water use efficiency.

G1274 (SEQ ID NO: 193)

30 Published Information

G1274 is a member of the WRKY family of transcription factors. The gene corresponds to WRKY51 (At5g64810). No information is available about the function(s) of G1274.

Experimental Observations

35 RT-PCR analysis was used to determine the endogenous expression pattern of G1274. Expression of G1274 was detected in leaf, root and flower tissues. The biotic stress related conditions,

Erysiphe and SA induced expression of G1274 in leaf tissue. The gene also appeared to be slightly induced by osmotic and cold stress treatments and perhaps by auxin.

The function of G1274 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. G1274 overexpressing lines were more tolerant to growth on low nitrogen containing media. In an assay intended to determine whether the transgene expression could alter C/N sensing, 35S::G1274 seedlings contained less anthocyanins (Figure 5A) than wild-type controls (Figure 5B) grown on high sucrose/N- and high sucrose/N/Gln plates. These data together indicated that overexpression of G1274 may alter a plant's ability to modulate carbon and/or nitrogen uptake and utilization.

G1274 overexpression and wild-type germination were also compared in a cold germination assay, the overexpressors appearing larger and greener (Figure 5C) than the controls (Figure 5D).

Figures 6A - 6D compare soil-based drought assays for G1274 overexpressors and wild-type control plants, which confirms the results predicted after the performance of the plate-based osmotic stress assays. 35S::G1274 lines fared much better after a period of water deprivation (Figure 6A) than control plants in (Figure 6B). This distinction was particularly evident in the overexpressor plants after once again being watered, said plants almost all fully recovered to a healthy and vigorous state in Figure 6C. Conversely, none of the wild-type plants seen in Figure 6D recovered after rewatering, as it was apparently too late for rehydration to rescue these plants.

In addition, 35S::G1274 transgenic plants were more tolerant to chilling compared to the wild-type controls, in both germination as well as seedling growth assays.

35S::G1274 overexpression plants were significantly greener and larger than wild-type control plants in a soil-based drought assay.

Overexpression of G1274 produced alterations in leaf morphology and inflorescence architecture. Four out of eighteen 35S::G1274 primary transformants were slightly small and developed inflorescences that were short, and showed reduced internode elongation, leading to a bushier, more compact stature than in wild-type.

In an experiment using T2 populations, it was observed that the rosette leaves from many of the plants were distinctly broad and appeared to have a greater rosette biomass than in wild type.

A similar inflorescence phenotype was obtained from overexpression of a potentially related WRKY gene, G1275. However, G1275 also caused extreme dwarfing, which was not apparent when G1274 was overexpressed.

Utilities

The phenotypic effects of G1274 overexpression could have several potential applications:

The enhanced performance of 35S::G1274 plants in a soil-based drought assay indicated that the gene or its equivalents may be used to enhance drought tolerance in plants.

The enhanced performance of 35S::G1274 seedlings under chilling conditions indicates that the gene or its equivalents might be applied to engineer crops that show better growth under cold conditions.

The morphological phenotype shown by 35S::G1274 lines indicate that the gene or its equivalents might be used to alter inflorescence architecture, to produce more compact dwarf forms that might afford yield benefits.

The effects on leaf size that were observed as a result of G1274 or equivalent overexpression might also have commercial applications. Increased leaf size, or an extended period of leaf growth, could increase photosynthetic capacity, and biomass, and have a positive effect on yield.

10 G1276 (SEQ ID NO: 195)

Published Information

G1276 (At5g60120) was identified as part of P1 clone: MGO3 (GenBank accession AB019231).

Experimental Observations

15 G1276 was found to be expressed ubiquitously in *Arabidopsis*. The function of this gene was analyzed using transgenic plants in which a G1276 cDNA clone was expressed under the control of the 35S promoter. Overexpression of G1276 in *Arabidopsis* delayed the onset of flowering by up to 2-3 weeks under continuous light conditions. No consistent differences were observed between the 35S::G1276 transgenics and the wild-type control plants in any of the physiology assays.

20 It is noteworthy that G1276 is a potential paralog of APETALA2 (G2) and that a number of genes from the G2 clade produced delayed flowering when overexpressed.

Utilities

25 The delayed flowering displayed by 35S::G1276 transformants indicated that the gene or its equivalents might be used to manipulate the flowering time of commercial species. Given the effects of G1276 overexpression, it is likely that the activity of the gene or its equivalents could be modified to accelerate flowering, or eliminate any requirement for vernalization.

G1313 (SEQ ID NO: 199)

30 Published Information

G1313 (At5g06100) corresponds to AtMYB33. Gocal et al. ((2001) *Plant Physiol.* 127: 1682-1693) showed that G1313 (AtMYB33) could bind to the GA (gibberellin) response element and activate the barley alpha-amylase promoter in a transient assay in barley aleurone cells. The gene was ubiquitously expressed in *Arabidopsis*. It was hypothesized that the gene could regulate GA responsive pathways that promote flowering in *Arabidopsis*. To test this hypothesis, Gocal et al. (*supra*) analyzed that whether AtMYB33 was capable of binding to the LFY gene promoter. LFY is a floral meristem identity gene that has a GA responsive element in its promoter. AtMYB33 was found to bind to the LFY

promoter suggesting that the action of gibberellins on flowering could be mediated through the activity of AtMYB33 (Gocal et al. *supra*).

Experimental Observations

5 The complete sequence of G1313 was determined. The function of this gene was analyzed using transgenic plants in which G1313 was expressed under the control of the 35S promoter. 35S::G1313 transgenics were wild-type in response to all physiological stress treatments performed.

Overexpression of G1313 produced an increase in seedling vigor in some of the T1 plants at an early seedling stage under normal growth conditions compared to the wild-type controls; transgenic
10 *Arabidopsis* seedlings were up to two-fold larger than the wild-type seedlings at early stages of development. Given that gibberellins are known to promote seed germination, the increased seedling vigor may be related to a GA response in seeds. The lack on an effect of G1313 on flowering time may result from the fact that an additional factor is required for the activity of the protein. All assays were performed under continuous light.

Utilities

The increase in seedling vigor in G1313 transgenics plants indicated this gene or its orthologs could be used to increased survivability and vigor of small seedlings under field conditions potentially leading to a greater yield in crops. Published results indicate that the gene might modify a plant's
20 response to the growth regulator gibberellic acid (Gocal et al. *supra*).

G1357 (SEQ ID NO: 207)

Published Information

G1357 corresponds to gene At3g44290, annotated by the *Arabidopsis* Genome Initiative. No
25 information is available about the function(s) of G1357.

Experimental Observations

The complete sequence of G1357 was experimentally determined. G1357 expression was not detected in wild-type plants under our experimental conditions. The function of this gene was analyzed
30 using transgenic plants in which G1357 was expressed under the control of the 35S promoter.

35S::G1357 seedlings were more tolerant to chilling stress in a growth assay and insensitive to ABA in a germination assay. Morphologically, overexpression of G1357 in *Arabidopsis* produced alterations in coloration, leaf shape, and a marked delay in the time to flowering. At the earliest stages, G1357 seedlings appeared normal, but towards the mid-rosette stage, the plants developed a darker green
35 coloration and the leaves became slightly rounder than those of wild-type. Additionally, many lines were also slightly smaller than controls. The majority of lines produced flower buds markedly late, with the

most severely affected individuals flowering approximately 1 month later than wild type under continuous light conditions.

In a soil based drought assay, G1357 overexpressing plants were significantly greener and larger than wild-type control plants.

5 It should be noted that a highly related gene, G1452 (analyzed in phase I) had similar endogenous expression patterns, and produced similar effects on coloration, leaf shape, flowering time, abiotic stress resistance, and ABA sensitivity.

Utilities

10 The results of physiological assays indicated that G1357 gene or its equivalents could be used to improve a plant's tolerance to chilling stress and drought.

Enhanced chilling tolerance could also extend the effective growth range of chilling sensitive crop species by allowing earlier planting or later harvest.

The delayed flowering displayed by 35S::G1357 transformants indicated that the gene or its
15 equivalents might be used to manipulate the flowering time of commercial species. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases.

Given the effects of G1357 overexpression, it is likely that the activity of the gene or its equivalents could be modified to accelerate flowering, or eliminate any requirement for vernalization.

20 Additionally, if the dark coloration of 35S::G1357 lines reflects an increase in biochemical composition, this gene or its equivalents might be used to improve the nutraceutical value of foodstuffs, or increase photosynthetic capacity to improve yield.

G1412 (SEQ ID NO: 215)

Published Information

25 G1412 is a member of the NAC family of transcription factors. G1412 was identified in the sequence of BAC clone F27G19, GenBank accession number AL078467, released by the *Arabidopsis* Genome Initiative. G1412 also corresponds to gene At4g27410, annotated by the *Arabidopsis* Genome Initiative, and to sequence 1543 from patent publication WO0216655 A2 on stress-regulated genes,
30 transgenic plants and methods of use. In the latter publication, G1412 was reported to be cold, osmotic and salt responsive in microarray analysis. No information is available about the function(s) of G1412.

Closely Related Genes from Other Species

35 G1412 is very similar in sequence to LEJA2 from tomato that is regulated by jasmonic acid. The level of sequence homology between these two proteins is significant enough to indicate they could have similar functions in the plant.

Experimental Observations

RT-PCR was used to analyze the endogenous expression pattern of G1412. G1412 appears to be constitutively expressed in all tissues tested. G1412 induction was observed in response to ABA, heat, drought, mannitol and *Erysiphe*, indicating the gene's expression is regulated by environmental conditions.

A T-DNA insertion mutant for G1412 was analyzed. The mutant displayed a wild-type morphology, and was wild-type in its response to the physiological analyses that were performed.

The effects of G1412 overexpression were also studied; the transformants displayed wild-type morphology. However, the 35S::G1412 transgenics were insensitive to ABA and were more tolerant to osmotic stress in a germination assay on media containing high concentrations of sucrose.

Utilities

The phenotypic effects of G1412 overexpression, such as the increase in seedling vigor observed in a germination assay on high sucrose media and insensitivity to germination on ABA media, indicated that the gene or its equivalents could be used to engineer plants with increased tolerance to abiotic stresses such as drought, salt, heat or cold.

G1420 (SEQ ID NO: 217)

Published Information

G1420 corresponds to gene AT5g49520, and it has also been described as WRKY48. No information is available about the function(s) of G1420.

Experimental Observations

G1420 is ubiquitously expressed in *Arabidopsis* and does not appear to be significantly induced by any of the conditions tested.

A T-DNA insertion mutant for G1420 was analyzed, and the mutant was phenotypically wild-type.

We have now generated 35S::G1420 lines. Overexpression of the gene in *Arabidopsis* produced marked alterations in the morphology of leaves and floral organs. 35S::G1420 seedlings typically displayed rather long narrow cotyledons. Later, the plants formed leaves that were often mildly serrated, narrow, slightly dark green, and rather contorted. Additionally many of the lines showed stunted growth and appeared markedly smaller than controls. Following the switch to reproductive growth, 35S::G1420 transformants developed rather thin spindly inflorescences. Flowers were often borne on particularly long pedicels, and floral organs, especially sepals and petals, were long, narrow and twisted in a comparable manner to the leaves. As a result of the reduced size, and floral abnormalities, the seed yield from most of the lines was very poor.

In addition to the developmental alterations produced as a consequence of G1420 overexpression, the 35S::G1420 seedlings displayed a sugar sensing phenotype in a germination assay on media containing high glucose.

5 Utilities

The results of physiological assays indicate that G1420 could be used to alter the sugar signaling in plants.

The effects of G1420 on plant development indicate that the gene could be used to manipulate architecture. In particular, the gene could be used to generate novel leaf and flower forms for the ornamental markets. Additionally, if the dark coloration of 35S::G1420 lines reflects an increase in biochemical composition, the gene might be used to improve the nutraceutical value of foodstuffs, or increase photosynthetic capacity to improve yield.

G1451 (SEQ ID NO: 223)

15 Published Information

G1451 is ARF8, a member of the ARF class of proteins with a VP1-like N-terminal domain and a C-terminal domain with homology to Aux/IAA proteins. ARF8, like several other ARFs, contains a glutamine-rich central domain that can function as a transcriptional activation domain (Ulmasov et al. (1999a) *Proc. Natl. Acad. Sci.* 96: 5844-5849). ARF8 was shown to bind to an auxin response element (Ulmasov et al. (1999b) *Plant J.* 19: 309-319). It was also shown that a truncated version of ARF8 lacking the DNA binding domain but containing the activation domain and the C-terminal domain could activate transcription on an auxin responsive promoter, presumably through interactions with another factor bound to the auxin response element (Ulmasov et al. 1999a, *supra*). ARF8 is closely related in sequence to ARF6 (Ulmasov et al. 1999b, *supra*).

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Experimental Observations

A line homozygous for a T-DNA insertion in G1451 exhibited a change in seed oil content. RT-PCR studies revealed that G1451 was expressed throughout the plant, with the highest expression in flowers. Transcripts of G1451 were induced in leaves by a variety of stress conditions.

30 The function of G1451 was analyzed using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1451 produced changes in leaf morphology and a general increase in the vegetative biomass of *Arabidopsis* plants. At early stages, 35S::G1451 transformants appeared normal. However, towards the end of the rosette phase, leaves became distinctly broader and longer than wild type leaves. Many of the plants showing this phenotype also exhibited a mild delay in the onset of flowering.

35

Utilities

G1451 or its orthologs can be used to increase plant biomass, thus improving yield. Additionally, the delay in flowering observed in some of the 35S::G1451 lines indicated that the gene might be used to manipulate the timing of reproductive growth.

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G1452 (SEQ ID NO: 225)Published Information

G1452 was identified in the sequence of clones T22O13, F12K2 with accession number AC006233 released by the *Arabidopsis* Genome Initiative. No information is available about the function(s) of G1452.

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Experimental Observations

The function of G1452 was analyzed using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1452 produced changes in leaf development and markedly delayed the onset of flowering. 35S::G1452 plants produced dark green, flat, rounded leaves, and typically formed flower buds between 2 and 14 days later than controls. Additionally, some of the transformants were noted to have low trichome density on leaves and stems. At later stages of life cycle, 35S::G1452 plants developed more slowly and senesced considerably later than wild-type controls. In addition, G1452 overexpressors were more tolerant to osmotic stress, and were insensitive to ABA in separate germination assays.

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G1452 expression was not detected in any tissue tested by RT-PCR and was not induced by any environmental stress-related condition tested.

Utilities

On the basis of the analyses performed to date, G1452 or its equivalents could be used to alter plant growth and development. In addition, G1452 or its equivalents could be used to alter a plant's response to water deficit conditions and therefore, could be used to engineer plants with enhanced tolerance to drought and salt stress.

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G1468 (SEQ ID NO: 227)Published Information

The genomic sequence of G1468 is located on the *Arabidopsis* BAC clone T7I23 (GenBank accession number U89959).

Experimental Observations30
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G1468 was predominantly expressed in flowers and embryos.

A line homozygous for a T-DNA insertion in G1468 was used to determine the function of this gene. The T-DNA insertion of G1468 was found to be within the first third of the coding sequence of the gene and therefore was likely to result in a null mutation. Furthermore, its expression level was unaffected by any of the conditions tested. G1468 knockout mutant plants behaved similarly to wild-type plants in all assays performed.

The function of G1468 was also studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1468 produced plants that were very tiny and rather dark in coloration compared to wild type controls at early stages. Severely affected individuals arrested growth early in vegetative development. Plants that survived formed narrow, gray leaves and showed a marked delay in the onset of flowering. Many of the late flowering plants had more axillary rosette leaves compared to controls leading to an increase in vegetative biomass.

Utilities

The alterations in leaf shape, size, and coloration shown by 35S::G1468 transformants indicated that the gene or its equivalents might be applied to modify plant architecture.

The delayed bolting indicated that gene or its equivalents might also be used to manipulate flowering time in commercial species. Conversely, it is possible that the activity of G1468 or its equivalents could be modified to accelerate flowering, or eliminate any requirement for vernalization.

G1476 (SEQ ID NO: 231)

Published Information

G1476 (At5g43540) was identified in the sequence of TAC clone K9D7 (GenBank accession number AB016875) based on its sequence similarity within the conserved domain to other C2H2 related proteins in *Arabidopsis*. There is no published or public information about the function of G1476.

Experimental Observations

G1476 is expressed in roots, flowers, embryos and germinating seeds.

The function of G1476 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1476 produced highly deleterious effects on growth and development. At early stages, while on media, 35S::G1476 seedlings appeared to grow more rapidly than controls.

Utilities

Based on the effects of its overexpression, G1476 could be used to regulate plant growth and development.

G1482 (SEQ ID NO: 233)Published Information

G1482 was identified as a gene in the sequence of BAC F10A5, GenBank accession number AC006434, released by the *Arabidopsis* Genome Initiative. There is no other published or public information about G1482.

Experimental Observations

The sequence of G1482 was experimentally determined. Homozygous plants harboring a T-DNA insertion in G1482 displayed significantly more root growth on MS control plates as well as on different stresses in three separate experiments.

The function of G1482 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. G1482 overexpression in *Arabidopsis* resulted in visually high levels of the anthocyanin pigment production throughout the plant.

Utilities

Based on the phenotypes produced when this gene is knocked out, G1482 or its orthologs can be used to manipulate root growth, particularly in response to environmental stresses such as drought and low nutrients.

In addition, G1482 or its orthologs could be used to modulate anthocyanin levels. The potential utilities of genes involved in anthocyanin production include alterations in pigment production for horticultural purposes and increase stress resistance perhaps in combination with other transcription factors. Flavonoids have antimicrobial activity and could be used to engineer pathogen resistance. In addition, several flavonoid compounds have health promoting effects such as the inhibition of tumor growth and cancer, prevention of bone loss and the prevention of the oxidation of lipids. Given that the phenylpropanoid biosynthetic pathway (from which anthocyanins are produced) feeds into the pathways for the production of a number of other classes of secondary metabolites, such as lignins and tannins, changing the activity of G1482 or its orthologs might also influence the levels of those types of compounds.

G1510 (SEQ ID NO: 241)Published Information

G1510 was identified in the sequence of P1 clone MPI10, GenBank accession number AB020747, released by the *Arabidopsis* Genome Initiative. There is no other published or public information about G1510.

Experimental Observations

The 5' and 3' ends of G1510 were experimentally determined by RACE. RT-PCR expression analysis showed that G1510 is expressed in all tissues except roots, suggesting that the gene could have a role within green tissues.

5 The function of this gene was analyzed using transgenic plants in which G1510 was expressed under the control of the 35S promoter. 35S::G1510 plants showed a dramatic change in coloration and were much darker green compared to controls. Green pigmentation also extended into the hypocotyls and roots from these plants, suggesting that the native function of G1510 could be related to plastid differentiation, chlorophyll production, or the regulation of chloroplast number. 35S::G1510 also
10 exhibited disproportionately long hypocotyls, indicating that the gene could influence light-regulated developmental processes.

Utilities

15 The increased pigmentation indicated that 35S::G1510 plants had altered levels of chlorophylls or carotenoids. As such the gene or its orthologs could have a number of valuable applications.

Enhanced chlorophyll and carotenoid levels could improve yield and nutritional value in crop plants. For instance lutein, like other xanthophylls such as zeaxanthin and violaxanthin, is an essential component in the protection of the plant against the damaging effects of excessive light. Specifically, lutein contributes to the rapid rise of non-photochemical quenching in plants exposed to high light. Crop
20 plants engineered to contain higher levels of lutein could therefore have improved photo-protection, possibly leading to less oxidative damage and better growth under high light. Additionally, elevated chlorophyll levels might increase photosynthetic capacity, and hence yield.

G1510 or its orthologs might be also applied to improve the nutraceutical value of foodstuffs. For example, consumption of dark green leafy vegetables has been shown in clinical studies to reduce the risk
25 of age-related macular degeneration (ARMD), the leading cause of blindness in elderly people.

G1538 (SEQ ID NO: 245)

Published Information

30 G1538 encodes a HD-ZIP class I homeodomain protein and corresponds to gene MSN2.9 within P1 clone MSN2 (chromosome 5, GenBank Accession AB018119). No published data are available pertaining to the function of this gene.

Experimental Observations

35 G1538 function was examined via analysis of a T-DNA insertion mutant for the gene. However, plants that were homozygous for this insertion displayed a wild-type phenotype in all assays performed. Nevertheless, RT-PCR studies on wild-type plants revealed G1538 expression to be induced in leaves by heat and salicylic acid treatments. Under normal physiological conditions, G1538 was expressed at

moderately high levels in roots, flowers and siliques, but at rather low levels in leaves, shoot stems, embryos, and germinating seeds.

We have now assessed the role of G1538 by analysis of transgenic *Arabidopsis* lines in which the gene was overexpressed. The boundaries of G1538 were identified by RACE experiments, a clone was amplified from cDNA derived from mixed tissues, and 35S::G1538 lines were generated. Approximately half of the T1 lines flowered earlier than wild-type controls under continuous light conditions, but this phenotype was not apparent in three of those lines, which were grown under a less inductive 12-hour photoperiod in the T2 generation. Interestingly, though, the plants from all three T2 lines did develop slightly longer leaf petioles than wild type. Such an effect had not been noted among the primary transformants, but it is noteworthy that increased petiole length is sometimes associated with accelerated or delayed flowering.

Given the alterations in flowering time, it is possible, that elevated G1538 activity can accelerate flowering specifically under inductive photoperiodic conditions. However, such effects on flowering time should be further examined by growing larger populations of plants from a number of different lines, under a variety of growth conditions.

Importantly, 35S::G1538 transformants also displayed a pronounced phenotype in the physiological assays: each of three independent T2 lines had improved tolerance to salt stress in a plate-based root growth assay. The 35S::G1538 seedlings were larger and displayed more secondary root growth than wild-type controls subjected to the same treatments.

Utilities

Based on the phenotypes observed in morphological and physiological assays, G1538 might be have a number of utilities.

Given the salt resistance exhibited by 35S::G1538 transformants, the gene might be used to engineer salt tolerant crops and trees that can flourish in saline soils, or under drought conditions.

The early flowering displayed by 35S::G1538 transformants indicates that the gene might be used to accelerate the flowering of commercial species, or to eliminate any requirements for vernalization.

Finally, as noted in our earlier reports, the RT-PCR experiments indicate that the gene and/or its promoter could be useful in designing plants that are more resilient to heat or physiological conditions that result in high levels of salicylic acid. The G1538 promoter might also be applied to create gene expression systems that are heat or salicylic acid inducible.

G1539 (SEQ ID NO: 247)

Published Information

G1539 was identified within a sequence released by the *Arabidopsis* genome initiative (gene MEB5.20, P1 clone MEB5, Chromosome 3, GenBank accession, AB019230,), as a gene encoding a

novel WUSCHEL-like homeodomain protein. No data regarding the function of this gene are available in the public literature.

Experimental Observations

5 The boundaries of G1539 were determined by RACE experiments, and transgenic lines were generated in which the gene was overexpressed from a 35S promoter. These plants displayed a wild-type response in all of the physiological assays, but showed some striking alterations in morphology compared to controls. 35S::G1539 lines exhibited a spectrum of developmental changes including alterations in leaf shape, phyllotaxy, coloration, growth rate, floral organ abnormalities, and a reduction in overall size. 10 However, the most prominent phenotype was seen in the inflorescence, where strange growths, which took on a carpelloid identity, developed from stems, pedicels and floral organs. Occasionally, on the stems of 35S::G1539 T1 plants, trichomes were positioned at the apex of gland-like structures.

 Similar results were previously obtained from overexpression of a related gene, WUSCHEL (G1540), which was found to induce the formation of callus like tissue that later took on a carpelloid 15 identity. WUSCHEL has a key role in the maintenance of stem cell identity within apical meristems, and during the reproductive phase, participates in a feedback loop with the AGAMOUS gene, which induces floral meristems to terminally differentiate into carpels (Mayer et al. (1998) *Cell* 95: 805-815; Schoof et al (2000) *Cell* 100: 635-644; Lohmann et al. (2001) *Cell* 105: 793-803). The similarity between the WUS and G1539 overexpression phenotypes indicated that the genes have similar roles in regulating apical 20 meristem activity.

 Two other WUS-like genes, G1591 and G2983, have also yielded similar overexpression phenotypes to G1539.

Utilities

25 Given its capacity to trigger ectopic carpel development in *Arabidopsis*, G1539 or its orthologs could be applied to commercial species to induce formation of increased numbers of carpels or fruits. A particular application might exist in saffron, one of the world's most expensive spices. Saffron filaments, or threads, are actually the dried stigmas of the saffron flower, *Crocus Sativus* Linneaus. Each flower contains only three stigmas, and more than 75,000 of these flowers are needed to produce just one pound 30 of saffron filaments. A gene such as G1539, which increased carpel numbers, could therefore substantially increase yield.

 Additionally, the overexpression phenotypes of G1539 indicate that it or its orthologs might be used to regulate meristem activity and stem cell identity. As such, the gene could have applications in the plant cell culture lines, or in transformation or micro-propagation systems, where generation of callus is 35 currently problematic but is required as part of the procedure.

The alterations in trichome development seen in occasional lines indicated that the gene or its orthologs could be used to manipulate the formation of those structures.

G1557 (SEQ ID NO: 255)

5 Published Information

G1557 was identified in the sequence of chromosome 4, GenBank accession number AL161501, released by the *Arabidopsis* Genome Initiative. It is not annotated in the public sequence. No functional information is available about G1557.

10 Experimental Observations

The function of G1557 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. G1557 overexpression in *Arabidopsis* resulted in increased seedling vigor in response to salt stress in a germination assay.

15 Utilities

G1557 or its orthologs may be useful for increasing salt tolerance. Salt (and drought) stress signal transduction consists of ionic and osmotic homeostasis signaling pathways. The pathway regulating ion homeostasis in response to salt stress has been reviewed recently by Xiong and Zhu ((2002) *Plant Cell Environ.* 25: 131-139). The osmotic component of salt stress involves complex plant reactions that are possibly overlapping with drought and/or cold stress responses. Common aspects of drought, cold and salt stress response have been reviewed recently by Xiong et al. (Xiong et al. (2002) *Plant Cell* 14 Suppl. S165-S183).

G1593 (SEQ ID NO: 261)

25 Published Information

G1593 was initially identified within a sequence released by the *Arabidopsis* genome initiative (gene T22O13.1 within clone T22O13, chromosome 2, GenBank accession, AC007290), as a gene encoding a novel homeodomain protein of the BEL1 class. The gene has been designated AGI number At2g27220, but no public data are available regarding its function.

30

Experimental Observations

The boundaries of G1593 were determined by RACE experiments, and transgenic lines were generated in which the gene was overexpressed from a 35S promoter. These transformants exhibited a wild-type response to physiological assays, but displayed a number of morphological phenotypes.

35 35S::G1593 lines were dark in coloration, displayed alterations in leaf shape, and formed shorter, more compact inflorescences than controls.

Utilities

The changes in morphology shown by the 35S::G1593 transformants indicate that the gene or its orthologs could be used to manipulate inflorescence architecture and branching patterns in commercial species, to create varieties with more compact forms. In particular, dwarf and compact forms of ornamental plants are extremely popular among consumers. They represent a lucrative market for breeders and growers alike, but currently for many varieties, suitable dwarf breeding lines are either unavailable or difficult to integrate into existing germ-lines. Therefore, currently, many ornamental plants are sprayed with expensive chemical growth regulators to reduce height and increase compactness. Overexpression of a gene with G1593 activity could potentially alleviate this requirement.

Additionally, if the altered coloration of 35S::G1593 plants reflects a change in biochemical composition, the gene or its orthologs might be used to improve the nutraceutical value of foodstuffs, or increase photosynthetic capacity to improve yield. For example, consumption of dark green leafy vegetables has been shown in clinical studies to reduce the risk of age-related macular degeneration (ARMD), the leading cause of blindness in elderly people.

G1660 (SEQ ID NO: 263)Published Information

G1660 was identified by amino acid sequence similarity to other DNA-binding proteins. G1660 is found in the sequence of the chromosome 2 BAC clone F5O4 (GenBank accession number AC005936, nid=g4038029), released by the *Arabidopsis* Genome Initiative. No information related to the functional characterization of G1660 is currently available from the public literature.

Experimental Observations

The 5' and 3' ends of G1660 were experimentally determined by RACE. The function of G1660 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Plants overexpressing G1660 had more root growth and seedling vigor when grown on media containing high salt, compared to wild-type control plants. Morphological analysis of transgenic plants revealed no phenotypic alterations.

Utilities

Based on the increased salt tolerance exhibited by the 35S::G1660 lines in physiology assays, this gene might be used to engineer salt tolerant crops and trees that can flourish in salinified soils, or under drought conditions.

G1730 (SEQ ID NO: 267)Published Information

G1730 was identified in the sequence of BAC T32F12, GenBank accession number AC005314, released by the *Arabidopsis* Genome Initiative. There is no other published or public information about G1730.

Experimental Observations

The full-length cDNA clone corresponding to G1730 was isolated from a gene library. Based on RT-PCR experiments, G1730 was highly expressed in all tissues except roots, but was markedly repressed in rosette leaves by cold or osmotic stress.

The function of G1730 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. 35S::G1730 plants showed wild-type morphology but displayed an enhanced performance compared to controls when subjected to osmotic stress in both mannitol and glucose germination assays. Given the expression profiles of the endogenous gene, and the putative role of RING C3H2C3 proteins in regulation of ubiquitin-dependent protein turnover, G1730 may act as a modulator of factors involved in the response to abiotic stress.

Utilities

The effects of osmotic stress on G1730 expression, and the phenotype seen in 35S::G1730 lines, indicated that the gene or its orthologs can be used to engineer plants with increased tolerance to abiotic stresses such as drought, salt, or cold.

G1753 (SEQ ID NO: 271)Published Information

G1753 (At2g36450) was identified as part of the chromosome 2 clone F1011 (GenBank accession AC006919).

Experimental Observations

The function of G1753 was analyzed using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1753 produced changes in *Arabidopsis* shoot architecture. 35S::G1753 transformants generally displayed reduced internode elongation in the inflorescence. Overall, this gave the plants a shorter, bushier appearance compared to wild type.

Two out of the three G1753 overexpressing lines showed an increase in the germination efficiency on media containing high concentrations of sucrose, indicating the gene is involved in sugar metabolism and/or signaling. In this context, it is striking that expression of the endogenous G1753 in wild-type

plants was only detected in siliques, indicating that G1753 could be involved in sugar sensing processes in early seed development.

Utilities

5 G1753 could be used to create dwarf and compact forms of ornamental plants in horticulture markets. Dwarf and compact forms of ornamental plants are extremely popular among consumers. They represent a lucrative market for breeders and growers alike, but currently for many varieties, suitable dwarf breeding lines are either unavailable or difficult to integrate into existing germ-lines. Therefore, currently, many ornamental plants are sprayed with expensive chemical growth regulators to reduce
10 height and increase compactness. Overexpression of a gene with G1753 activity could potentially alleviate this requirement.

The results of physiological assays indicate that G1753 could be used to alter the sugar signaling in plants.

If the physiological phenotype is related to osmotic stress, the gene could be used to engineer
15 cold and dehydration tolerance.

G1779 (SEQ ID NO: 275)

Published Information

G1779 was identified from the *Arabidopsis* genomic sequence (GenBank accession number
20 AL049483) based on its sequence similarity within the conserved domain to other GATA related proteins in *Arabidopsis*.

Experimental Observations

The function of this gene was initially studied by knockout analysis. Plants homozygous for a T-DNA insertion in G1779 were wild type for all assays performed.
5

Gene expression profiling using RT-PCR showed that G1779 is expressed in all tissues, albeit at higher levels in leaves.

The function of G1779 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1779 resulted in plants that showed enhanced
0 tolerance to chilling stress when grown under low temperatures for an extended period of time. The majority of 35S::G1779 plants were wild type in morphological analyses that were performed.

Utilities

G1779 might be used to improve chilling tolerance.

G1792 (SEQ ID NO: 277)Published Information

G1792 was identified in the sequence of BAC clone K14B15 (AB025608, gene K14B15.14). No information is available about the function(s) of G1792.

Closely Related Genes from Other Species

G1792 shows sequence similarity, outside of the conserved AP2 domain, with a protein from tomato, represented by EST sequence AI776626 (AI776626 EST257726 tomato resistant, Cornell *Lycopersicon esculentum* cDNA clone cLER19A14, mRNA sequence). No functional information is available about this tomato gene.

Experimental Observations

The function of G1792 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. 35S::G1792 plants were more tolerant to the fungal pathogens *Fusarium oxysporum* and *Botrytis cinerea* : they showed fewer symptoms after inoculation with a low dose of each pathogen. These results were confirmed using individual T2 lines. Figure 7C shows a G1792 overexpressing line (labeled G1792-12; on left) and wild-type plants (on right) five days after inoculation with *Botrytis cinerea*, showing the chlorosis and hyphal growth in the latter control plants but not in the former overexpressors. Additional, experiments have confirmed that 35S::G1792 plants also showed increased tolerance to challenge with *Erysiphe*. Five days after inoculation with *Fusarium oxysporum*, the G1792 overexpressors, as seen on the left in Figure 7D, showed little or no chlorosis , as compared with wild-type plants on the right of Figure 7D.

The effect of G1792 overexpression in increasing tolerance to pathogens received further, incidental confirmation. T2 plants of 35S::G1792 lines 5 and 12 were being grown (for other purposes) in a room that suffered a serious powdery mildew infection. For each line, a pot of 6 plants was present in a flat containing 9 other pots of lines from unrelated genes. In either of the two different flats, the only plants that were free from infection were those from the 35S::G1792 line. This observation indicated that G1792 overexpression might increase resistance to powdery mildew. Interestingly, G1792 was ubiquitously expressed, but appeared to be induced by salicylic acid.

35S::G1792 overexpressing plants showed more tolerance to growth under nitrogen-limiting conditions. In a root growth assay under conditions of limiting N, 35S::G1792 lines were less stunted. In a germination assay that monitors the effect of C on N signaling through anthocyanin production on high sucrose plus and minus glutamine (Hsieh et al. (1998) *Proc. Natl. Acad. Sci. U.S.A*) 95: 13965-13970), the 35S::G1792 lines made less anthocyanin , showed greater cotyledon expansion and had more root growth on high sucrose medium supplemented with glutamine (Figure 7A) than control plants (Figure 7B), indicating that the gene could be involved in the plants' ability to monitor their carbon and nitrogen status.

35S::G1792 overexpressing plants were larger and greener than wild-type control plants in a soil-based drought assay.

G1792 overexpressing plants showed several mild morphological alterations: leaves were dark green and shiny, and plants bolted, subsequently senesced, slightly later than wild-type controls. Among the T1 plants, additional morphological variation (not reproduced later in the T2 plants) was observed: many showed reductions in size as well as aberrations in leaf shape, phyllotaxy, and flower development.

Utilities

G1792 or its equivalents could be used to engineer pathogen-resistant plants.

In addition, G1792 or its equivalents could also be used to improve seedling germination and performance under conditions of limited nitrogen, and plants with enhanced drought tolerance.

G1796 (SEQ ID NO: 279)

Published Information

G1796 (At1g12980) is found in the sequence of BAC clone F3F19, GenBank accession number AC007357 (nid=4662618). G1796 was identified by Banno et al. ((2001) *Plant Cell* 13: 2609-2618) as ESR1 (Enhancer of Shoot Regeneration) in a screening for *Arabidopsis* cDNAs that can confer cytokinin-independent shoot formation from root cultures when overexpressed. The authors found enhanced shoot regeneration when a chemically inducible system was used for transient expression of ESR1. Transformation of *Arabidopsis* plants with a 35S::ESR1 construct using the flower vacuum infiltration method strongly inhibited normal leaf development. Only one transgenic 35S::ESR1 plant was obtained which produced dark green calli suggesting that ESR1 enhances shoot regeneration but interferes with the subsequent differentiation of plant cells.

G1796 was found to be included in patent application W00200903.

Experimental Observations

The intronless G1796 gene was cloned from genomic DNA for overexpression. The function of the gene was analyzed using transgenic plants in which G1796 was expressed under the control of the 35S promoter. Overexpression of G1796 caused severe growth defects: seedlings were generally distinctly small and formed rather dark curled leaves. The growth arrest at very early seedling stages was also found by Banno et al. (2001) *supra*. The thickened club-like carpels, and the changes found in the structure of the inflorescences could be related to the function of G1796 in organogenesis, but were not specifically described by Banno et al. (2001) *supra*.

G1796 was expressed at low level in root, flower and rosette, but not in stems, siliques, embryos or germinating seeds.

Utilities

The use of G1796 for plant regeneration after transformation has been described by Banno et al. (2001) *supra*.

G1796 might be used to manipulate fruit size and shape.

- 5 Additionally, if the dark coloration of 35S::G1796 lines reflects an increase in biochemical composition, the gene might be used to improve the nutraceutical value of foodstuffs, or increase photosynthetic capacity to improve yield.

G1797 (SEQ ID NO: 281)

10 Published Information

G1797 was identified within P1 clone MJM18 (chromosome 5, GenBank accession AB025623) as one of a pair of novel, highly related, tandemly arranged MADS box genes (the other gene was G1798). A functional characterization of G1797 remains to be published.

Experimental Observations

- 15 To assess the function of G1797, transgenic *Arabidopsis* lines were analyzed in which the gene was overexpressed from a CaMV promoter. 35S::G1797 transformants were very early flowering, had curled leaves, and retained outer whorl floral organs for a prolonged period following pollination and silique outgrowth. These phenotypes indicated that G1797 might influence genetic pathways that regulate flowering time or floral organ senescence and abscission. However, despite these changes in growth and
20 development, 35S::G1797 lines displayed a wild type response in all of the physiological assays.

It should be noted that accelerated flowering and changes in flower morphology were also observed as a result of overexpression of the putative paralog, G1798, indicating that the two genes have related functions. Two other related genes, G627 and G1011, also produced very similar effects to G1797 and G1798 when overexpressed.

- 25 Interestingly, equivalent effects on perianth organs to those described above were obtained by Fernandez et al. ((2000) *Plant Cell* 12: 183-198) through overexpression of AGAMOUS-LIKE 15 (AGL15). G1797 and AGL15 occupy different clades within the MADS family, but the similarity in phenotype may indicate that they act in common pathways.

Utilities

- 30 The accelerated switch to reproductive growth seen in 35S::G1797 plants, indicated that the gene or its equivalents could be used to manipulate flowering time in commercial species. Specifically, G1797 could be used to accelerate flowering, or eliminate any requirement for vernalization. Conversely, it is possible that the activity of G1797 or its equivalents could be modified to delay flowering. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield
35 increases.

The effects on flower development are also of commercial interest; the persistence of outer whorl organs following pollination in 35S::G1797 lines indicated that the gene or its equivalents could be applied to ornamental plants to prolong the life of blooms.

5 **G1798 (SEQ ID NO: 283)**

Published Information

G1798 was identified within P1 clone MJM18 (chromosome 5, GenBank accession AB025623) as one of a pair of novel, highly related, tandemly arranged MADS box genes (the other gene was G1797). A functional characterization of G1798 remains to be published.

10 Experimental Observations

To assess the function of G1798, we analyzed transgenic *Arabidopsis* lines in which the gene was overexpressed from a CaMV promoter. 35S::G1798 transformants were very early flowering, had curled leaves, were very small and displayed severe abnormalities in flower development. As a result of such defects, the plants showed very poor fertility and insufficient seed was obtained to perform physiological assays. Additionally, a number of 35S::G1798 lines displayed terminal flowers, indicating that the gene could influence meristem determinacy.

It should be noted that accelerated flowering and changes in flower development were also observed as a result of overexpression of the putative paralog, G1797, indicating that the two genes have related functions. Interestingly, 35S::G1797 lines exhibited delayed floral organ abscission; such a phenotype might also have been prevalent in 35S::G1798 plants, but could have been masked by the severe sterility of these lines. Two other related genes, G627 and G1011 also produced very similar effects to G1797 and G1798 when overexpressed.

Utilities

The accelerated switch to reproductive growth seen in 35S::G1798 plants, indicated that the gene or its equivalents could be used to manipulate flowering time in commercial species. Specifically, G1798 could be used to accelerate flowering, or eliminate any requirement for vernalization. Conversely, it is possible that the activity of G1798 or its equivalents could be modified to delay flowering. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases.

The effects on flower and inflorescence development are also of commercial interest and indicated that the gene or its equivalents might be used to manipulate floral traits such as sterility or fruit development, or to produce novel plant architectures.

G1816 (SEQ ID NO: 287)

35 Published Information

G1816 is a member of the MYB-related class of transcription factors. The gene corresponds to TRIPTYCHON (TRY), and has recently been shown to be involved in the lateral inhibition during

epidermal cell specification in the leaf and root (Schellmann et al. (2002) *EMBO J.* 21: 5036-5046). The model proposes that TRY (G1816) and CPC (G225) function as repressors of trichome and atrichoblast cell fate. TRY loss-of-function mutants form ectopic trichomes on the leaf surface. TRY gain-of-function mutants are glabrous and form ectopic root hairs.

5

Experimental Observations

The complete sequence of G1816 was determined. The function of the gene was studied using transgenic plants in which G1816 was expressed under the control of the 35S promoter. Consistent with the morphological phenotypes published for the 35S::TRY overexpressors, the transgenic plants were glabrous and form ectopic root hairs. These transgenic lines were also more tolerant to growth under nitrogen-limiting conditions, both in a germination assay as well as a root growth assay on older seedlings. In addition to the nitrogen-limiting tolerance phenotypes observed in these transgenic lines, the 35S::G1816 plants were also insensitive to growth retardation effects of germination on conditions of high glucose, indicating that this gene could play a role in sugar sensing responses in the plant or osmotic stress tolerance. Genes for many sugar-sensing mutants are allelic to genes involved in abscisic acid and ethylene signaling (Rolland et al. (2002) *Plant Cell* 14: Suppl. S185-S205). Therefore, G1816 could also be involved in hormone signaling pathways.

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Utilities

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The phenotypic effects of G1816 overexpression, such as the increase in root hair formation and the increase in seedling vigor observed in a germination assay on high glucose media, indicated that the gene or its orthologs can be used to engineer plants with increased tolerance to abiotic stresses such as drought, salt, heat or cold.

25

In addition, the enhanced performance of G1816 overexpression lines under low nitrogen conditions indicated that the gene or its orthologs could be used to engineer crops that could thrive under conditions of reduced nitrogen availability.

The effect of G1816 overexpression on insensitivity to glucose in a germination assay, indicated that the gene or its orthologs could be involved in sugar sensing responses in the plant.

30

G1816 or its orthologs could also be used to alter anthocyanin production and trichome formation in leaves.

35

The potential utilities of genes involved in anthocyanin production include alterations in pigment production for horticultural purposes and increase stress resistance perhaps in combination with other transcription factors. Flavonoids have antimicrobial activity and could be used to engineer pathogen resistance. In addition, several flavonoid compounds have health promoting effects such as the inhibition of tumor growth and cancer, prevention of bone loss and the prevention of the oxidation of lipids.

Given that the phenylpropanoid biosynthetic pathway (from which anthocyanins are produced) feeds into the pathways for the production of a number of other classes of secondary metabolites, such as lignins and tannins, changing the activity of G1816 or its orthologs might also influence the levels of those types of compounds.

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G1837 (SEQ ID NO: 295)Published Information

G1837 (At5g54480) was identified as part of the BAC clone F24B18, GenBank accession number AB026634 (nid=4757390).

10

Experimental Observations

The function of the gene was analyzed using transgenic plants in which a G1837 genomic clone was expressed under the control of the 35S promoter. Transgenic plants overexpressing G1837 showed increased tolerance to NaCl in the root inhibition assay, and also a potential enhancement of chilling tolerance. Under normal growth conditions, 35S::G1837 lines showed wild-type morphology.

15

Utilities

G1837 could be used to engineer increased salt stress tolerance.

20 **G1840 (SEQ ID NO: 297)**Published Information

G1840 (At5g67010) was identified as part of TAC clone K8A10 (GenBank accession AB026640).

25 Experimental Observations

Overexpression of G1840 induced necrosis and death of patches of tissue in aerial part of the plant, indicating that it might be influence pathways of disease response, programmed cell death, or senescence. At early stages of development, 35S::G1840 seedlings appeared normal. However, towards the end of the rosette phase, these plants displayed rather broad flat dark leaves with short petioles.

30 Randomly distributed, brown specks of necrotic tissue became visible on the leaves at around this time. Similar effects were noted in the inflorescence; in severely affected plants, the entire inflorescence tips became brown and withered away without producing seeds. This phenomenon was seen in both primary and secondary inflorescences, and plants with a strong phenotype developed a very short, bushy architecture.

35 A related AP2 family gene, G1749, was analyzed, and found to produce similar effects to G1840 when overexpressed.

Utilities

The overexpression phenotype indicates G1840 could have a role in regulating programmed cell death. Such a function could have various applications. The gene, its targets, or its equivalents could be used to induce cell death in a controlled manner in specific tissues or in response to pathogen attack. For example, if the gene was specifically active in gametes or reproductive organs, the gene or its equivalents might be used to achieve male or female sterility. Alternatively, in the latter scenario, the gene or its equivalents might restrict the spread of a pathogen infection through a plant.

G1863 (SEQ ID NO: 303)**10 Published Information**

G1863 was identified by amino acid sequence similarity to rice Growth-regulating-factor1 (GRF1), which has a potential role in the regulation of stem growth (Knaap et al. (2000) *Plant Physiol.* 122: 695-704). G1863, which has also been referred to as *Arabidopsis* GRL3, is found in the sequence of chromosome II section 199 of 255 (GenBank accession AC006919.5 GI:6598632), released by the *Arabidopsis* Genome Initiative. No information related to the functional characterization of G1863 is currently available from the public literature.

Experimental Observations

G1863 was found to be ubiquitously expressed, but had lower levels of expression in the stems of shoots than in other tissues. It was also determined that homozygotes for a T-DNA insertion within G1863 showed increased sensitivity to NaCl in germination assays.

35S::G1863 overexpressing transformants displayed a wild-type response in the physiology assays, but did display a number of morphological phenotypes. Plants that overexpress G1863 had larger leaves that had higher levels of chlorophyll per unit area. These plants were dark in coloration, showed changes in leaf shape, and delayed flowering.

Utilities

G1863 or its orthologs could be used to generate salt or drought tolerant crops.

The overexpression data indicate that the gene could have a number of additional applications.

30 The delayed flowering displayed by 35S::G1863 transformants indicated that the gene or its orthologs might be used to manipulate the flowering time of commercial species. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases.

Conversely, the activity of G1863 or its orthologs might be modified to accelerate flowering, or eliminate any requirement for vernalization.

This transcription factor or its orthologs could be used to improve plant productivity through increased biomass or yield and/or improve the nutraceutical value of foodstuffs, or increase photosynthetic capacity to improve yield. With regard to the former, consumption of dark green leafy vegetables has been shown in clinical studies to reduce the risk of age-related macular degeneration (ARMD), the leading cause of blindness in elderly people.

The changes in leaf shape shown by 35S::G1863 plants also indicated that the gene or its orthologs could be used to engineer changes in plant form.

G1893 (SEQ ID NO: 305)

Published Information

G1893 (At1g03790) was identified in the sequence of P1 clone MOE17 (GenBank accession number AB025629) based on its sequence similarity within the conserved domain to other C2H2 related proteins in *Arabidopsis*. There is no published or public information about the function(s) of G1893.

Experimental Observations

G1893 is expressed ubiquitously at moderately low levels and was weakly induced by cold. The function of G1893 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1893 resulted in seedlings with square cotyledons. True leaves were small with serrated margins. Many initial transformants did not survive past early stages of growth. Those that did survive were small and produced few seeds. These seedlings also contained more anthocyanin.

G1893 is a paralog of G3062 and G1976. Similar to what was seen with overexpression of G1893, overexpression of G3062 produced highly deleterious effects on *Arabidopsis* growth and development. It was nearly impossible to obtain 35S::G3062 transformants. Only one line survived to maturity, but was markedly smaller than wild-type controls at all stages of development, and yielded few seeds. Overexpression of G1976 also produced alterations in leaf morphology and flower development, as well as causing an extreme decrease in overall plant size and fertility. Severely affected 35S::G1976 lines were tiny, and died at early stages. More moderate phenotypes that were observed were very small plants with dark green leaves with serrated leaf margins. Inflorescences were short and lacked internode elongation. Floral organs were mostly very poorly developed with short pedicels. Fertility of 35S::G1976 transformants was very poor and many plants completely failed to set seed.

Utilities

G1893 or its equivalents may have a utility in modifying fertility, cotyledon shape or plant architecture.

G1928 (SEQ ID NO: 311)Published Information

G1928 was identified in the sequence of P1 clone MCP4, GenBank accession number AB028610, released by the *Arabidopsis* Genome Initiative. There is no other published or public information about the function(s) of G1928.

Experimental Observations

The function of G1928 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Transgenic *Arabidopsis* plants overexpressing G1928 grew much more vigorously than wild-type plants at 4° C; the plants were larger, less chlorotic and showed fewer symptoms of stress.

Utilities

Based on the effects of G1928 overexpression, the gene or its orthologs might be used to protect crops against low temperature conditions.

G1968 (SEQ ID NO: 321)Published Information

G1968 (At1g26610) was identified in the sequence of BAC T1K7 (GenBank accession number AC013427), based on its sequence similarity within the conserved domain to other C2H2 related proteins in *Arabidopsis*. There is no published or public information about the function of G1968.

Experimental Observations

The function of G1968 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1968 resulted in plants that were small and slow developing. Flowers were also small and had defects in organ formation. G1968 overexpressing lines contained more anthocyanins when grown under low nitrogen, or low nitrogen plus glutamine, in a germination assay. When grown on control plates, two lines exhibited size segregation. One line was wild type.

Utilities

On the basis of the response of G1968 to low nitrogen media, the gene might be useful in developing plants that are more tolerant to poor nutrient growth conditions.

G1983 (SEQ ID NO: 323)Published Information

G1983 (At1g03790) was identified in the sequence of BAC F21M11 (GenBank accession number AC003027) based on its sequence similarity within the conserved domain to other C3H related proteins in *Arabidopsis*. There is no published or public information about the function of G1983.

Experimental Observations

The function of G1983 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1983 resulted in plants that were small, darker green and flowered late. 35S::G1983 plants were wild type in all physiological analyses that were performed.

Utilities

Based on the delayed flowering of G1983 overexpression lines, the gene might be used to manipulate the flowering time of commercial species. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases.

If the dark coloration of 35S::G1983 lines reflects an increase in biochemical composition, the gene might be used to improve the nutraceutical value of foodstuffs, or increase photosynthetic capacity to improve yield.

G1985 (SEQ ID NO: 325)

Published Information

G1985 was identified in the sequence of BAC F3L24, GenBank accession number AC011436, released by the *Arabidopsis* Genome Initiative. There is no other published or public information about G1985.

Experimental Observations

The 5' and 3' ends of G1985 were determined by RACE PCR, and the gene function was analyzed via overexpression lines.

Overexpression of G1985 produced a spectrum of alterations in *Arabidopsis* development. However, the most dramatic effect was observed in the inflorescence, where G1985 appeared to inhibit reproductive development and caused a reversion towards vegetative growth. 35S::G1985 plants were very small, slow developing, formed rather dark curled leaves. The inflorescences from these plants were generally stunted, and carried flowers that often had underdeveloped organs and poor pollen production. Strikingly, however, inflorescences typically showed an increase in vegetative characteristics and often formed small aerial rosettes. Additionally, in some cases, the inflorescence meristem apparently reverted back to initiating leaf primordia once it had entered the phase of flower initiation.

Floral reversion is extremely rare in *Arabidopsis*, especially under inductive light conditions such as those in which these experiments were performed. In wild-type plants, the shoot meristem, on becoming an inflorescence meristem, usually forms 2-3 single cauline leaf primordia (which develop secondary shoots in their axils) and then initiates floral meristems until senescence occurs. The inflorescence meristem displays a strong commitment to flower formation, and usually never switches

back into a phase of leaf production once flower initiation has commenced. However, in some species (e.g. *Impatiens*) floral reversion does occur, and is an important means by which the plant achieves developmental plasticity in response to changing environmental conditions (Battey et al. (2002). *Curr. Opin. Plant Biol.* 5: 62-68; Battey (2000) *J. Exp. Bot.* 51: 1769-1780).

5 Utilities

The experimental results obtained with G1985 overexpressors indicate that the gene or its orthologs can modulate the developmental programs, which regulate phase change and developmental plasticity of the shoot meristem. In particular, the gene might be used to manipulate seasonality and influence whether plants display an annual or perennial habit.

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G1988 (SEQ ID NO: 327)

Published Information

G1988 (At3g21150) is in P1 clone MSA6 (GenBank accession number AP000604) and was identified based on its sequence similarity within the conserved domain to other CONSTANS-like related proteins in *Arabidopsis*. There is no published or public information about the function of G1988.

15

Experimental Observations.

The function of G1988 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Evidence from physiological and morphological assays indicates that G1988 may play a role in developmental processes regulated by light; 35S::G1988 seedlings displayed longer hypocotyls, elongated petioles, and a number of lines flowered early.

20

When grown on limited phosphate, all lines appeared larger and had more root growth than controls. Seedlings germinated on plates that contained limited nitrogen (supplemented with glutamine) appeared less stressed than controls.

Utilities

Based on the results from physiological assays, G1988 might be used to engineer plants that show enhanced growth and survivability in low nutrient environments.

25

G1988 could also have a role in modulating developmental processes regulated by light, such as shade avoidance. Eliminating shading responses could lead to increased planting densities with subsequent yield enhancement. The gene might also be useful in manipulating flowering time.

30

G1995 (SEQ ID NO: 333)

Published Information

G1995 (At3g58070) is in BAC T10K17 (GenBank accession number AL132977) and was identified based on its sequence similarity within the conserved domain to other zinc finger DOF-related proteins in *Arabidopsis*. There is no published or public information about the function of G1995.

35

Experimental Observations

The function of G1995 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1995 resulted in plants that had flowers with increased trichome density on sepals and ectopic trichomes on carpels. The flowers also had rather poor pollen production and many of the lines yielded only relatively small quantities of seed. One line displayed aerial rosette like structures and had floral organs that were converted towards a bract-like identity. In physiological analyses, G1995 overexpressors showed size segregation and a slight increase in sensitivity to nutrient limitation.

10 Utilities

Based on the results from physiological assays, G1995 might be used to engineer plants that show enhanced growth and survivability in low nutrient environments.

The morphological effects of G1995 overexpression indicate a number of potential applications relating to increasing or changing trichome density:

15 Trichome glands on the surface of many higher plants produce and secrete exudates that give protection from the elements and pests such as insects, microbes and herbivores. These exudates may physically immobilize insects and spores, may be insecticidal or anti-microbial or they may produce allergens or irritants to protect against herbivores. Trichomes have also been suggested to decrease transpiration by decreasing leaf surface airflow, and by exuding chemicals that protect the leaf from the sun.

20 Depending on the plant species, varying amounts of diverse secondary biochemicals (often lipophilic terpenes) are produced and exuded or volatilized by trichomes. These exotic secondary biochemicals, which are relatively easy to extract because they are on the surface of the leaf, have been widely used in such products as flavors and aromas, drugs, pesticides and cosmetics. One class of secondary metabolites, the diterpenes, can effect several biological systems such as tumor progression, prostaglandin synthesis and tissue inflammation. In addition, diterpenes can act as insect pheromones, termite allomones, and can exhibit neurotoxic, cytotoxic and antimitotic activities. As a result of this functional diversity, diterpenes have been the target of research several pharmaceutical ventures. In most cases where the metabolic pathways are impossible to engineer, increasing trichome density or size on leaves may be the only way to increase plant productivity.

30 Thus, the use of G1995 and its homologs to increase trichome density, size or type may therefore have profound utilities in so called molecular farming practices and increasing the yield of cotton fibers.

If the effects on trichome patterning and/or aerial rosette formation reflect a general change in heterochronic processes, G1995 or other clade members, might be used to modify the way meristems and/or cells develop during different phases of the plant life cycle. In particular, altering the timing of phase changes could afford positive effects on yield and biomass production.

G2041 (SEQ ID NO: 341 and SEQ ID NO: 2110)Published Information

The transcriptional regulator G2041 was identified by amino acid sequence similarity to proteins of the SWI/SNF family of chromatin remodeling factors. G2041 is found in the sequence of the chromosome 3, BAC clone T12K4 (AL138640.1 GI:6899910), released by the *Arabidopsis* Genome Initiative. No additional public information related to the functional characterization of G2041 is available.

Experimental Observations

The function of G2041 was analyzed through its overexpression in *Arabidopsis*; 35S::G2041 lines displayed no consistent morphological changes when compared to control plants. However, the overexpression lines were more tolerant to salt stress in a germination assay. It should be noted that since a truncated version of the gene (SEQ ID NO: 2110) was overexpressed, the phenotype obtained could be a dominant negative type effect.

Utilities

The results of physiological assays indicate that G2041 or its equivalents could be modify abiotic stress responses. Given the salt resistance exhibited by 35S::G2041 transformants, the gene or its equivalents might be used to engineer salt tolerant crops and trees that can flourish in saline soils, or under drought conditions.

G2051 (SEQ ID NO: 343)Published Information

G2051 corresponds to AT1G32510, annotated by the *Arabidopsis* Genome initiative. No information is available about the function(s) of G2051.

Experimental Observations

The function of G2051 was analyzed using transgenic plants in which the gene was expressed under the control of the 35S promoter. The phenotypes of the 35S::G2051 transgenic *Arabidopsis* plants were wild-type in morphology.

G2051 overexpressing lines were more tolerant of chilling stress in a germination assay. Two of the three lines analyzed showed the response.

Utilities

Based on the phenotype observed in 35S::G2051 transgenic plants, the gene or its equivalents could be engineered to manipulate the response to abiotic stresses, such as cold during germination. For

example, a gene that enhanced germination and seedling vigor in the cold would have tremendous utility in allowing seeds to be planted earlier in the season with a higher survival rate.

G2060 (SEQ ID NO: 345)

5 Published Information

G2060 corresponds to gene AT1g69810, and it has also been described as WRKY36. No information is available about the function(s) of G2060.

Experimental Observations

10 G2060 is ubiquitously expressed in *Arabidopsis*, with slightly higher levels of transcript being found in roots than in other samples.

A T-DNA insertion mutant for G2060 was analyzed and shown to display a wild-type morphology, and was also wild-type in its response to the physiological analyses that were performed.

Transgenic plants in which G2060 was expressed under the control of the 35S promoter were
15 then generated. No consistent morphological or developmental alterations were observed as a consequence of G2060 overexpression. However, 35S::G2060 seedlings were more tolerant to salt stress in a root inhibition assay when compared to the wild-type controls.

Utilities

20 Based on the increased salt tolerance exhibited by the 35S::G2060 lines in physiology assays, this gene might be used to engineer salt tolerant crops and trees that can flourish in salinified soils, or under drought conditions.

G2085 (SEQ ID NO: 355)

25 Published Information

G2085 was identified in the sequence of BAC T22A6, GenBank accession number AL078637, released by the *Arabidopsis* Genome Initiative.

G2085 appears to correspond to ZIM (at residue 306 near the carboxyl terminus, leucine is replaced by methionine in ZIM, compared to isolated cDNA, and the genomic sequence released by
30 AGI). Nishii et al. ((2000) *Biosci. Biotechnol. Biochem.* 64: 1402-1409) isolated ZIM by differential screening of an arrayed normalized cDNA library from inflorescence tissue of *Arabidopsis* (Takemura et al. (1999) *DNA Res.* 6: 275-282). In addition to the GATA domain, ZIM contains a basic region with a sequence resembling a nuclear localization signal, and an acidic region. The nuclear localization of ZIM was detected using GFP as a reporter. Based on its expression pattern, zinc finger domain, and nuclear
35 localization, the authors suggest that ZIM is involved in inflorescence and flower development.

Experimental Observations

G2085 was determined to be constitutively expressed throughout the plant, and that its expression is markedly repressed by a variety of stress conditions such as abscisic acid, cold, osmotic stress, and *Erysiphe*. G2085 was analyzed via a homozygous T-DNA insertion mutant and that line appeared wild-type in all assays.

The complete sequence of G2085 was determined, and G2085 overexpression lines were generated. Many of the plants overexpressing G2085 had small, dark colored, hirsute, inner rosette leaves. Altered seed morphology and increased seed size was also noted. Trichome density was increased.

In each set of primary transformants, many of the lines were smaller than wild type controls. In particular, the adult rosette leaves of around half of the plants from the second set were noted to be small, dark in coloration, and have a rather high trichome density. Additionally, alterations in morphology were observed in the seeds from a small number of T1 lines from each set. From the first set, seeds from 2/18 lines were larger than controls, and in the second set, 4/16 lines had rather pale seeds, and two of these showed seeds that were also large.

Utilities

The promoter of G2085 may also have utility as a promoter that can be down-regulated in response to a variety of stresses.

Based on the overexpression phenotypes, G2085 or its orthologs might be used to manipulate plant growth and development. Based on the increase in seed size of the 35S::G2085 transgenic lines, G2085 could be increasing the size of the embryo and that could enhance seed traits such as seed oil or seed protein content or yield. Additionally, G2085 might be used to modify trichome density. Additionally, if the dark coloration of 35S::G2085 lines reflects an increase in biochemical composition, the gene might be used to improve the nutraceutical value of foodstuffs, or increase photosynthetic capacity to improve yield.

The morphological effects of G2085 overexpression indicate a number of potential applications relating to increasing or changing trichome density: Thus, the use of G2085 and its equivalents to increase trichome density, size or type may therefore have profound utilities in so called molecular farming practices and increase the yield of cotton fibers.

G2133 (SEQ ID NO: 1495)

Published Information

G2133 corresponds to gene F26A9.11 (AAF23336). No information is available about the function(s) of G2133.

Closely Related Genes from Other Species

G2133 does not show extensive sequence similarity with known genes from other plant species outside of the conserved AP2/EREBP domain.

5 Experimental Observations

The function of G2133 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter.

G2133 expression was detected in a variety of tissues: flower, leaf, embryo, and silique samples. Its expression might be altered by several conditions, including auxin treatment, osmotic stress, and
10 *Fusarium* infection. Overexpression of G2133 caused a variety of alterations in plant growth and development: delayed flowering, altered inflorescence architecture, and a decrease in overall size and fertility.

At early stages, 35S::G2133 transformants were markedly smaller than controls and displayed curled, dark-green leaves. Most of these plants remained in a vegetative phase of development
15 substantially longer than controls, and produced an increased number of leaves before bolting. In the most severely affected plants, bolting occurred more than a month later than in wild type (24-hour light). In addition, the plants displayed a reduction in apical dominance and formed large numbers of shoots simultaneously, from the axils of rosette leaves. These inflorescence stems had short internodes, and carried increased numbers of cauline leaf nodes, giving them a very leafy appearance. The fertility of
20 35S::G2133 plants was generally very low. In addition, G2133 overexpressing lines were found to be more resistant to the herbicide glyphosate in initial and repeat experiments.

No alterations were detected in 35S::G2133 plants in the biochemical analyses that were performed.

G2133 is a paralog of G47, the latter having been known from earlier studies to confer a drought
25 tolerance phenotype when overexpressed. It was thus not surprising when G2133 was also shown to induce drought tolerance in a number of 35S::G2133 lines challenged in soil-based drought assays. Results with two of these lines are shown in Figures 10A and 10B, which compare the recovery of these lines from eight days of drought treatment with that of wild-type controls. After re-watering, all of the plants of both G2133 overexpressor lines became reinvigorated, and all of the control plants died or were
30 severely affected by the drought treatment.

Utilities

G2133 could be used for the generation of glyphosate resistant plants, and to increase plant resistance to oxidative stress.

35 G2133 can be used to increase the tolerance of plants to drought and likely to other osmotic stresses as well.

G2142 (SEQ ID NO: 365)Published Information

G2142 was identified by amino acid sequence similarity to other HLH/MYC proteins. G2142 is found in the sequence of the chromosome 1 BAC clone T6L1 (GenBank accession number AC011665, 5 nid=g6358759), released by the *Arabidopsis* Genome Initiative. No information related to the functional characterization of G2142 is currently available from the public literature.

Experimental Observations

The function of G2142 was studied using transgenic plants in which the gene was expressed 10 under the control of the 35S promoter. A small number of the 35S::G2142 plants displayed a slight acceleration of flowering compared to controls. Additionally, G2142 overexpressors were more tolerant to phosphate deprivation in a root growth assay, but this effect was rather subtle.

Utilities

15 The results of physiological assays indicate that G2142 could be used to improve plant performance in conditions of limited phosphate.

G2146 (SEQ ID NO: 367)Published Information

20 The sequence of G2146 was obtained from *Arabidopsis* genomic sequencing project, GenBank accession number AC012393, nid=6143859, based on its sequence similarity within the conserved domain to other bHLH related proteins in *Arabidopsis*.

Experimental Observations

25 The function of G2146 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G2146 resulted in plants that displayed a mild increase in the time to flowering, darker coloration, and inflorescences that were shorter and bushier than those of wild-type plants.

Utilities

30 G2146 could be used to generate plants that flower late or have altered leaf coloration and plant architecture. The delayed flowering displayed by 35S::G2146 transformants indicates that the gene might be used to manipulate the flowering time of commercial species. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases.

35 Additionally, the dark coloration of 35S::G2146 lines may reflect an increase in biochemical composition; the gene may thus be used to improve the nutraceutical value of foodstuffs, or increase photosynthetic capacity to improve yield.

G2207 (SEQ ID NO: 371)Published Information

G2207 (At1g20640) was identified as part of the BAC clone F5M15, GenBank accession number
5 AC027665 (nid=8096769).

Experimental Observations

The complete sequence of G2207 was determined. The function of the gene was analyzed using
transgenic plants in which a genomic clone for G2207 was expressed under the control of the 35S
10 promoter. In germination assays, 35S::G2207 lines showed increased tolerance to osmotic stress under
conditions of high salt or high sucrose and were less sensitive to abscisic acid. All these phenotypes
indicate that G2207 is involved in the plant response to dehydration stress. A small number of the lines
also showed delayed flowering, indicating that the gene regulates the timing of the floral transition.

The bZIP-NIN gene G2207 does not share significant homology to any of the bZIP genes, for
15 some of which a role in abscisic acid signaling has been reported (ABF1=G2071, ABF2=G3028,
ABF3=G570, ABF4=G1058; Choi et al. (2000) *J. Biol. Chem.* 275: 1723-1730).

Utilities

G2207 appears to affect ABA sensitivity. ABA is one of the key signal molecules in the stress
20 response pathways. G2207 may have a utility in modifying ABA responses such as seed dormancy, seed
development, and cold and/or drought tolerances.

In particular, based on the increased tolerance to high levels of salt or sucrose, exhibited by the
35S::G2207 lines in physiology assays, this gene might be used to engineer crops and trees that can
flourish in salinified soils, or under drought conditions.

25 Although the increased sucrose tolerance observed for 35S::G2207 lines is most likely related to
a general dehydration stress tolerance, the gene might be involved in sugar sensing. Thus G2207 might
also be used to generate crop plants with altered sink source relations.

The late flowering shown by 35S::G2207 lines indicates that the gene might be used to
manipulate the flowering time of commercial species. In particular, an extension of vegetative growth
30 can significantly increase biomass and result in substantial yield increases.

Additionally, if the dark coloration of 35S::G2207 lines reflects an increase in biochemical
composition, the gene might be used to improve the nutraceutical value of foodstuffs, or increase
photosynthetic capacity to improve yield.

G2239 (SEQ ID NO: 379)Published Information

G2239 was identified in the sequence of BAC T12H1, GenBank accession number AC009177, released by the *Arabidopsis* Genome Initiative.

G2239 corresponds to ATL6, a member of the ATL (RHE) gene family (Jensen et al. (1998) *FEBS Lett.* 436: 283-287; Martinez-Garcia et al. (1996) *Mol. Gen. Genet.* 252: 587-596; Salinas-Mondragon et al. (1999) *Plant Mol. Biol.* 40: 579-590). Members of the ATL gene family contain, in addition to the RING C3H2C3 domain, an n-terminal transmembrane domain. Fungal elicitors and cycloheximide applications caused rapid induction of ATL6 and ATL2 (G649) expression. However, induced ATL6 expression was found to be more stable than that of ATL2. This difference might be accounted for by the fact that the ATL6 3' UTR lacks a DST element (an mRNA stability determinant found in SAUR transcripts), whereas this element is found in the 3' UTR of ATL2. The authors suggest that ATL6 and ATL2 may function in plant-pathogen interactions.

Experimental Observations

The complete sequence of G2239 was determined and its function was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter.

G2239 overexpression lines were greener and contained less anthocyanin when grown on low nitrogen media supplemented with sucrose or sucrose plus glutamine. However, the phenotype of 35S::G2239 plants was wild-type in all morphological assays performed.

Utilities

The enhanced performance of G2239 overexpression lines under low nitrogen conditions indicated that the gene or its orthologs could be used to engineer crops that could thrive under conditions of reduced nitrogen availability.

The observation that 35S::G2239 lines made less anthocyanin on high sucrose plus glutamine, indicated that G2239 might be used to modify carbon and nitrogen status, and hence assimilate partitioning.

G2317 (SEQ ID NO: 389)

Published Information

G2317 is a novel member of the Myb-related family of transcription factors. G2317 corresponds to gene At1g18330, annotated by the *Arabidopsis* Genome Initiative. No information is available about the function(s) of G2317.

Experimental Observations

The complete sequence of G2317 was determined. The function of G2317 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. 35S::G2317 plants did not show consistent alterations in morphology or development.

When analyzed in physiological assays, each of three 35S::G2317 lines showed more tolerance to salt stress by displaying more root growth in a root growth assay. G2317 overexpressing lines also displayed larger size and less chlorosis in high salt (150mM) at the seedling stage when compared to wild-type plants.

One transgenic line showed enhanced performance when germinated under cold conditions.

Utilities

The results of physiological assays indicate that G2317 could be modify abiotic stress responses.

Given the salt resistance exhibited by 35S::G2317 transformants, the gene or its orthologs might be used to engineer salt tolerant crops and trees that can flourish in saline soils, or under drought conditions.

The enhanced performance of a line of 35S::G2317 seedlings under chilling conditions indicated that the gene or its orthologs might be applied to engineer crops that show better growth under cold conditions.

G2319 (SEQ ID NO: 391 and SEQ ID NO: 2112)

Published Information

G2319 corresponds to AT3G09600, annotated by the *Arabidopsis* Genome initiative. No information is available about the function(s) of G2319.

Experimental Observations

The function of G2319 was analyzed using transgenic plants in which the gene was expressed under the control of the 35S promoter. Two different G2319 constructs were transformed into *Arabidopsis*.

P13388 contained a truncated version of the gene (SEQ ID NO: 2112) whereas P13446 contained a full-length clone. Transformants harboring P13446 exhibited wild-type morphology and exhibited wild-type phenotypes in response to the physiology assays. A marked delay in the onset of flowering was observed in ten of the eighteen lines transformed with the P13388 construct. Three lines co-transformed with P13388 showed more tolerance to salt stress in a root growth inhibition assay. When the assay was repeated, all thereof these lines repeated the phenotype.

Given that all of the phenotypic effects resulted from overexpression of a truncated version (SEQ ID NO: 2112) of the G2319 product, it might represent a dominant negative phenotype.

Utilities

Based on the phenotypes observed in morphological and physiological assays, G2319 or its equivalents might be have a number of utilities.

Given the salt resistance exhibited by 35S::G2319 transformants, the gene or its equivalents might be used to engineer salt tolerant crops and trees that can flourish in saline soils, or under drought conditions.

The late flowering displayed by 35S::G2319 transformants indicated that the gene or its equivalents might be used to delay the flowering of commercial species.

10 G2334 (SEQ ID NO: 393)

Published Information

G2334 was identified by amino acid sequence similarity to the rice Growth-regulating-factor1 (GRF1), which has a potential role in the regulation of stem growth in rice (Knapp et al (2000) *Plant Physiol.* 122: 695-704). It is found in the sequence of chromosome 3, BAC clone F8J2 (AL132969.2 GI:7629988), released by the *Arabidopsis* Genome Initiative. No information related to the functional characterization of G2334 is currently available from the public literature.

Experimental Observations

The function of G2334 was analyzed through its overexpression in *Arabidopsis*; 35S::G2334 lines displayed marked delay in the onset of flowering, developed large wrinkled dark green leaves, and had substantially greater vegetative biomass than wild-type controls.

It should be noted that the effects of G2334 overexpression are very similar to those produced by overexpression of a related gene G1863, indicating that the two genes might have overlapping functions.

25 Utilities

The overexpression data indicate that G2334 could have a number of applications.

The phenotypes displayed by 35S::G2334 transformants indicated that the gene or its equivalents might be used to increase size or manipulate the flowering time of commercial species. Conversely, the activity of G2334 or its equivalents might be modified to accelerate flowering, or eliminate any requirement for vernalization.

Additionally, if the altered coloration of 35S::G2334 plants reflects a change in biochemical composition, the gene or its equivalents might be used to improve the nutraceutical value of foodstuffs, for example, by reducing the risk of ARMD, or increase photosynthetic capacity to improve yield.

The changes in leaf shape shown by 35S::G2334 plants indicated that the gene or its equivalents could be used to engineer changes in plant form.

G2382 (SEQ ID NO: 401)Published Information

The sequence of G2382 was obtained from *Arabidopsis* genomic sequencing project, GenBank accession number AB020746, nid=3985949, based on its sequence similarity within the conserved
5 domain to other triple-helix related proteins in *Arabidopsis*.

Experimental Observations

The function of G2382 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G2382 resulted in plants that were insensitive
10 to ABA treatment in a germination assay.

Utilities

G2382 appears to affect ABA sensitivity. ABA is one of key signal molecules in the stress response pathways. Therefore, G2382 may have a utility in modifying ABA responses such as seed
15 development, seed dormancy, and cold and dehydration tolerance.

G2432 (SEQ ID NO: 407)Published Information

G2432 (At1g29160) is in the sequence of BAC F28N24 (GenBank accession number
20 AC021043) based on its sequence similarity within the conserved domain to other DOF related proteins in *Arabidopsis*. There is no published or public information about the function of G2432.

Experimental Observations

The function of G2432 was studied using transgenic plants in which the gene was expressed
25 under the control of the 35S promoter. Overexpression of G2432 resulted in very small plants with narrow cotyledons and poorly developed roots. As 35S::G2432 plants matured, tiny, round, vertically oriented leaves with extremely long petioles were observed, and flowering was delayed. Such features often indicate alterations in light regulated development. Many lines senesced without setting seed. The lines that did flower produced inflorescences with infertile flowers. Consequently, no seed was obtained
30 for physiological analysis.

Utilities

The phenotype of plants overexpressing G2432 or its paralog G736 indicate that the former gene or its equivalents might be used to manipulate developmental processes regulated by light, such as shade
35 avoidance. Eliminating shading responses could lead to increased planting densities with subsequent yield enhancement. The gene might also be useful in modifying flowering time.

G2453 (SEQ ID NO: 411, SEQ ID NO: 2113 and SEQ ID NO: 2114)

Published Information

The YABBY transcription factor G2453 is referenced in the public literature as INNER NO OUTER (INO), and has an established role in the abaxial-adaxial patterning of *Arabidopsis* ovules (Baker et al. (1997) *Genetics* 145: 1109-1124; Villanueva et al. (1999) *Genes Dev.* 13: 3160-3169). In common with other transcription factors from the YABBY gene family, INO has an important function in specifying abaxial cell fate in organs (Baker et al. (1997) *supra*; Villanueva et al. (1999) *supra*; Siegfried et al. (1999) *Development* 126: 4117-4128). G2453 is found in the sequence of the chromosome 1 BAC F28C11 (AC007945.3 GI:8096767), released by the *Arabidopsis* Genome Initiative.

Experimental Observations

The function of G2453 was analyzed through its ectopic overexpression in *Arabidopsis*. The sequences that were used to confer the phenotypes disclosed here were SEQ ID NOs: 2113 and SEQ ID NO: 2114, which are both variants of the G2453 sequence. These experiments revealed a number of morphological changes that are consistent with the previously defined role of YABBYs in abaxial cell fate determination in leaves, floral organs and ovules. The plants were generally small, slow developing, and produced rather dark, curled leaves that had a wrinkled surface texture compared to those of wild type. Additionally, an effect was observed which has not been discussed in the public literature: G2453 overexpression resulted in accumulation of high levels of anthocyanins, particularly at early stages of seedling development.

A number of lines in which an antisense version of G2453 was overexpressed were also examined. These lines exhibited wild-type morphology but displayed enhanced tolerance to salt stress in a germination assay.

Utilities

Based on the published data, the gene or its equivalents could potentially be used to modify leaf and flower development. In particular, the gene might be used to manipulate fruit traits.

The increased pigment levels and dark coloration observed in 35S::G2453 transformants point towards a number of utilities reducing the risk of ARMD by consumption of plants so altered.

Given that the 35S::G2453 plants likely had increased chlorophyll levels, the gene or its equivalents might also be used to enhance photosynthetic capacity and yield.

G2453 or its equivalents could also be applied to alter pigment production for horticultural purposes and to increase stress resistance. Flavonoids have antimicrobial activity and could be used to engineer pathogen resistance. Since the phenylpropanoid biosynthetic pathway (from which anthocyanins are produced) feeds into the pathways for the production of a number of other classes of secondary metabolites, such as lignins and tannins, changing the activity of G2453 or its equivalents might also influence the levels of those types of compounds.

Given the increased salt tolerance exhibited by the 35S::G2453 antisense lines, the gene or its equivalents might be used to engineer salt tolerant crops and trees that can flourish in salinified soils, or under drought conditions.

5 **G2457 (SEQ ID NO: 417)**

Published Information

 G2457 is known in the public literature as CRABS CLAW (CRC), which in common with other members of the YABBY family, plays an important role in specifying abaxial cell fate in leaves and floral organs (Alvarez et al (1999) *Development*: 126: 2377-2386; Bowman et al. (1999)

10 *Development*:126: 2387-2396; Eshed et al. (1999) *Cell* 99: 199-209; Siegfried (1999) *Development* 126: 4117-4128). G2457 is found in the sequence of the chromosome 1, BAC F23O10 (GenBank accession number AC018364.5; GI:12325073), released by the *Arabidopsis* Genome Initiative.

Experimental Observations

15 The function of G2457 was analyzed through its ectopic overexpression in *Arabidopsis*; 35S::G2457 lines exhibited a number of morphological changes, which are consistent with the previously defined role of CRC in abaxial cell fate determination in leaves, floral organs, and ovules. These plants showed distinctly narrow and curled leaves and a variety of floral defects.

 The overexpression lines revealed an additional potential role for G2457 in the response to
20 abiotic stress which has not previously been recognized in the published literature; all three of the 35S::G2457 lines tested performed better than wild-type controls on plates containing sodium chloride.

Utilities

 Based on the effects of G2457 overexpression and the published data, the gene or its orthologs
25 could potentially be used to modify leaf and flower, and fruit development.

 Given the increased salt tolerance exhibited by the 35S::G2457 lines, the gene may be used to engineer salt tolerant crops and trees that can flourish in salinified soils, or under drought conditions.

G2459 (SEQ ID NO: 419)

30 Published Information

 G2459 was identified by amino acid sequence similarity to the *Arabidopsis* YABBY1. Transcription factors from the YABBY family play an important role in specifying abaxial cell fate in leaves and floral organs (Siegfried et al. (1999) *Development* 126: 4117-4128). G2459 is found in the sequence of the chromosome 2 clone T9J22 map B68 (AC002505.3 GI:20196938), released by the
35 *Arabidopsis* Genome Initiative.

Experimental Observations

The function of G2459 was analyzed through its ectopic overexpression in *Arabidopsis*. The overexpression of G2459 revealed a number of morphological changes, which were consistent with the previously defined role of YABBYs in abaxial cell fate determination in leaves, floral organs and ovules.

5 All the T1 plants were generally small, slow developing, and produced rather dark, curled leaves compared to those of wild type.

Additionally, an effect was observed which has not been discussed in the public literature: G2459 overexpression resulted in accumulation of high levels of anthocyanins, particularly at early stages of seedling development. This effect was exacerbated by stress conditions such as high levels of glucose.

Utilities

Based on the published data, the gene could potentially be used to modify leaf and flower development. In particular, the gene or its equivalents might be used to manipulate fruit traits.

The increased pigment levels and dark coloration observed in 35S::G2453 transformants point towards a number of utilities reducing the risk of ARMD by consumption of plants so altered. Given that the 35S::G2453 plants likely had increased chlorophyll levels, the gene might also be used to enhance photosynthetic capacity and yield. G2453 or its equivalents could also be applied to alter pigment production for horticultural purposes and to increase stress resistance. Flavonoids have antimicrobial activity and could be used to engineer pathogen resistance. In addition, several flavonoid compounds have health promoting effects such as the inhibition of tumor growth, prevention of bone loss and the prevention of the oxidation of lipids. Since the phenylpropanoid biosynthetic pathway (from which anthocyanins are produced) feeds into the pathways for the production of a number of other classes of secondary metabolites, such as lignins and tannins, changing the activity of G2453 or its equivalents might also influence the levels of those types of compounds.

G2505 (SEQ ID NO: 425)

Published Information

G2505 is a novel member of the NAC family of transcription factors. G2505 corresponds to gene At4g10350, annotated by the *Arabidopsis* Genome Initiative. No information is available about the function(s) of G2505.

Experimental Observations

G2505 was expressed at low or non-detectable levels in most tissue types. Higher levels of transcript were found in roots compared to other tissues. No induction of G2505 expression in leaf tissue was detected in response to environmental stress-related conditions.

The effects of G2505 overexpression (overexpression construct P1533) were analyzed. Despite numerous repeated attempts, 35S::G2505 transformants could not be obtained and it was concluded that overexpression of the gene caused lethality during embryo or early seedling development.

5 Upon repeating the transformation with a new overexpression construct (P2776), the transformation frequency was very low and the few lines that were obtained were distinctly small and dark in coloration. Only two of these lines produced sufficient seed for physiology assays to be performed. However, both of those lines displayed enhanced performance in a severe drought assay.

Utilities

10 The reduced sensitivity of 35S::G2505 lines in the dehydration stress assay indicated that the gene or its orthologs might be used to engineer crops with increased tolerance to drought, salt, freezing and chilling stress, or increased water use efficiency.

G2536 (SEQ ID NO: 431)

15 Published Information

G2536 is a novel member of the NAC family of transcription factors. G2536 corresponds to gene At3g44350, annotated by the *Arabidopsis* Genome Initiative. No information is available about the function(s) of G2536.

20 Experimental Observations

The complete sequence of G2536 was determined. The function of the gene was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. 35S::G2536 plants did not show consistent alterations in their response to the physiological analyses that were performed.

25 Overexpression of G2536 produced a striking effect on leaf development and caused both an increase in leaf size as well as an apparent delay in the onset of leaf senescence. At early stages, 35S::G2536 transformants appeared normal, except for a small number of lines, which displayed rather long petioles. However, towards the end of the rosette stage and the start of the inflorescence stage, a marked alteration in rosette morphology was noticeable; leaves were generally larger and broader than in
30 wild type and often exhibited mild serrations on the margins. This effect became increasingly apparent as the plants aged. At the end of the lifecycle, the leaves of 35S::G2536 plants also remained green and showed a delay in senescence compared to wild type. Some of the 35S::G2536 lines showed a mild delay in the onset of flowering (up to about seven days in continuous light).

Utilities

The effects on leaf size and shape that were observed as a result of G2536 overexpression might also have commercial applications. Increased leaf size, or an extended period of leaf growth as a result of G2536 or ortholog expression modification, could increase photosynthetic capacity, and biomass, and have a positive effect on yield. The observed stay green phenotype or delay in the onset of senescence could also result in yield increases by increasing the period of photosynthetic productivity in source tissues.

G2550 (SEQ ID NO: 435)Published Information

G2550 was initially identified within sequence released by the *Arabidopsis* genome initiative (gene F1B16.6 within BAC clone F1B16, chromosome I, GenBank accession, AC023754), as a gene encoding a novel homeodomain protein of the BEL1 class. No public data are available pertaining to the function of this gene.

Experimental Observations

The boundaries of G2550 were determined by RACE experiments, and transgenic lines were generated in which the gene was overexpressed from a 35S promoter. These transformants exhibited a wild-type response to physiological assays, but displayed a number of morphological phenotypes. 35S::G2550 lines were dark in coloration, displayed alterations in leaf shape, and formed shorter more compact inflorescences than controls.

Utilities

The changes in morphology shown by the 35S::G2550 transformants indicated that the gene or its orthologs could be used to manipulate inflorescence architecture and branching patterns in commercial species, to create varieties with more compact forms. In particular, dwarf and compact forms of ornamental plants are extremely popular among consumers. They represent a lucrative market for breeders and growers alike, but currently for many varieties, suitable dwarf breeding lines are either unavailable or difficult to integrate into existing germ-lines. Therefore, currently, many ornamental plants are sprayed with expensive chemical growth regulators to reduce height and increase compactness. Overexpression of a gene with G2550 activity could potentially alleviate this requirement.

The altered coloration of 35S::G2550 plants reflects a change in biochemical composition, and thus the gene or its orthologs might be used to improve the nutraceutical value of foodstuffs. For example, consumption of dark green leafy vegetables has been shown in clinical studies to reduce the risk of age-related macular degeneration (ARMD), the leading cause of blindness in elderly people. Given

that the 35S::G2550 plants likely had increased chlorophyll levels, the gene might be used to enhance photosynthetic capacity and yield.

G2567 (SEQ ID NO: 441)

5 Published Information

G2567 corresponds to ARF16 (Hagen and Guilfoyle (2002) *Plant Mol. Biol.* 49: 373-385; Liscum and Reed (2002) *Plant Mol. Biol.* 49: 387-400). G2567 was identified in genomic sequence (BAC accession number AL161576).

10 Experimental Observations

The complete cDNA sequence of G2567 was determined. The function of this gene was analyzed using transgenic plants in which G2567 was expressed under the control of the 35S promoter. Plants overexpressing G2567 showed enhanced tolerance to chilling stress in a growth assay. These plants were wild-type in morphology.

15

Utilities

G2567 may be used to engineer crop plants that are more tolerant to chilling stress.

G2571 (SEQ ID NO: 445)

20 Published Information

G2571 (At1g64380) is part of the BAC clone F15H21, GenBank accession number AC066689 (nid=10645388).

Experimental Observations.

25 The complete sequence of G2571 was determined and the gene was cloned from cDNA for overexpression. The function of the gene was analyzed using transgenic plants in which G2571 was expressed under the control of the 35S promoter. Overexpression of G2571 resulted reduced size, changes in coloration, branching patterns, and leaf and flower development. In particular, some of the lines showed a sympodial-like growth pattern in the inflorescence, similar to that shown by tomato
30 plants. Thus, the gene could have a key role in regulating shoot meristem activity and branching patterns. G2571 overexpressing lines behaved similarly to the wild-type controls in all physiological assays performed.

Utilities

35 The alterations in shoot architecture seen in 35S::G2571 lines indicate that the gene might be used to manipulate inflorescence branching patterns. This could influence yield and could offer the potential for more effective harvesting techniques. For instance, the self pruning mutation of tomato

results in a determinate growth pattern and facilitates mechanical harvesting (Pnueli et al. (1998) *Plant Cell* 13: 2687-2702.

G2579 (SEQ ID NO: 451)

5 Published Information

G2579 was identified as part of the clone T28N17 (GenBank accession AC069328).

Experimental Observations

The function of G2579 was analyzed using transgenic plants in which a cDNA clone of the gene was expressed under the control of the 35S promoter. Overexpression of G2579 produced striking
10 changes in leaf shape and flower development. 35S::G2579 transformants were rather small in stature and formed narrow curled leaves with short petioles. The flowers from these plants exhibited markedly wider carpels than those of wild type, which gave rise to somewhat stumpy club-like siliques. Interestingly, although the fertility of these lines was very poor, siliques appeared to grow out fairly extensively in many instances, indicating that the gene might be producing parthenocarpic effects (fruit
15 development in the absence of seed set).

It is perhaps noteworthy that overexpression of G2579 produced similar effects on carpels to overexpression of another member of the AP2 family, G1796.

Additionally, one of three 35S::G2579 lines examined in physiology assays showed increased tolerance to chilling in a plate-based growth assay.

20 Utilities

Based on the morphological phenotypes associated with the overexpression of G2579, the gene or its equivalents could be used to engineer plants with altered fertility or altered fruit size and shape. For example, the parthenocarpic effects that were apparently induced indicated that the gene or its equivalents might be used to aid the production of seedless fruit varieties.

25 The results of physiological assays indicate that G2579 or its equivalents could also be used to generate crop plants that have increased abiotic stress tolerance, and in particular, better growth under cold conditions.

G2585 (SEQ ID NO: 453)

30 Published Information

G2585 corresponds to gene At5g01900, and it has also been described as WRKY62. No information is available about the function(s) of G2585.

Experimental Observations

The complete sequence of G2585 was experimentally determined. The function of the gene was
35 studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Seeds from four out of eighteen of the 35S::G2585 primary transformants were larger than those of

control plants grown in the same flats. However, in all other respects, G2585 overexpression lines appeared wild-type.

Utilities

5 G2585 could be used to alter seed size, shape and composition resulting in higher yielding crop plants.

G2617 (SEQ ID NO: 467)

Published Information

10 G2617 (At5g06070) was identified in the sequence of TAC clone K16F4 (GenBank accession number AP002030) based on its sequence similarity within the conserved domain to other C2H2 related proteins in *Arabidopsis*. There is no published or public information about the function of G2617.

Experimental Observations

The function of G2617 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter.

15 Overexpression of G2617 severely affected plant growth and development and produced changes in seedling growth rate, rosette phyllotaxy, leaf and flower morphology, overall plant size, and seed yield. At early stages, many of the 35S::G2617 T1 plants appeared to develop faster and seemed more advanced than wild-type, but later became small and stunted. However, this effect on seedling development was not observed in the T2 lines.

20 Utilities

The developmental effects on G2617 overexpression indicated that the gene might be used to modify growth rate and architecture. Accelerated seedling growth would allow a crop to become established faster. This would minimize exposure to stress conditions at early stages of growth, when the plants are most sensitive. Additionally, it might allow a crop to grow faster than competing weed species.
25 Furthermore, the changes in silique shape displayed by the 35S::G2617 plants, indicated that the gene may be used to alter fruit traits.

G2650 (SEQ ID NO: 483)

Published Information

30 G2650 is in the sequence of BAC T22D6, GenBank accession number AL357612, released by the *Arabidopsis* Genome Initiative. No information regarding the function of G2650 is available.

Experimental Observations.

The full-length cDNA sequence of G2650 was determined, after which the function of this gene was analyzed in transgenic plants in which G2650 was expressed under the control of the 35S promoter.
35 Plants overexpressing G2650 showed a number of effects that indicate that the gene can influence light regulated developmental processes. 35S::G2650 plants displayed long hypocotyls, elongated petioles, and formed narrow leaves that were held in a more upright orientation than those of controls. About half

of the T1 lines and all of the T2 lines examined flowered earlier than wild type. Under 12-hour conditions, the T2 plants developed excessive numbers of small axillary rosette leaves, which may eventually result in an overall increase in biomass. G2650 overexpressing lines also showed enhanced tolerance to chilling stress in a growth assay.

5

Utilities

Based on the overexpression phenotypes, G2650 could have a number of applications.

(1) Manipulation of light regulated development:

10 G2650 could influence shade avoidance. Eliminating shading responses might allow increased planting densities with subsequent yield enhancement.

(2) The gene might also be useful in manipulating flowering time. In particular, G2650 could be applied to accelerate flowering or eliminate any requirements for vernalization.

(3) Enhanced chilling stress tolerance.

15 (4) Altered meristem activity. The increased activity of axillary meristems in the rosettes of 35S::G2650 plants indicates that the gene might be used to increase leaf numbers and biomass. Alternatively, the gene might be used to modulate branching patterns.

G2661 (SEQ ID NO: 487)

Published Information

20 The sequence of G2661 was obtained from the *Arabidopsis* genome sequencing project, GenBank accession number AL161746, nid=7327833, based on its sequence similarity within the conserved domain to other bHLH related proteins in *Arabidopsis*.

Experimental Observations

25 The function of this gene was analyzed using transgenic plants in which G2661 was expressed under the control of the 35S promoter. G2661 overexpressors showed greener cotyledons on media containing high glucose compared to wild-type controls. This result indicated that G2661 may be involved in sugar sensing. Plants overexpressing G2661 were also found to be slightly smaller, darker, and slower developing than control plants in a small number of transgenic lines.

30

Utilities

The sugar sensing phenotype of G2661 indicated that this gene may be useful for altering source-sink relationships or other sugar regulated processes.

G2691 (SEQ ID NO: 497)

Published Information

G2691 (At1g25470) was identified as part of the BAC clone F2J7, GenBank accession number AC079281 (nid=10092314).

Experimental Observations

5 The complete sequence of G2691 was determined. The gene was cloned from cDNA for overexpression. The function of the gene was analyzed using transgenic plants in which G2691 was expressed under the control of the 35S promoter. G2691 overexpressing lines were morphologically wild-type. One out of three lines overexpressing G2691 showed increased seedling vigor (manifested by increased expansion of the cotyledons) in germination assays on high salt compared to wild-type
10 controls.

Utilities

15 G2691 could potentially be used to increase or facilitate seed germination and seedling growth under adverse environmental conditions, in particular salt stress.

G2694 (SEQ ID NO: 499)

Published Information

20 G2694 (At3g35770) belongs to a set of transcription factors termed OTHER. This group is comprised of regulatory genes that have been shown to bind DNA in a sequence specific manner and/or are presumed to be transcription factors based on their biochemical properties. In addition, the genes in this category do not belong to an established gene family and are, in effect, singletons in the genome. G2694 corresponds to STERILE APETALA (SAP) that was identified by Byzova et al. ((1999) *Genes Dev.* 13: 1002-1014). A mutation in SAP in *Arabidopsis* affects several aspects of reproductive growth including inflorescence, floral organ and ovule development. Mutants in the SAP gene fail to make
25 female gametophytic tissue, and megasporogenesis arrests after the first meiotic division. The internode distance in sap mutants is also reduced, petals are narrow, stamens are short and malformed, and petals and stamens are reduced in number. SAP genetically interacts with both AG and AP2 during inflorescence development. While SAP seems to function synergistically with AP2, the authors hypothesize that SAP is a negative regulator of AG (Byzova et al. (1999) *supra*).

30

Experimental Observations

35 The function of this gene was analyzed using transgenic plants in which G2694 was expressed under the control of the 35S promoter. Overexpression of G2694 produced very striking alterations in seedling size, leaf shape, delayed flowering, and changes in inflorescence and flower morphology. Some of the effects observed in the inflorescence were somewhat similar to those seen in sap mutants by Byzova et al. (1999) *supra*. However, the effects observed during the vegetative phase were not described for sap. No additional phenotypes were observed in physiological assays.

At the earliest stages, 35S::G2694 seedlings appeared larger than wild type. About two weeks after planting, the seedlings displayed markedly long petioles, narrow leaf blades, and had leaves held in a more vertical orientation than in wild type. Such effects indicated that the gene influences light-regulated developmental programs. Leaves were slightly dark in color and developed an extremely curled and twisted morphology as they expanded. In addition to these effects, the plants produced visible flower buds approximately 5 days later than controls under continuous light conditions. Following the switch to flowering, 35S::G2694 transformants formed inflorescences that had a very leafy appearance; typically an increased number of coflorescence nodes, and a higher order of branching was apparent. Changes in flower morphology were also seen; sepals were frequently enlarged and bract-like, petals and stamens were somewhat contorted, pollen production was low, and carpels were wider than in wild type. Such abnormal flowers were of low fertility and fewer siliques set than in control plants. However, siliques that did develop had a wide flattened appearance.

The morphological effects observed in overexpression lines fit with the hypothesis that SAP interacts with genes such as AGAMOUS, APETALA2 and CURLY LEAF. However, given the pleiotropy of the phenotype, such interactions are likely to be complex, and clearly affect many aspects of plant development.

Utilities

Based on the morphological effects of G2694 overexpression, a wide range of potential commercial applications for the gene or its orthologs exist, including:

- (1) Modification of light regulated developmental processes such as shade avoidance.
- (2) Modification of vegetative growth and flowering time.

The late flowering and excessive vegetative growth shown by 35S::G2694 lines indicated that the gene or its orthologs might be used to manipulate the flowering time of commercial species. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases.

That 35S::G2694 seedlings were larger than wild type at early stages, indicated that the gene could be used to confer a growth advantage at early stages and allow a crop to attain more rapid ground cover. Additionally, if the slightly dark coloration of 35S::G2694 plants reflects enhanced chlorophyll and/or carotenoid levels, this could enhance photosynthetic capacity and thereby lead to yield improvements. Finally, the changes in leaf shape seen in transgenic lines indicated that the gene could be used to produce novel ornamental forms.

- (3) Modification of flower and fruit structure

The dark coloration of 35S::G2694 lines may reflect an increase in biochemical composition, and thus G2694 or its orthologs may be used to improve the nutraceutical value of foodstuffs, or increase photosynthetic capacity to improve yield.

G2717 (SEQ ID NO: 505)Published Information

G2717 corresponds to gene At1g49950, and it has also been described as Telomere Repeat Binding Factor 1 (TRBF1). No information is available about the function(s) of G2717.

5

Experimental Observations

The function of the gene was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. 35S::G2717 lines were wild type with respect to their morphology and development. However, the G2717 overexpressors appeared to be more tolerant to osmotic stress in germination assays. Seedlings from all three transgenic lines were larger than wild-type seedlings at the same developmental stage on control media.

10

In a soil based drought assay, G2717 overexpressing plants were significantly larger and greener than wild-type control plants.

15 Utilities

Based on the increased salt, osmotic stress and drought tolerance exhibited by the 35S::G2717 plants in physiology assays, this gene or its equivalents may be used to engineer salt tolerant crops and trees that can flourish in salinified soils, or under drought conditions.

Since 35S::G2717 seedlings were slightly larger than controls, the gene or its equivalents could also be used to accelerate the rate of germination and growth of plants.

20

G2718 (SEQ ID NO: 507)Published Information

G2718 (AT1G01380) was identified in the BAC clone, F6F3 (GenBank accession AC023628). Two highly related genes, TRY and CPC have been implicated in epidermal cell specification. A lateral inhibition model proposes that TRY (G1816) and CPC (G225) function as repressors of trichome and atrichoblast cell fate (Shellmann et al. (2002) *EMBO J.* 21: 5036-5046). A comprehensive review on epidermal cell-fate specification has been published recently (Schiefelbein (2003) *Curr. Opin. Plant Biol.* 6: 74-78).

30

Experimental Observations

The function of G2718 was studied using plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G2718 resulted in a glabrous phenotype. The effect was highly penetrant, being observed in all primary transformants and each of three independent T2 lines. All of the T1 lines showed a very strong phenotype and completely lacked trichomes on leaves and stems. A comparably severe effect was observed in one of the three T2 populations, whereas the other two T2 populations each exhibited a weaker phenotype, indicating that the effect might have become partially

35

silenced between the generations. Trichomes were present in these weaker lines, but at a much lower density than in wild type.

In addition to the effects on trichome density, 35S::G2718 transformants were also generally slightly smaller than wild type controls.

5 The phenotypic effects above were observed in the 35S::G2718 as well as in all 35S lines from members of the G2718 clade (G225, G226, G1816, and G682). Similarly, 35S::TF lines from the G2718 clade all had increased root hair formation, reduced anthocyanin levels, and showed improved growth under nitrogen limiting conditions, indicating that the genes improve nutrient uptake. It should be noted however, that due to the apparent silencing of the transgene in the T2 generation, only two of three
10 35S::G2718 lines examined displayed these phenotypes.

Utilities

The phenotypic effects of G2718 overexpression, such as the increase in root hair formation and the increase in seedling vigor observed in a root growth assay on N-limiting media, indicates that the
15 gene or its equivalents could be used to engineer plants with increased tolerance to abiotic stresses such as nutrient limitation, drought, salt, heat or cold.

The enhanced performance of G2718 overexpression lines under low nitrogen conditions indicates that the gene or its equivalents could be used to engineer crops that could thrive under conditions of reduced nitrogen availability.

20 G2718 or its equivalents could also be used to alter anthocyanin production or trichome formation, and production of secondary biochemicals (e.g., lipophilic terpenes) by trichomes.

G2723 (SEQ ID NO: 509)

Published Information

25 G2723 is a member of the Myb-related family of transcription factors. The gene corresponds to gene At1g19490, annotated by the *Arabidopsis* Genome Initiative. No information is available about the function(s) of G2723.

Experimental Observations

30 The complete sequence of G2723 was confirmed, and the function of the gene was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. 35S::G2723 plants did not show consistent alterations in their response to the physiological analyses that were performed.

With respect to the morphology and development of the transgenic plants, overexpression of
35 G2723 produced a moderate delay in the onset of flowering in *Arabidopsis* by up to approximately two weeks under continuous light conditions. The phenotype was apparent in eleven out of eighteen of the primary transformants and each of three T2 populations that were examined.

Utilities

The delayed flowering displayed by 35S::G2723 transformants indicates that the gene or its orthologs can be used to manipulate the flowering time of commercial species. In particular, an extension
5 of vegetative growth can significantly increase biomass and result in substantial yield increases

Given the effects of G2723 overexpression, it is likely that the activity of the gene or its orthologs can be modified to accelerate flowering or eliminate any requirement for vernalization.

G2741 (SEQ ID NO: 511)10 Published Information

G2741 was identified in the sequence of BAC F12A12, GenBank accession number AL133314, released by the *Arabidopsis* Genome Initiative. No functional information is available about G2741.

Experimental Observations

15 The function of G2741 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Five of the eighteen 35S::G2741 lines were significantly delayed in flowering and exhibited greater vegetative biomass than wild-type. No altered phenotypes were detected in any of the physiological assays.

It should be noted that G2741 is closely related to G1435, which also produced late flowering
20 plants when overexpressed.

Utilities

The delayed flowering displayed by 35S::G2741 transformants indicated that the gene or its
equivalogs might be used to manipulate the flowering time of commercial species. In particular, an
25 extension of vegetative growth can significantly increase biomass and result in substantial yield increases. Given the effects of G2741 overexpression, it is possible that the activity of the gene or its
equivalogs could be modified to accelerate flowering, or eliminate any requirement for vernalization.

G2754 (SEQ ID NO: 517)30 Published Information

The transcription regulator G2754 was identified by amino acid sequence similarity to proteins of the SWI/SNF family of chromatin remodeling factors. G2754 is found in the sequence of the chromosome 5, P1 clone MSN2 (GenBank accession number AC005936.1; nid=3702737), released by the *Arabidopsis* Genome Initiative. No additional public information related to the functional
35 characterization of G2754 is available.

Experimental Observations

The function of G2754 was analyzed through its ectopic overexpression in *Arabidopsis*; 35S::G2754 seedlings were slightly pale in coloration, displayed long hypocotyls, elongated petioles, and had leaves held in a more upright orientation. Many of the lines also flowered noticeably earlier than controls. Following the switch to flowering, the inflorescences from 35S::G2754 plants had a spindly appearance and exhibited somewhat increased internode elongation compared to wild type. The above effects were observed in ten out of eighteen of the primary transformants and each of three independent T2 lines.

10 Utilities

The phenotype of plants overexpressing G2754 indicated that the gene or its orthologs might be used to manipulate developmental processes regulated by light, such as shade avoidance. Eliminating shading responses could lead to increased planting densities with subsequent yield enhancement.

The gene or its orthologs might also be useful in modifying flowering time. In particular, G2754 could be applied to accelerate flowering or eliminate any requirements for vernalization.

G2763 (SEQ ID NO: 521)

Published Information

The sequence of G2763 was obtained from *Arabidopsis* genomic sequencing project, GenBank accession number AB026636, nid=4757392, based on its sequence similarity within the conserved domain to other bHLH related proteins in *Arabidopsis*.

Experimental Observations

The 5' and 3' ends of G2763 were experimentally determined by RACE. The full-length cDNA clone corresponding to G2763 was isolated in-house from the screening of *Arabidopsis* cDNA libraries.

The function of G2763 was assessed by analysis of transgenic *Arabidopsis* lines in which the cDNA was constitutively expressed from the 35S CaMV promoter. Overexpression of G2763 resulted in plants that displayed a mild delay in the onset of flowering, compared to wild-type controls. Additionally, a number of the plants were slightly small and appeared dark in coloration, particularly at later stages of development. In the physiological assays, G2763 overexpressors have a sugar sensing phenotype in a germination assay on media containing high glucose. The small seedling phenotype was confirmed in a repeat experiment on all three individual line. In addition, all three lines of G2763 were more sensitive to chilling stress in the chilling growth assay. Seedlings were small and in the case of line 5 had more anthocyanin accumulation.

The sugar sensing phenotype of G2763 overexpressing plants may be related to the late flowering phenotype. Sugars are central regulatory molecules that control several aspects of plant physiology, metabolism, and development, including flowering.

Utilities

The delayed flowering displayed by 35S::G2763 transformants indicates that the gene might be used to manipulate the flowering time of commercial species. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases.

G2763 might be used to generate crop plants with altered sugar sensing.

G2763 could also be used to generate crop plants enhanced resistance to chilling.

If the dark coloration of 35S::G2763 lines reflects an increase in biochemical composition, the gene might be used to improve the nutraceutical value of foodstuffs, or increase photosynthetic capacity to improve yield.

G2768 (SEQ ID NO: 525 and SEQ ID NO: 2118)

Published Information

The sequence of G2768 was obtained from the *Arabidopsis* genome sequencing project, GenBank accession number AB018117 (nid=3702735). It corresponds to At5g47430, annotated by the *Arabidopsis* Genome Initiative.

Experimental Observations

The function of G2768 was assessed by analysis of transgenic *Arabidopsis* lines in which the cDNA was constitutively expressed from the 35S CaMV promoter.

The G2768 clone within the overexpression construct (P15431; comprising SEQ ID NO: 2118) encodes a product that lacks 227 amino acids at the carboxy-terminus compared to the full-length wild-type protein. Thus, it is possible that the morphological phenotypes seen in plants transformed with P15431 represent dominant negative type effects.

Overexpression of G2768 produced dramatic changes in flower morphology; flowers from 35S::G2768 transformants were strikingly similar to those of mutants for the MADS-box gene, AGAMOUS (AG, Bowman et al. (1989) *Plant Cell* 1: 37-52; Bowman et al. (1991a) *Development* 112: 1-20; Yanofsky et al. (1990) *Nature* 346: 35-39; Coen and Meyerowitz (1991) *Nature* 353: 31-37).

In a typical 35S::G2768 flower, a general loss of determinate floral meristem growth was apparent, such that a new flower bud developed within, or in place of, the central carpels. This pattern was then reiterated and the fourth whorl of the secondary flower in turn gave rise to a tertiary flower bud and so on, resulting in a chain of flowers, each emerging from the center of the previous one. The phenotype was observed to varying extents, and in the most severe cases, a central carpel was converted completely into a new flower bud. In other instances, however, the conversion was incomplete; fourth whorl organs developed as a contorted pair of carpel-like structures, which when dissected open, were seen to contain the vestigial floral organs of a secondary flower. Additionally, stamen development was

compromised, and in the severest cases, six petals developed in place of stamens in the third whorls. As a result of these changes, 35S::G2768 flowers were infertile and failed to yield seed.

The features described above are identical to those displayed by AG mutants, indicating that G2768 might interact with AG during the development of wild type flowers. In particular, AG is specifically expressed in the third and fourth whorls of developing flowers, where it specifies stamen and carpel identity respectively, and prevents indeterminate growth of the floral meristem (Bowman et al. (1991b) *Plant Cell* 3: 749-758; Drews et al. (1991) *Cell* 65: 991-1002). Thus, in wild-type plants, G2768 might have a role in preventing AG expression in first and second floral whorls.

Additionally, G2768 overexpression produced changes in leaf shape, such that those organs became larger and flatter than in wild type.

Utilities

Based on the effects of G2768 overexpression, the gene or its equivalents could be used to manipulate flower structure and development. A wide range of applications could be envisaged, including the following:

- (1) production of larger showier flowers for the ornamental market;
- (2) the gene or its equivalents might be used to engineer sterility in trees and grasses to prevent escape of pollen from genetically engineered plants;
- (3) the sterility of the 35S::G2768 flowers, and failure of seed set, delays senescence, which would increase duration of the flowering period in ornamentals;
- (4) the gene or its equivalents could be applied to artichokes to eliminate the choke;
- (5) the gene or its equivalents could be applied to roses; increased numbers of petals might be of interest to the rose oil industry.

Given the increase in leaf size observed in 35S::G2768 lines, the gene or its equivalents may also be applied to increase biomass and yield in crop plants.

G2771 (SEQ ID NO: 527 and SEQ ID NO: 2119)

Published Information

G2771 corresponds to gene AT4G28810, annotated by the *Arabidopsis* Genome Initiative. No information is available about the function(s) of G2771.

Experimental Observations

The function of G2771 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G2771 produced striking alterations in leaf morphology and a marked delay in the onset of flowering. The leaves of 35S::G2771 lines were noticeably narrower, darker, and more curled than were those of controls, particularly at late stages. At early stages, plants grown on plates were observed to show long hypocotyls and were rather pale in

coloration, indicating that G2771 might influence light-regulated development. These lines also showed reduced accumulation of anthocyanins when subjected to a chilling growth assays.

It should be noted that the G2771 overexpression construct, contained a truncated clone of the gene (SEQ ID NO: 2119); the above phenotypes might therefore represent dominant negative effects.

5

Utilities

Based on the morphological effects of overexpression, G2771 or its equivalents might be used to manipulate leaf shape. In particular, this could be used to create novel forms for the ornamental plant market. This effect might also have other commercial applications. Increased leaf size, or an extended period of leaf growth, could increase photosynthetic capacity, and biomass, and have a positive effect on yield. The dark coloration observed in 35S::G2771 transformants point towards a number of utilities. Consumption of dark green leafy vegetables has been shown in clinical studies to reduce the risk of ARMD.

Additionally, the delayed flowering displayed by 35S::G2771 transformants indicated that the gene or its equivalents might be used to manipulate the flowering time of commercial species. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases.

G2771 or its equivalents could also have a role in modulating developmental processes regulated by light, such as shade avoidance. Eliminating shading responses could allow for increased planting densities with subsequent yield enhancement.

G2771 or its equivalents might also be used to generate crop plants that have better growth under cold conditions. The growth of many crops is very sensitive to cool temperatures. A gene that enhances growth under chilling conditions could result in enhanced yields.

25 G2776 (SEQ ID NO: 529)

Published Information

The sequence of G2776 was obtained from the *Arabidopsis* genome sequencing project, GenBank accession number AL161592, nid=7270751, based on its sequence similarity within the conserved domain to other bHLH related proteins in *Arabidopsis*.

30

Experimental Observations

The function of G2776 was assessed by analysis of transgenic *Arabidopsis* lines in which the cDNA was constitutively expressed from the 35S CaMV promoter. G2776 overexpressors have a sugar sensing or osmotic tolerant phenotype in a germination assay on media containing high sucrose.

Seedlings of 35S::G2776 transgenic lines were larger with green cotyledons compared with wild-type seedlings grown on sucrose. The result could indicate that G2776 may be involved in sugar sensing and/or osmotic stress tolerance.

Utilities

The sugar sensing phenotype of G2776 indicates that this gene may be useful for altering source-sink relationships or other sugar regulated processes.

5 If the phenotype of 35S::G2776 seedlings on sucrose plates reflects a general resistance to osmotic stress conditions, the gene might be used to engineer plants that are more resilient to abiotic stresses such as drought, salt and/or freezing.

G2784 (SEQ ID NO: 537 and SEQ ID NO: 2120)

Published Information

10 G2784 corresponds to gene AT5G57770, annotated by the *Arabidopsis* Genome Initiative.

Experimental Observations

The 5' and 3' ends of G2784 were determined by RACE. The function of G2784 was analyzed using transgenic plants in which G2784 was expressed under the control of the 35S promoter.

15 Overexpression of G2784 (SEQ ID NO: 2120) produced marked changes in overall plant architecture. 35S::G2784 transformants, were small, slow developing and exhibited curled dark leaves. Additionally, plants from two of the T2 lines exhibited abnormal inflorescence morphology and produced secondary shoots that grew downwards.

20 35S::G2784 lines showed more tolerance to cold stress in a germination assay. When the assay was repeated on individual lines, all three lines showed enhanced seedling vigor when germinated under cold conditions.

Utilities

25 G2784 or its equivalents could be used to engineer enhanced cold germination in plants. The germination of many crops is very sensitive to cold temperatures. A gene that would enhance germination and seedling vigor in the cold would have tremendous utility in allowing seeds to be planted earlier in the season with a higher survival rate.

The morphological changes exhibited by 35S::G2784 plants indicated that the gene or its equivalents might be used to manipulate plant architecture. In particular, G2784 could be applied to produce novel leaf and shoot morphologies for the ornamental markets.

30 Additionally, if the altered coloration of 35S::G2784 plants reflects a change in biochemical composition, the gene or its equivalents may be used to improve the nutraceutical value of foodstuffs, or increase photosynthetic capacity to improve yield.

G2826 (SEQ ID NO: 545)

Published Information

35 G2826 (At1g68360) is in BAC T22E19 (GenBank accession number AC016447) and was identified based on its sequence similarity within the conserved domain to other zinc finger C2H2-related proteins in *Arabidopsis*. There is no published or public information about the function of G2826.

Experimental Observations

The function of G2826 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Few primary transformants were produced, indicating that the gene can be lethal when overexpressed at high levels. Overexpression of G2826 resulted in plants that were small and slow developing. Some individuals developed aerial rosettes at cophorescence nodes, indicating a disruption in phase change in the inflorescence. Flowers were also small and had defects in organ formation, pollen production, and yielded few seeds. Strikingly, flowers also displayed increased trichome density on sepals and often possessed ectopic trichomes on the carpels. On dissecting the carpels, trichome-like structures developing from the internal walls were also apparent. Some plants also had floral organs converted towards a bract-like identity. The changes in morphology produced by overexpression of this gene is indicative of heterochronic shifts (i.e., cells in various lineages and tissues adopt fates that are normally associated with cells from other developmental stages). For example, trichomes are normally associated with vegetative rather than reproductive organs. Additionally, aerial rosettes occur when a secondary inflorescence meristem develops in a manner comparable to a primary shoot meristem during the vegetative phase of growth.

Utilities

The morphological effects of G2826 overexpression indicate a number of potential applications relating to increasing or changing trichome density: Thus, the use of G2826 and its homologs to increase trichome density, size or type may therefore have profound utilities in so called molecular farming practices and increasing the yield of cotton fibers.

If the effects on trichome patterning and/or aerial rosette formation reflect a general change in heterochronic processes, G2826 or other clade members might be used to modify the way meristems and/or cells develop during different phases of the plant life cycle. In particular, altering the timing of phase changes could afford positive effects on yield and biomass production.

G2830 (SEQ ID NO: 547)

Published Information

G2830 (At5g42640) was identified in the sequence of P1 clone MFO20, GenBank accession number AB013391, released by the *Arabidopsis* Genome Initiative. There is no published or public information about the function of G2830.

Experimental Observations

G2830 is expressed at a low level in embryos and siliques as determined by RT-PCR analysis. Expression of G2830 was not detected in other tissues. Previously, a line homozygous for a T-DNA

insertion in G2830 was used to determine the function of this gene. G2830 mutant plants showed an increase in seed oil content.

The phenotype of 35S::G2830 lines has now been analyzed. No consistent effects on *Arabidopsis* growth and development were found in morphological assays. However, a proportion of plants from a single 35S::G2830 T2 line performed better than wild-type plants when germinated on media with low nitrogen supplemented with sucrose or with sucrose plus glutamine.

Utilities

G2830 or its equivalents may be used to increase seed oil content of plants, which may be used to improve seed oil yield or increase the caloric content of foods.

Because expression of G2830 is embryo and silique specific, its promoter could be useful for targeted gene expression in these tissues. That fact that 35S::G2830 transformants produced less anthocyanin on high sucrose plus glutamine indicated that G2830 might be used to modify carbon and nitrogen status, and hence assimilate partitioning.

G2838 (SEQ ID NO: 555)

Published Information

G2838 was identified in the sequence of BAC F15M7, GenBank accession number AP002543, released by the *Arabidopsis* Genome Initiative. There is no other published or public information about the function of G2838.

Experimental Observations

The 5' and 3' ends of G2838 were determined by RACE PCR. The complete sequence of G2838 was determined. The function of G2838 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Many of the 35S::G2838 seedling transformants had large cotyledons compared to control plants. As plants matured, many lines became rather dark in coloration, showed a delay in the onset of flowering, and an increase in vegetative characteristics in the inflorescence. In some instances, aerial rosettes were seen at cophorescence nodes, and in other cases flowers had shoot like characteristics. Sepals from some flowers had a bract-like appearance and an increase in trichome density. Many lines showed non-specific flower abnormalities; floral organs were often small and contorted and pollen production was poor. As a result, seed yield from many of the lines was rather poor.

Utilities

The morphological effects of G2838 overexpression indicate a number of applications relating to increasing or changing trichome density by modification of the expression of this transcription factor or

its equivalents. Thus, the use of G2838 and its homologs to increase trichome density, size or type may therefore have profound utilities in so-called molecular farming practices and increasing the yield of cotton fibers. Since the mallow family is closely related to the Brassica family in which *Arabidopsis* is located, genes involved in trichome formation are likely to have homologs that function in cotton.

5 If the effects on trichome patterning and/or aerial rosette formation reflect a general change in heterochronic processes, G2838 or other clade members, might be used to modify the way meristems and/or cells develop during different phases of the plant life cycle, or manipulate flowering time. In particular, altering the timing of phase changes could afford positive effects on yield and biomass production. The enlarged size of 35S::G2838 seedlings might also be interpreted as a heterochronic shift, and indicated that the gene might be applied to crops in order to expedite ground coverage.

10 The dark coloration of 35S::G2838 lines might reflect a change in biochemical composition or chlorophyll content. Thus, the gene might be applied to improve the nutraceutical value of foodstuffs, or increase photosynthetic capacity in crop plants, to improve yield.

15 G2839 (SEQ ID NO: 557)

Published Information

G2839 (At3g46080) was identified in the sequence of BAC F12M12 (GenBank accession number AL355775) based on its sequence similarity within the conserved domain to other C2H2 related proteins in *Arabidopsis*. There is no published or public information about the function of G2839.

20 Experimental Observations

The function of G2839 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Few primary transformants were generated. This indicates that G2839 overexpression can be lethal. T1 lines displayed stunted growth and development, and yielded very few or zero seeds. Inflorescences were poorly developed. In one line, flower pedicels were very short and flowers and siliques were oriented downwards. G2839 overexpressors showed a phenotype in a germination assay on media containing high sucrose: seedlings were green and had high germination rates. Thus, the gene appeared to influence sugar sensing and/or osmotic stress responses.

25 G2839 is closely related to G354 and G353. Flower phenotypes in which pedicels were very short and flowers and siliques were oriented downwards have been described for G353 and G354 and are also similar to the brevipedicellus mutant (Koornneef et al. (1983) *J. Heredity* 1983; 74: 265-272; Venglat et al. (2002) *Proc. Natl Acad Sci U S A.* 99:4730-4735; Douglas et al. (2002) *Plant Cell* 14:547-558. Interestingly 35S::G353 lines also showed increased resistance to osmotic stress.

Utilities

35 The phenotypes observed in physiology assays indicate that G2839 might be used to generate crop plants with altered sugar sensing. If the physiological phenotype is related to osmotic stress, the gene could be used to engineer cold and dehydration tolerance.

The morphological phenotype shown by 35S::G2839 lines indicate that the gene might be used to alter inflorescence architecture. In particular, a reduction in pedicel length and a change in the position at which flowers and fruits are held, might influence harvesting or pollination efficiency. Additionally, such changes might produce attractive novel forms for the ornamental markets.

5

G2854 (SEQ ID NO: 567)Published Information

The sequence of G2854 was obtained from the *Arabidopsis* genome sequencing project, GenBank accession number AL161566, nid=7269538, based on its sequence similarity within the conserved domain to other ACBF-like related proteins in *Arabidopsis*.

10

Experimental Observations

The 5' and 3' ends of G2854 were determined by RACE. The function of G2854 was analyzed using transgenic plants in which G2854 was expressed under the control of the 35S promoter.

35S::G2854 transformants showed increased germination efficiency on sucrose plates compared to wild-type controls.

15

Utilities

G2854 may be used to generate crop plants with altered sugar sensing.

20

G2859 (SEQ ID NO: 569)Published Information

G2859 corresponds to gene AT1G73830, annotated by the *Arabidopsis* Genome Initiative. No information is available about the function(s) of G2859.

25

Experimental Observations

The function of G2859 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. 35S:: G2859 transgenic plants produced marked changes in *Arabidopsis* seedling morphology, coloration, leaf shape, and inflorescence development. 35S::G2859 transformants appeared pale in coloration during all phases of the life cycle. At early stages, the seedlings displayed rather long hypocotyls and long oval shaped cotyledons. Such a phenotype could indicate that G2859 was influencing light regulated developmental programs. Later, the plants formed leaves were rather flat and had mild serrations on the margins. Following the switch to reproductive growth, 35S::G2859 inflorescences became increasingly proliferated and bushy as the plants aged, exhibited very thin stems, long narrow curled cauline leaves, and carried flowers that were rather small and had poorly developed organs.

30

35

G2859 overexpressing lines behaved similarly to the wild-type controls in all physiological assays performed.

Utilities

5 Based on the effects of G2859 overexpression, the gene or its orthologs could be used to modify light-regulated developmental processes such as shade avoidance. Additionally, G2859 could be used to manipulate inflorescence architecture and generate plants with a denser bushier shoot structure.

G2885 (SEQ ID NO: 579)

10 Published Information

G2885 was identified in the sequence of genomic clone K21L19.7, GenBank accession number AB024029, released by the *Arabidopsis* Genome Initiative. It is a member of the response regulator class of GARP proteins, and was recently named ARR18 (Hwang et al. (2002) *Plant Physiol.* 129: 500-515). No functional information is available about G2885.

15

Experimental Observations

The function of G2885 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G2885 produced highly pleiotropic effects on *Arabidopsis* development, including alterations in meristem initiation and growth, cell differentiation, leaf shape, flower morphology, overall plant size, and rate of senescence. Most strikingly, two T2 lines showed secondary rosettes of leaves developing from the adaxial surface of cotyledons. This phenotype was identical to that seen with overexpression of a truncated ARR1 (G1493) protein lacking its response regulator domain. Callus-like outgrowths were also noted on the stems of two T1 plants, consistent with the observation of disordered cell proliferation in the plants overexpressing a truncated ARR1 (Sakai et al. (2001) *Science* 294: 1519-1521). ARR1 is known to function in cytokinin signal transduction, and G2885 is therefore also likely to function in cytokinin response. G2885 may be a stronger activator than ARR1, since the ectopic rosettes did not appear in plants expressing an intact ARR1 protein (Sakai et al. (2001) *supra*; G1493). In physiology assays, 35S::G2885 lines were more sensitive to cold conditions than wild-type plants, indicating that the gene can influence the response to abiotic stress.

30

Utilities

The overexpression phenotypes of G2885 indicated that the gene regulates meristem activity and stem cell identity. As such, the gene or its orthologs could have applications in cell cultures lines, or in transformation or micro-propagation systems, where regeneration of shoots from callus is currently problematic.

35

Based on the increased sensitivity to cold exhibited by the 35S::G2885 lines, this gene or its orthologs could be used to engineer cold tolerance. The germination of many crops is very sensitive to cold temperatures. A gene that altered sensitivity to cold would have utility in understanding the sensory transduction pathway for the regulation of growth and development by temperature. Understanding how plants respond to temperature could lead to plants with enhanced germination and seedling vigor in the cold and have utility in allowing seeds to be planted earlier in the growing season with a higher survival rate.

G2907 (SEQ ID NO: 587 and SEQ ID NO: 2122)

10 Published Information

G2907 has been described as AtSR1 (*Arabidopsis thaliana* Signal-Responsive genes; Yang and Poovaiah (2002) *J. Biol. Chem.* 277: 45049-45058). The authors have shown that the protein contains a functional calmodulin-binding domain in addition to the DNA binding domain. AtSR1 specifically recognizes a novel 6-bp motif (CGCC box). Expression analysis indicates that AtSR1 transcript levels increase in response to different signals and stresses such as ethylene, methyl jasmonate, hydrogen peroxide, heat, cold, UV light and sodium chloride (Yang and Poovaiah (2002) *supra*). G2907 also corresponds to sequence 2286 from patent publication WO0216655 A2 (2001) on stress-regulated genes, transgenic plants and methods of use. No functional characterization in planta has been published so far.

20 Experimental Observations

The function of G2907 was analyzed using transgenic plants in which a cDNA clone of the gene was expressed under the control of the 35S promoter. Overexpression of G2907 (SEQ ID NO: 2122) markedly accelerated the onset of leaf senescence in *Arabidopsis*. This phenotype was apparent in three independent 35S::G2907 T2 lines, and was confirmed when the lines were re-grown for a second time. For unknown reasons, however, the phenotype was not noted in the T1 generation.

35S::G2907 plants were indistinguishable from wild-type controls in all physiology assays performed.

Utilities

30 G2907 or its equivalents may have utility in altering senescence-related processes. Although leaf senescence is thought to be an evolutionary adaptation to recycle nutrients, the ability to control senescence in an agricultural setting may have value. For example, a delay in leaf senescence in some maize hybrids is associated with a significant increase in yields and a delay of a few days in the senescence of soybean plants can have a large impact on yield as well. Delayed flower senescence may also generate plants that retain their blossoms longer, this could impact yield and may be of potential interest to the ornamental horticulture industry.

G2913 (SEQ ID NO: 589)Published Information

G2913 (Atlg76110) was identified as part of the BAC clone T23E18 (GenBank accession AC009978).

5

Experimental Observations

The function of G2913 was analyzed using transgenic plants in which a cDNA clone of the gene was expressed under the control of the 35S promoter. In an assay intended to determine whether the transgene expression could alter carbon and nitrogen sensing, 35S::G2913 seedlings contained less anthocyanins (and in some cases were larger) than wild-type controls grown on high sucrose/N- plates. The transgenic seedlings were also greener on high sucrose/N-/Gln plates.

10

Utilities

The enhanced performance of G2913 overexpression lines under low nitrogen conditions indicated that the gene or its orthologs can be used to engineer crops that could thrive under conditions of reduced nitrogen availability.

15

G2930 (SEQ ID NO: 591)Published Information

The sequence of G2930 was obtained from the *Arabidopsis* genome sequencing project, GenBank accession number AC016972, nid=6714311, based on its sequence similarity within the conserved domain to other bHLH related proteins in *Arabidopsis*.

20

Experimental Observations

The complete sequence of G2930 was determined experimentally. The function of G2930 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G2930 resulted in plants that were more tolerant to chilling stress in a growth assay compared to control plants. However, overexpression of G2930 produced no consistent effects on *Arabidopsis* morphology.

25

Utilities

G2930 could be used to generate crop plants that are more tolerant to chilling stress.

30

G2933 (SEQ ID NO: 593)Published Information

The sequence of G2933 was obtained from *Arabidopsis* genomic sequencing project, GenBank accession number AL138655, nid=6899905, based on its sequence similarity within the conserved domain to other bHLH related proteins in *Arabidopsis*.

35

Experimental Observations

The function of G2933 was assessed by analysis of transgenic *Arabidopsis* lines in which the cDNA was constitutively expressed from the 35S CaMV promoter. A small number of G2933 overexpression lines produced larger seeds than wild-type controls. The result indicates that G2933 is involved in the regulation of sink-source relationship in plants. In addition, seedlings of 35S::G2933 transgenic lines showed more tolerance to chilling stress in a growth assay. When the assay was repeated on individual lines, all three lines analyzed showed the phenotype.

Utilities

G2933 might be used to modify sink-source relationship and thereby enhance seed yield.

This gene could also be used to generate crop plants that have better growth under cold conditions. The growth of many crops is very sensitive to cool temperatures. A gene that enhances growth under chilling conditions could result in enhanced yields.

G2969 (SEQ ID NO: 603)

Published Information

G2969 (At2g29660) was identified in the sequence of *Arabidopsis thaliana* chromosome 2 clone T27A16 (GenBank accession number AC005496) based on its sequence similarity within the conserved domain to other C2H2 related proteins in *Arabidopsis*. There is no published or public information about the function of G2969.

Experimental Observations

The function of G2969 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. G2969 overexpressing lines showed increased tolerance to sucrose and ABA in germination assays. The ABA and sucrose insensitivity indicates that the effect of overexpressing G2969 might cause tolerance to osmotic stress. 35S::G2969 plants were wild type in morphological analyses that were performed.

Utilities

G2969 appears to affect ABA sensitivity. ABA is one of key signal molecules in the stress response pathways. Therefore, G2969 may have a utility in modifying ABA responses such as seed dormancy, seed development, and cold and drought tolerances.

G2969 might also be used to generate crop plants with altered sugar sensing.

G2972 (SEQ ID NO: 605)

Published Information

G2972 (At3g29340) was identified in the sequence of P1 clone MUO10 (GenBank accession number AP001309) based on its sequence similarity within the conserved domain to other C2H2 related proteins in *Arabidopsis*. There is no published or public information about G2972.

Experimental Observations

The function of G2972 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. G2972 overexpressing lines showed more tolerance to growth under low phosphate conditions. 35S::G2972 plants were wild type in morphological analyses that were performed.

Utilities

The response of 35S::G2972 seedlings to low phosphate conditions indicates that the gene could be used to manipulate nutrient uptake, or the ability to grow in poor nutrient soils.

G2979 (SEQ ID NO: 607)

Published Information

The transcription factor G2979 was identified by amino acid sequence similarity to the mammalian E2F proteins. It has been referenced in the public literature both as E2L2 and E2Ff (Kosugi and Ohashi, (2002) *J. Biol. Chem.* 277: 16553-16558; Mariconti et al. (2002) *J. Biol. Chem.* 277: 9911-9919). G2979 is found in the sequence of the chromosome 3 BAC T22N4 (AC010676.6 GI:1240872), released by the *Arabidopsis* Genome Initiative. The G2979 product is thought to function as a repressor and be involved in restricting cell proliferation (Kosugi and Ohashi (2002) *supra*).

Experimental Observations

The function of G2979 was analyzed through its overexpression in *Arabidopsis*; 35S::G2979 lines displayed a mild delay in the onset of flowering, a marked increase in vegetative biomass, and increases in floral organ number. It seems more likely that increased floral organ number and leaf size are related effects, and could both be due to a change in meristem activity, such as increased numbers of cells being allocated to organ primordia, or such cells going through additional rounds of cell division.

Utilities

Based on the substantially increased size of 35S::G2979 organs, the gene or its equivalents could be used to increase plant biomass, thus improving yield. The increased flower size seen in such plants indicated that G2979 or its equivalents could be applied to produce desirable flower and fruit traits.

Additionally, the slight delay in flowering observed in some of the 35S::G2979 lines indicated that the gene or its equivalents might be used to manipulate the timing of reproductive growth. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases. Conversely, it is possible that the activity of G2979 or its equivalents could be modified to accelerate flowering, or eliminate any requirement for vernalization.

G2981 (SEQ ID NO: 609)Published Information

G2981 is similar in its amino acid sequence to the mammalian DP2a, a dimerization partner to E2F required for the progression and arrest of the cell cycle in animals and plants. G2981 is in chromosome 5, BAC clone F12E4 (GenBank accession AL162751.1 GI:7378607), released by the *Arabidopsis* Genome Initiative. No public information related to the functional characterization of G2981 is available.

Experimental Observations

The boundaries of G2981 were determined by RACE (Rapid Amplification of cDNA Ends; a PCR-based method that facilitates the cloning of full-length cDNA sequences when a partial cDNA sequence is known) and its function was analyzed through overexpression in *Arabidopsis*. 35S::G2981 seedlings were larger and appeared to have less anthocyanin on plates that were nitrogen deficient, but which were supplemented with glutamine and high sucrose levels. This assay monitors the effect of carbon on nitrogen signaling through anthocyanin production.

Utilities

The enhanced performance of G2981 overexpression lines under low nitrogen conditions indicate that the gene could be used to engineer crops that could thrive under conditions of reduced nitrogen availability.

That 35S::G2981 lines make less anthocyanin on high sucrose plus glutamine, indicates G2981 might be used to modify carbon and nitrogen status, and hence assimilate partitioning.

G2982 (SEQ ID NO: 611)Published Information

G2982 is found in the sequence of the chromosome 5, BAC clone T22P11 (GenBank accession AL162971.1 GI:7413630), released by the *Arabidopsis* Genome Initiative. The gene appears to have a role in cell cycle control (Magyar et al. (2000) *FEBS Lett.* 486:79-87) and its sequence has recently been included in patent publication WO0185946 A2.

Experimental Observations

The function of G2982 was analyzed through overexpression of a genomic clone in *Arabidopsis*. 35S::G2982 transformants displayed increased tolerance to dehydration stress. In all other respects, these transgenic lines appeared wild type.

In a soil based drought assay, G2982 overexpressing *Arabidopsis* plants were significantly greener and larger than wild-type control plants.

Utilities

The response of 35S::G2982 plants to dehydration stress indicated that G2982 or its equivalents could be used to improve plant tolerance to cold, freezing, drought, and salt conditions.

5 **G2983 (SEQ ID NO: 613)**

Published Information

G2983 was initially identified within a sequence released by the *Arabidopsis* genome initiative (gene F2G19.11 within BAC clone F2G19, Chromosome 1, GenBank accession, AC083835), as a gene encoding a novel WUSCHEL-like homeodomain protein. No data are available regarding the function of
10 this locus.

Experimental Observations

The boundaries of G2983 were initially determined by RACE experiments, and transgenic lines were generated in which the gene was overexpressed from a 35S promoter. These plants displayed some
15 striking alterations in morphology compared to wild type. 35S::G2983 lines exhibited a spectrum of developmental changes including alterations in leaf shape, phyllotaxy, coloration, growth rate, floral organ abnormalities, and a reduction in overall size. However, the most prominent phenotype was seen in the inflorescence, where strange growths developed from stems, pedicels and floral organs. In some cases, such outgrowths showed stigmatic tissue or took on a trichome-like identity.

20 Similar results from overexpression of a related gene, WUSCHEL had previously been obtained, in which the latter gene was found to induce the formation of callus like outgrowths. WUSCHEL has a key role in the maintenance of stem cell identity within apical meristems, and during the reproductive phase, participates in a feedback loop with the AGAMOUS gene, which induces floral meristems to terminally differentiate into carpels (Mayer et al. (1998) *Cell* 95: 805-815; Schoof et al (2000) *Cell* 100:
25 635-644; Lohmann et al. (2001) *Cell* 105: 793-803). The similarity between the WUS and G2983 overexpression phenotypes indicated that the genes might have similar roles in regulating apical meristem activity. Two other WUS-like genes, G1539 and G1591, have also yielded similar effects on the inflorescence to G2983.

An additional, potentially related phenotype was observed in the roots of 35S::G2983 lines in
30 physiology experiments. During assays which involved the monitoring of root growth on vertical plates, following inversion of plates, it was noted that 35S::G2983 roots displayed an abnormal gravitropic response; rather than growing downwards, the roots grew in a spiral pattern, and appeared to proliferate and generate an increased number of root hairs.

35

Utilities

The overexpression phenotypes of G2983 indicated that this transcription factor or its orthologs might be used to regulate meristem activity and stem cell identity. As such, the gene could have applications in the plant cell culture lines, or in transformation or micro-propagation systems, where generation of callus is currently problematic but is required as part of the procedure. Additionally, the effects on root morphology seen in 35S::G2983 plants, indicated that the gene might be used to manipulate root hair development and thereby enhance the ability of crops to survive abiotic stresses such as drought. Finally, the alterations in trichome development seen in occasional lines indicated that the gene could be used to manipulate the formation of those structures.

Given its potential capacity to trigger ectopic carpel development in *Arabidopsis*, G2983 or its orthologs can be applied to commercial species to induce formation of increased numbers of carpels or fruits. A particular application might exist in saffron, one of the world's most expensive spices. Saffron filaments, or threads, are actually the dried stigmas of the saffron flower, *Crocus Sativus* Linnaeus. Each flower contains only three stigmas, and more than 75,000 of these flowers are needed to produce just one pound of saffron filaments. A gene such as G2983, which increased carpel numbers, could therefore substantially increase yield.

G2990 (SEQ ID NO: 615)Published Information

G2990 corresponds to gene MKM21.8 within P1 clone MKM21 (GenBank accession AB016876) derived from chromosome 5. We identified this locus as a novel member of the ZF-HB family and no data regarding its function are currently in the public domain (as of 8/5/02).

Experimental Observations

The boundaries of G2990 were identified by RACE experiments performed and a full-length clone was then PCR-amplified from cDNA derived from mixed tissue samples. Full-length cDNA sequences for this gene have recently been deposited in GenBank (Accessions AY091034 and AY117347), and the coding sequences are identical to that identified by us.

The function of G2990 was assessed by analysis of transgenic *Arabidopsis* lines in which the cDNA was constitutively expressed from a 35S CaMV promoter. Under normal growth circumstances, 35S::G2990 transformants displayed wild-type morphology. However, two of three independent T2 populations showed an altered response to nitrogen deprivation in plate-based assays, indicating that the gene might be involved in the response to conditions of nutrient limitation.

Utilities

The data from physiological assays, revealing that G2990 can influence the response to nitrogen deprivation, indicate that the gene might have utility in engineering commercial species that can be successfully cultivated in low nitrogen soils or growth media.

G2992 (SEQ ID NO: 617)Published Information

G2992 corresponds to gene F24J1.29 within BAC clone F24J1 (GenBank accession AC021046) derived from chromosome 1. No data regarding its function are currently in the public domain.

5 Experimental Observations

This locus was identified as a member of the ZF-HB family. The boundaries of G2992 were determined by RACE, and a clone was PCR-amplified from cDNA derived from mixed tissue samples. The function of G2992 was then assessed by analysis of transgenic *Arabidopsis* lines in which the cDNA was constitutively expressed from a 35S CaMV promoter. 35S::G2992 T2 populations displayed an enhanced ability to germinate on plates containing high levels of sodium chloride, and on plates containing high levels of ABA. Thus, G2992 can function as part of response pathway to abiotic stress. 35S::G2992 seedlings were also noted to be rather pale in coloration, and appeared more sensitive than wild type to conditions of nitrogen deprivation. Furthermore, 35S::G2992 seedlings also showed altered root morphology; fewer lateral roots were present. Additionally, morphological studies revealed that overexpression of G2992 can accelerate the onset of reproductive development, reduce plant size, and produce changes in leaf shape.

Utilities

Based on the phenotypes observed in morphological and physiological assays, G2992 might be have a number of applications.

20 Given the salt resistance and ABA insensitivity exhibited by 35S::G2992 transformants, the gene might be used to engineer salt tolerant crops and trees that can flourish in salinified soils, or under drought conditions.

G2992 appears to affect ABA sensitivity; therefore the gene may have a utility in modifying ABA responses such as seed development and dormancy, as well as cold and dehydration tolerance.

25 The data from physiological assays, revealing that G2992 can influence the response to nitrogen deprivation, indicate that the gene might have utility in engineering commercial species that can be successfully cultivated in low nitrogen soils or growth media.

The early flowering exhibited by 35S::G2992 lines, indicates that the gene might be used to manipulate flowering time in commercial species. In particular, G2992 could be applied to accelerate flowering or eliminate any requirements for vernalization.

30 Finally, the effects of G2992 overexpression on leaf shape indicate that the gene might be used to modify plant architecture.

G2996 (SEQ ID NO: 621)35 Published Information

No data regarding the function of this gene are presently known or available.

Experimental Observations.

This locus was identified as a novel member of the ZF-HB family. The boundaries of G2996 were identified from partial EST sequences in the public databases and were confirmed by RACE experiments. A full-length clone was then PCR-amplified from cDNA derived from mixed tissue samples. The function of G2996 was assessed by analysis of transgenic *Arabidopsis* lines in which the cDNA was constitutively expressed from a 35S CaMV promoter. Under normal growth conditions, 35S::G2996 transformants displayed wild-type morphology. However, each of three independent T2 populations showed increased sensitivity to mannitol in plate-based root growth inhibition assays, indicating that G2996 can influence osmotic stress responses.

Utilities

The data from physiological assays, revealing that G2996 can influence osmotic stress responses, indicate that the gene might have utility in engineering commercial species that have increased survivability and yield under adverse osmotic conditions.

G2998 (SEQ ID NO: 623)Published Information

The gene is a member of the ZF-HB family. No data have been presented publicly regarding the function of this gene.

Experimental Observations

The boundaries of G2998 were determined by RACE, and a clone was PCR-amplified from cDNA derived from mixed tissue samples. A full-length cDNA sequence has recently been deposited in GenBank (Accession AY084462), and its coding sequence is identical that identified by us. The function of G2998 was assessed by analysis of transgenic *Arabidopsis* lines in which the cDNA was constitutively expressed from a 35S CaMV promoter. All three of the 35S::G2998 T2 populations analyzed, displayed an enhanced ability to germinate on plates containing high levels of sodium chloride. Thus, G2998 can function as part of response pathway to abiotic stress. Additionally, morphological studies revealed that overexpression of G2998 can produce a delay in the onset of reproductive development, indicating that the gene can have a role in determining flowering time in *Arabidopsis*.

Utilities

Based on the increased salt tolerance exhibited by the 35S::G2998 lines in physiology assays, this gene might be used to engineer salt tolerant crops and trees that can flourish in salinified soils, or under drought conditions.

The delayed flowering displayed by 35S::G2998 transformants indicates that the gene might be used to manipulate the flowering time of commercial species. In particular, an extension of vegetative growth can significantly increase biomass and result in substantial yield increases.

Given the effects of G2998 overexpression, it is likely that the activity of the gene (or its orthologs) could be modified to accelerate flowering, or eliminate any requirement for vernalization.

G2999 (SEQ ID NO: 625)

Published Information

G2999 was identified within a sequence released by the *Arabidopsis* Genome Initiative (Chromosome 2, GenBank accession AC006439).

Experimental Observations

The boundaries of G2999 were determined by RACE experiments and a full-length clone was PCR-amplified out of cDNA derived from mixed tissues. The function of G2999 was then assessed by analysis of transgenic *Arabidopsis* lines in which the cDNA was constitutively expressed from a 35S CaMV promoter. 35S::G2999 transformants displayed wild-type morphology, but two of three T2 lines showed increased tolerance to salt stress in the physiology assays. Root growth assays with G2999 overexpressing seedlings and controls in a high sodium chloride medium showed that a majority of 35S::G2999 *Arabidopsis* seedlings appeared larger, greener, and had more root growth than the control seedlings on the right (Figure 8C, four control seedling are on the right). G2998, a paralogous *Arabidopsis* sequence, also showed a salt phenotype and performed similarly in the plate-based salt stress assay (Figure 8B). Thus, G2998 and G2999 could act in the same pathways, and have a role in the response to abiotic stress.

Utilities

Given the salt resistance exhibited by 35S::G2999 transformants, the gene might be used to engineer salt tolerant crops and trees that can flourish in saline soils, or under drought conditions.

G3070 (SEQ ID NO: 653)

Published Information

G3070 was identified in the sequence of BAC T23J18, GenBank accession number AC011661, released by the *Arabidopsis* Genome Initiative. There is no other published or public information about the function of G3070.

Experimental Observations

The 5' end of G3070 was determined by RACE PCR. The function of G3070 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. 35S::G3070

transformants had leaves with distinctive steely gray coloration at all stages of the life cycle. In all other respects, however, the plants appeared morphologically normal. This dramatic change in leaf color might have arisen from a variety of possible causes, including a change in the level of pigments, alterations in wax accumulation/composition at the leaf surface, or by a change in the histology of the leaves.

- 5 Alterations in cell shape or changes in the adhesion of epidermis to underlying cell layers have been found to result in coloration changes (Cornish and Zeevart (1986) *Plant Physiol* 81: 1017-1021; Glover et al. (1998) *Development* 125: 3497-3508; Heys et al. (1997) *Planta* 202: 85-92). There was no consistent difference in physiological assays between 35S::G3070 transformants and wild-type seedlings.

10 Utilities

Depending on the basis of the color change seen in 35S::G3070 lines, a number of applications could be envisaged.

If the phenotype is due to loosening of epidermal cell layers, the gene or its equivalents might be used to produce fruits, vegetables, and other plant products, which can be more easily peeled.

- 15 If the effects are due to changes in wax composition and/or accumulation, G3070 or its equivalents might be used to afford protection against pests or abiotic stresses such as drought.

If the phenotype is due to changes in pigment levels within the leaf, the gene or its equivalents may be applied to alter photosynthetic capacity and yield.

20 **G3076 (SEQ ID NO: 655)**

Published Information

G3076 (At4g18650) was identified as part of the BAC clone F28A21 (GenBank accession AL035526).

Experimental Observations

- 25 The function of G3076 was studied using plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G3076 produced no consistent alterations in *Arabidopsis* growth and development. However, G3076 overexpressing lines showed more tolerance to a severe drought stress treatment.

Utilities

- 30 The reduced sensitivity of 35S::G3076 lines in the dehydration assay indicated that the gene or its equivalents might be used to engineer crops with increased water use efficiency or increased tolerance to stresses such as drought, salt, freezing and/or chilling stress.

G3083 (SEQ ID NO: 657)

35 Published Information

G3083 (At3g14880) is part of BAC clone K15M2, GenBank accession number AP000370 (nid=5541653).

Experimental Observations

The 5'- and 3'- ends of G3083 were determined by RACE and the function of the gene was assessed by analysis of transgenic *Arabidopsis* lines in which a genomic clone was constitutively expressed from a 35S promoter. In the physiological analysis, two out of the three 35S::G3083 lines tested, displayed an enhanced ability to germinate on plates containing high levels of sodium chloride. Thus, G3083 can function as part of a response pathway to abiotic stress. 35S::G3083 plants were indistinguishable from wild-type controls in the morphological analysis.

Utilities

Based on the increased salt tolerance exhibited by the 35S::G3083 lines in physiology assays, this gene might be used to engineer salt tolerant crops and trees that can flourish in salinified soils, or under drought conditions.

G3086 (SEQ ID NO: 661)

Published Information

G3086 corresponds to gene AT1G51140, annotated by the *Arabidopsis* Genome Initiative. No information is available about the function(s) of G3086.

Experimental Observations

The function of G3086 was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G3086 in *Arabidopsis* produced a pronounced acceleration in the onset of flowering. 35S::G3086 transformants produced visible flower buds 5-7 days early (in inductive 24-hour light conditions), and were markedly smaller than wild-type controls.

G3086 overexpressing lines were larger and more tolerant of heat stress. Figure 9A shows the effects of a heat assay on *Arabidopsis* wild-type and G3086-overexpressing plants. The overexpressors on the left were generally larger, paler, and exhibited earlier bolting than the wild type plants seen on the right of this plate.

35S::G3086 transformants were also larger and displayed more root growth when grown under high salt conditions. G3086 overexpressors, as exemplified by the eight seedlings on the right of Figure 9B, were larger, greener, and had more root growth than control plants, as exemplified by the four seedlings on the right in Figure 9B.

Utilities

Based on the phenotypes observed in morphological and physiological assays, G3086 might be have a number of utilities.

Given the salt resistance exhibited by 35S::G3086 transformants, the gene or its orthologs might be used to engineer salt tolerant crops and trees that can flourish in saline soils, or under drought conditions.

Based on the response of 35S::G3086 lines to heat stress, the gene or its orthologs might be used to engineer crop plants with increased tolerance to abiotic stresses such as high temperatures, a stress that often occurs simultaneously with other environmental stress conditions such as drought or salt stress.

The early flowering displayed by 35S::G3086 transformants indicated that the gene or its orthologs might be used to accelerate the flowering of commercial species, or to eliminate any requirements for vernalization.

Example IX: Identification of Homologous Sequences

This example describes identification of genes that are orthologous to *Arabidopsis thaliana* transcription factors from a computer homology search.

Homologous sequences, including those of paralogs and orthologs from *Arabidopsis* and other plant species, were identified using database sequence search tools, such as the Basic Local Alignment Search Tool (BLAST) (Altschul et al. (1990) *J. Mol. Biol.* 215: 403-410; and Altschul et al. (1997) *Nucleic Acid Res.* 25: 3389-3402). The tblastx sequence analysis programs were employed using the BLOSUM-62 scoring matrix (Henikoff and Henikoff (1992) *Proc. Natl. Acad. Sci.* 89: 10915-10919). The entire NCBI GenBank database was filtered for sequences from all plants except *Arabidopsis thaliana* by selecting all entries in the NCBI GenBank database associated with NCBI taxonomic ID 33090 (Viridiplantae; all plants) and excluding entries associated with taxonomic ID 3701 (*Arabidopsis thaliana*).

These sequences are compared to sequences representing genes of the Sequence Listing, for example, SEQ ID NO: 2N - 1, wherein N = 1-335, using the Washington University TBLASTX algorithm (version 2.0a19MP) at the default settings using gapped alignments with the filter "off". For each of these gene sequences, individual comparisons were ordered by probability score (P-value), where the score reflects the probability that a particular alignment occurred by chance. For example, a score of $3.6e-40$ is 3.6×10^{-40} . In addition to P-values, comparisons were also scored by percentage identity. Percentage identity reflects the degree to which two segments of DNA or protein are identical over a particular length. Examples of sequences so identified are presented in Tables 7, 8 and 9. Paralogous or orthologous sequences were readily identified from proprietary databases and in GenBank. The percent sequence identity among these sequences can be as low as 47%, or even lower sequence identity.

Candidate paralogous sequences were identified among *Arabidopsis* transcription factors through alignment, identity, and phylogenetic relationships. A list of paralogs is shown in Table 8. Candidate orthologous sequences were identified from proprietary unigene sets of plant gene sequences in *Zea mays*, *Glycine max* and *Oryza sativa* based on significant homology to *Arabidopsis* transcription factors. These candidates were reciprocally compared to the set of *Arabidopsis* transcription factors. If the

candidate showed maximal similarity in the protein domain to the eliciting transcription factor or to a paralog of the eliciting transcription factor, then it was considered to be an ortholog. Identified non-*Arabidopsis* sequences that were shown in this manner to be orthologous to the *Arabidopsis* sequences are provided in Tables 7 and 9.

5

Example X: Screen of Plant cDNA library for Sequence Encoding a Transcription Factor DNA Binding Domain That Binds To a Transcription Factor Binding Promoter Element and Demonstration of Protein Transcription Regulation Activity.

The "one-hybrid" strategy (Li and Herskowitz (1993) *Science* 262: 1870-1874) is used to screen for plant cDNA clones encoding a polypeptide comprising a transcription factor DNA binding domain, a conserved domain. In brief, yeast strains are constructed that contain a lacZ reporter gene with either wild-type or mutant transcription factor binding promoter element sequences in place of the normal UAS (upstream activator sequence) of the GALL promoter. Yeast reporter strains are constructed that carry transcription factor binding promoter element sequences as UAS elements are operably linked upstream (5') of a lacZ reporter gene with a minimal GAL1 promoter. The strains are transformed with a plant expression library that contains random cDNA inserts fused to the GAL4 activation domain (GAL4-ACT) and screened for blue colony formation on X-gal-treated filters (X-gal: 5-bromo-4-chloro-3-indolyl-β-D-galactoside; Invitrogen Corporation, Carlsbad CA). Alternatively, the strains are transformed with a cDNA polynucleotide encoding a known transcription factor DNA binding domain polypeptide sequence.

Yeast strains carrying these reporter constructs produce low levels of beta-galactosidase and form white colonies on filters containing X-gal. The reporter strains carrying wild-type transcription factor binding promoter element sequences are transformed with a polynucleotide that encodes a polypeptide comprising a plant transcription factor DNA binding domain operably linked to the acidic activator domain of the yeast GAL4 transcription factor, "GAL4-ACT". The clones that contain a polynucleotide encoding a transcription factor DNA binding domain operably linked to GLA4-ACT can bind upstream of the lacZ reporter genes carrying the wild-type transcription factor binding promoter element sequence, activate transcription of the lacZ gene and result in yeast forming blue colonies on X-gal-treated filters.

Upon screening about 2×10^6 yeast transformants, positive cDNA clones are isolated; i.e., clones that cause yeast strains carrying lacZ reporters operably linked to wild-type transcription factor binding promoter elements to form blue colonies on X-gal-treated filters. The cDNA clones do not cause a yeast strain carrying a mutant type transcription factor binding promoter elements fused to LacZ to turn blue. Thus, a polynucleotide encoding transcription factor DNA binding domain, a conserved domain, is shown to activate transcription of a gene.

Example XI: Gel Shift Assays.

The presence of a transcription factor comprising a DNA binding domain which binds to a DNA transcription factor binding element is evaluated using the following gel shift assay. The transcription factor is recombinantly expressed and isolated from *E. coli* or isolated from plant material. Total soluble protein, including transcription factor, (40 ng) is incubated at room temperature in 10 µl of 1 x binding buffer (15 mM HEPES (pH 7.9), 1 mM EDTA, 30 mM KCl, 5% glycerol, 5% bovine serum albumin, 1 - mM DTT) plus 50 ng poly(dI-dC):poly(dI-dC) (Pharmacia, Piscataway NJ) with or without 100 ng competitor DNA. After 10 minutes incubation, probe DNA comprising a DNA transcription factor binding element (1 ng) that has been ³²P-labeled by end-filling (Sambrook et al. (1989) *supra*) is added and the mixture incubated for an additional 10 minutes. Samples are loaded onto polyacrylamide gels (4% w/v) and fractionated by electrophoresis at 150V for 2h (Sambrook et al. *supra*). The degree of transcription factor-probe DNA binding is visualized using autoradiography. Probes and competitor DNAs are prepared from oligonucleotide inserts ligated into the BamHI site of pUC118 (Vieira et al. (1987) *Methods Enzymol.* 153: 3-11). Orientation and concatenation number of the inserts are determined by dideoxy DNA sequence analysis (Sambrook et al. *supra*). Inserts are recovered after restriction digestion with EcoRI and HindIII and fractionation on polyacrylamide gels (12% w/v) (Sambrook et al. *supra*).

Example XII. Introduction of Polynucleotides into Dicotyledonous Plants

Any of the transcription factor sequences of the invention listed in the Sequence Listing, and paralogous, and orthologous sequences, may be recombined into pMEN20 or pMEN65 expression vectors and then are transformed into a plant for the purpose of modifying plant traits. The cloning vector may be introduced into a variety of cereal plants by means well known in the art such as, for example, direct DNA transfer or *Agrobacterium tumefaciens*-mediated transformation. It is now routine to produce transgenic plants using most dicot plants (see Weissbach and Weissbach, (1989) *supra*; Gelvin et al. (1990) *supra*; Herrera-Estrella et al. (1983) *supra*; Bevan (1984) *supra*; and Klee (1985) *supra*). Methods for analysis of traits are routine in the art and examples are disclosed above.

Example XIII: Transformation of Cereal Plants with an Expression Vector

Cereal plants such as, but not limited to, corn, wheat, rice, sorghum, or barley, may also be transformed with the present polynucleotide sequences in pMEN20 or pMEN65 expression vectors for the purpose of modifying plant traits. For example, pMEN020 may be modified to replace the NptII coding region with the BAR gene of *Streptomyces hygroscopicus* that confers resistance to phosphinothricin. The KpnI and BglII sites of the Bar gene are removed by site-directed mutagenesis with silent codon changes.

The cloning vector may be introduced into a variety of cereal plants by means well known in the art such as, for example, direct DNA transfer or *Agrobacterium tumefaciens*-mediated transformation. It

is now routine to produce transgenic plants of most cereal crops (Vasil (1994) *Plant Mol. Biol.* 25: 925-937) such as corn, wheat, rice, sorghum (Cassas et al. (1993) *Proc. Natl. Acad. Sci.* 90: 11212-11216, and barley (Wan and Lemeaux (1994) *Plant Physiol.* 104:37-48. DNA transfer methods such as the microprojectile can be used for corn (Fromm et al. (1990) *Bio/Technol.* 8: 833-839); Gordon-Kamm et al. (1990) *Plant Cell* 2: 603-618; Ishida (1990) *Nature Biotechnol.* 14:745-750), wheat (Vasil et al. (1992) *Bio/Technol.* 10:667-674; Vasil et al. (1993) *Bio/Technol.* 11:1553-1558; Weeks et al. (1993) *Plant Physiol.* 102:1077-1084), rice (Christou (1991) *Bio/Technol.* 9:957-962; Hiei et al. (1994) *Plant J.* 6:271-282; Aldemita and Hodges (1996) *Planta* 199:612-617; and Hiei et al. (1997) *Plant Mol. Biol.* 35:205-218). For most cereal plants, embryogenic cells derived from immature scutellum tissues are the preferred cellular targets for transformation (Hiei et al. (1997) *Plant Mol. Biol.* 35:205-218; Vasil (1994) *Plant Mol. Biol.* 25: 925-937).

Vectors according to the present invention may be transformed into corn embryogenic cells derived from immature scutellar tissue by using microprojectile bombardment, with the A188XB73 genotype as the preferred genotype (Fromm et al. (1990) *Bio/Technol.* 8: 833-839; Gordon-Kamm et al. (1990) *Plant Cell* 2: 603-618). After microprojectile bombardment the tissues are selected on phosphinothricin to identify the transgenic embryogenic cells (Gordon-Kamm et al. (1990) *Plant Cell* 2: 603-618). Transgenic plants are regenerated by standard corn regeneration techniques (Fromm et al. (1990) *Bio/Technol.* 8: 833-839; Gordon-Kamm et al. (1990) *Plant Cell* 2: 603-618).

The plasmids prepared as described above can also be used to produce transgenic wheat and rice plants (Christou (1991) *Bio/Technol.* 9:957-962; Hiei et al. (1994) *Plant J.* 6:271-282; Aldemita and Hodges (1996) *Planta* 199:612-617; and Hiei et al. (1997) *Plant Mol. Biol.* 35:205-218) that coordinately express genes of interest by following standard transformation protocols known to those skilled in the art for rice and wheat (Vasil et al. (1992) *Bio/Technol.* 10:667-674; Vasil et al. (1993) *Bio/Technol.* 11:1553-1558; and Weeks et al. (1993) *Plant Physiol.* 102:1077-1084), where the bar gene is used as the selectable marker.

Example XIV: Identification of Orthologous and Paralogous Sequences

Orthologs to *Arabidopsis* genes may identified by several methods, including hybridization, amplification, or bioinformatically. This example describes how one may identify homologs to the *Arabidopsis* AP2 family transcription factor CBF1 (polynucleotide SEQ ID NO: 2238, encoded polypeptide SEQ ID NO: 2239), which confers tolerance to abiotic stresses (Thomashow et al. (2002) US Patent No. 6,417,428), and an example to confirm the function of homologous sequences. In this example, orthologs to CBF1 were found in canola (*Brassica napus*) using polymerase chain reaction (PCR).

Degenerate primers were designed for regions of AP2 binding domain and outside of the AP2 (carboxyl terminal domain):

Mol 368 (reverse) 5'- CAY CCN ATH TAY MGN GGN GT -3' (SEQ ID NO: 2246)

Mol 378 (forward) 5'- GGN ARN ARC ATN CCY TCN GCC -3' (SEQ ID NO: 2247)

5 (Y: C/T, N: A/C/G/T, H: A/C/T, M: A/C, R: A/G)

Primer Mol 368 is in the AP2 binding domain of CBF1 (amino acid sequence: His-Pro-Ile-Tyr-Arg-Gly-Val) while primer Mol 378 is outside the AP2 domain (carboxyl terminal domain) (amino acid sequence: Met-Ala-Glu-Gly-Met-Leu-Leu-Pro).

10 The genomic DNA isolated from *B. napus* was PCR-amplified by using these primers following these conditions: an initial denaturation step of 2 min at 93°C; 35 cycles of 93°C for 1 min, 55°C for 1 min, and 72°C for 1 min ; and a final incubation of 7 min at 72°C at the end of cycling.

The PCR products were separated by electrophoresis on a 1.2% agarose gel and transferred to nylon membrane and hybridized with the AT CBF1 probe prepared from *Arabidopsis* genomic DNA by
15 PCR amplification. The hybridized products were visualized by colorimetric detection system (Boehringer Mannheim) and the corresponding bands from a similar agarose gel were isolated using the Qiagen Extraction Kit (Qiagen). The DNA fragments were ligated into the TA clone vector from TOPO TA Cloning Kit (Invitrogen) and transformed into *E. coli* strain TOP10 (Invitrogen).

Seven colonies were picked and the inserts were sequenced on an ABI 377 machine from both
20 strands of sense and antisense after plasmid DNA isolation. The DNA sequence was edited by sequencer and aligned with the AtCBF1 by GCG software and NCBI blast searching.

The nucleic acid sequence and amino acid sequence of one canola ortholog found in this manner (bnCBF1; polynucleotide SEQ ID NO: 2244 and polypeptide SEQ ID NO: 2245) identified by this process is shown in the Sequence Listing.

25 The aligned amino acid sequences show that the bnCBF1 gene has 88% identity with the *Arabidopsis* sequence in the AP2 domain region and 85% identity with the *Arabidopsis* sequence outside the AP2 domain when aligned for two insertion sequences that are outside the AP2 domain.

Similarly, paralogous sequences to *Arabidopsis* genes, such as *CBF1*, may also be identified.

Two paralogs of CBF1 from *Arabidopsis thaliana*: *CBF2* and *CBF3*. *CBF2* and *CBF3* have been
30 cloned and sequenced as described below. The sequences of the DNA SEQ ID NO: 2240 and 2242 and encoded proteins SEQ ID NO: 2241 and 2243 are set forth in the Sequence Listing.

A lambda cDNA library prepared from RNA isolated from *Arabidopsis thaliana* ecotype Columbia (Lin and Thomashow (1992) *Plant Physiol.* 99: 519-525) was screened for recombinant clones that carried inserts related to the *CBF1* gene (Stockinger et al. (1997) *Proc. Natl. Acad. Sci.* 94:1035-
35 1040). CBF1 was ³²P-radiolabeled by random priming (Sambrook et al. *supra*) and used to screen the library by the plaque-lift technique using standard stringent hybridization and wash conditions (Hajela et al. (1990) *Plant Physiol.* 93:1246-1252; Sambrook et al. *supra*) 6 X SSPE buffer, 60°C for hybridization and 0.1 X SSPE buffer and 60°C for washes). Twelve positively hybridizing clones were obtained and

the DNA sequences of the cDNA inserts were determined. The results indicated that the clones fell into three classes. One class carried inserts corresponding to *CBF1*. The two other classes carried sequences corresponding to two different homologs of *CBF1*, designated *CBF2* and *CBF3*. The nucleic acid sequences and predicted protein coding sequences for *Arabidopsis CBF1*, *CBF2* and *CBF3* are listed in the Sequence Listing (SEQ ID NOs: 2238, 2240, 2242 and SEQ ID NOs: 2239, 2241, and 2243, respectively). The nucleic acid sequences and predicted protein coding sequence for *Brassica napus CBF* ortholog is listed in the Sequence Listing (SEQ ID NOs: 2244 and 2245, respectively).

A comparison of the nucleic acid sequences of *Arabidopsis CBF1*, *CBF2* and *CBF3* indicate that they are 83 to 85% identical as shown in Table 11.

TABLE 11

	Percent identity ^a	
	DNA ^b	Polypeptide
cbf1/cbf2	85	86
cbf1/cbf3	83	84
cbf2/cbf3	84	85

^a Percent identity was determined using the *Clustal* algorithm from the Megalign program (DNASTAR, Inc.).

^b Comparisons of the nucleic acid sequences of the open reading frames are shown.

Similarly, the amino acid sequences of the three CBF polypeptides range from 84 to 86% identity. An alignment of the three amino acid sequences reveals that most of the differences in amino acid sequence occur in the acidic C-terminal half of the polypeptide. This region of CBF1 serves as an activation domain in both yeast and *Arabidopsis* (not shown).

Residues 47 to 106 of CBF1 correspond to the AP2 domain of the protein, a DNA binding motif that to date, has only been found in plant proteins. A comparison of the AP2 domains of CBF1, CBF2 and CBF3 indicates that there are a few differences in amino acid sequence. These differences in amino acid sequence might have an effect on DNA binding specificity.

Example XV: Transformation of Canola with a Plasmid Containing CBF1, CBF2, or CBF3

After identifying homologous genes to CBF1, canola was transformed with a plasmid containing the *Arabidopsis CBF1*, *CBF2*, or *CBF3* genes cloned into the vector pGA643 (An (1987) *Methods Enzymol.* 253: 292). In these constructs the CBF genes were expressed constitutively under the CaMV 35S promoter. In addition, the CBF1 gene was cloned under the control of the *Arabidopsis COR15* promoter in the same vector pGA643. Each construct was transformed into *Agrobacterium* strain GV3101. Transformed *Agrobacteria* were grown for 2 days in minimal AB medium containing appropriate antibiotics.

Spring canola (*B. napus* cv. Westar) was transformed using the protocol of Moloney et al. ((1989) *Plant Cell Reports* 8: 238) with some modifications as described. Briefly, seeds were sterilized and plated on half strength MS medium, containing 1% sucrose. Plates were incubated at 24° C under 60-80 $\mu\text{E}/\text{m}^2\text{s}$ light using a 16 hour light/ 8 hour dark photoperiod. Cotyledons from 4-5 day old seedlings were collected, the petioles cut and dipped into the *Agrobacterium* solution. The dipped cotyledons were placed on co-cultivation medium at a density of 20 cotyledons/plate and incubated as described above for 3 days. Explants were transferred to the same media, but containing 300 mg/l timentin (SmithKline Beecham, PA) and thinned to 10 cotyledons/plate. After 7 days explants were transferred to Selection/Regeneration medium. Transfers were continued every 2-3 weeks (2 or 3 times) until shoots had developed. Shoots were transferred to Shoot-Elongation medium every 2-3 weeks. Healthy looking shoots were transferred to rooting medium. Once good roots had developed, the plants were placed into moist potting soil.

The transformed plants were then analyzed for the presence of the NPTII gene/ kanamycin resistance by ELISA, using the ELISA NPTII kit from 5Prime-3Prime Inc. (Boulder, CO).

Approximately 70% of the screened plants were NPTII positive. Only those plants were further analyzed.

From Northern blot analysis of the plants that were transformed with the constitutively expressing constructs, showed expression of the CBF genes and all CBF genes were capable of inducing the *Brassica napus* cold-regulated gene BN115 (homolog of the *Arabidopsis* COR15 gene). Most of the transgenic plants appear to exhibit a normal growth phenotype. As expected, the transgenic plants are more freezing tolerant than the wild-type plants. Using the electrolyte leakage of leaves test, the control showed a 50% leakage at -2 to -3° C. Spring canola transformed with either CBF1 or CBF2 showed a 50% leakage at -6 to -7° C. Spring canola transformed with CBF3 shows a 50% leakage at about -10 to -15° C. Winter canola transformed with CBF3 may show a 50% leakage at about -16 to -20° C.

Furthermore, if the spring or winter canola are cold acclimated the transformed plants may exhibit a further increase in freezing tolerance of at least -2° C.

To test salinity tolerance of the transformed plants, plants were watered with 150 mM NaCl. Plants overexpressing CBF1, CBF2 or CBF3 grew better compared with plants that had not been transformed with CBF1, CBF2 or CBF3.

These results demonstrate that homologs of *Arabidopsis* transcription factors can be identified and shown to confer similar functions in non-*Arabidopsis* plant species.

Example XVI: Cloning of transcription factor promoters

Promoters are isolated from transcription factor genes that have gene expression patterns useful for a range of applications, as determined by methods well known in the art (including transcript profile analysis with cDNA or oligonucleotide microarrays, Northern blot analysis, semi-quantitative or quantitative RT-PCR). Interesting gene expression profiles are revealed by determining transcript

abundance for a selected transcription factor gene after exposure of plants to a range of different experimental conditions, and in a range of different tissue or organ types, or developmental stages. Experimental conditions to which plants are exposed for this purpose includes cold, heat, drought, osmotic challenge, varied hormone concentrations (ABA, GA, auxin, cytokinin, salicylic acid, brassinosteroid), pathogen and pest challenge. The tissue types and developmental stages include stem, root, flower, rosette leaves, cauline leaves, siliques, germinating seed, and meristematic tissue. The set of expression levels provides a pattern that is determined by the regulatory elements of the gene promoter.

Transcription factor promoters for the genes disclosed herein are obtained by cloning 1.5 kb to 2.0 kb of genomic sequence immediately upstream of the translation start codon for the coding sequence of the encoded transcription factor protein. This region includes the 5'-UTR of the transcription factor gene, which can comprise regulatory elements. The 1.5 kb to 2.0 kb region is cloned through PCR methods, using primers that include one in the 3' direction located at the translation start codon (including appropriate adaptor sequence), and one in the 5' direction located from 1.5 kb to 2.0 kb upstream of the translation start codon (including appropriate adaptor sequence). The desired fragments are PCR-amplified from *Arabidopsis* Col-0 genomic DNA using high-fidelity Taq DNA polymerase to minimize the incorporation of point mutation(s). The cloning primers incorporate two rare restriction sites, such as NotI and SfiI, found at low frequency throughout the *Arabidopsis* genome. Additional restriction sites are used in the instances where a NotI or SfiI restriction site is present within the promoter.

The 1.5-2.0 kb fragment upstream from the translation start codon, including the 5'-untranslated region of the transcription factor, is cloned in a binary transformation vector immediately upstream of a suitable reporter gene, or a transactivator gene that is capable of programming expression of a reporter gene in a second gene construct. Reporter genes used include green fluorescent protein (and related fluorescent protein color variants), beta-glucuronidase, and luciferase. Suitable transactivator genes include LexA-GAL4, along with a transactivatable reporter in a second binary plasmid (as disclosed in US patent application 09/958,131, incorporated herein by reference). The binary plasmid(s) is transferred into *Agrobacterium* and the structure of the plasmid confirmed by PCR. These strains are introduced into *Arabidopsis* plants as described in other examples, and gene expression patterns determined according to standard methods known to one skilled in the art for monitoring GFP fluorescence, beta-glucuronidase activity, or luminescence.

The promoter region for G1753 is obtained from *Arabidopsis* chromosome 2 clone F1011 (AC006919), gene At2g36450, from position 43906-45410 of the genomic clone. The complement of this sequence is the promoter oriented in the 5'-3' direction, with the translation start codon for G1753 the complement of positions 43903-43905.

The present invention is not limited by the specific embodiments described herein. The invention now being fully described, it will be apparent to one of ordinary skill in the art that many changes and

modifications can be made thereto without departing from the spirit or scope of the appended claims. Modifications that become apparent from the foregoing description and accompanying figures fall within the scope of the claims.

5 All references, publications, patent documents, web pages, and other documents cited or mentioned herein are hereby incorporated by reference in their entirety for all purposes. Although the invention has been described with reference to specific embodiments and examples, it should be understood that one of ordinary skill can make various modifications without departing from the spirit of the invention. The scope of the invention is not limited to the specific embodiments and examples provided.

10

What is claimed is:

1. A recombinant polynucleotide selected from the group consisting of:

- (a) a nucleotide sequence encoding a polypeptide, wherein said nucleotide sequence is selected from the group consisting of SEQ ID NO: 2N - 1, where N = 1- 335, SEQ ID NOs: 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 684, 685, 686, 687, 688, 689, 691, 692, 693, 694, 695, 696, 697, 698, 699, 701, 702, 704, 705, 706, 708, 709, 710, 711, 712, 713, 714, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 764, 765, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 866, 867, 868, 869, 870, 871, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 899, 900, 901, 902, 903, 904, 905, 906, 907, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 920, 921, 922, 923, 924, 926, 927, 928, 929, 930, 931, 938, 939, 940, 941, 942, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 972, 973, 974, 975, 976, 977, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1005, 1006, 1007, 1008, 1009, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1051, 1052, 1053, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1080, 1081, 1082, 1083, 1084, 1085, 1088, 1089, 1090, 1091, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1146, 1147, 1148, 1149, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1196, 1199, 1200, 1201, 1203, 1204, 1205, 1206, 1207, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1277, 1278, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1302, 1303, 1304, 1305, 1306, 1307, 1310, 1311, 1312, 1313, 1314, 1316, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1349, 1351, 1353,

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1385, 1387, 1389, 1391, 1393, 1395, 1397, 1399, 1401, 1403, 1405, 1407, 1409, 1411, 1413,
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(b) a nucleotide sequence encoding a polypeptide, wherein said polypeptide is selected from the
10 group consisting of SEQ ID NO: 2N, where N = 1- 335, SEQ ID NOs: 681, 682, 683, 690, 700,
703, 707, 715, 729, 730, 731, 743, 760, 761, 762, 763, 766, 767, 782, 783, 784, 785, 807, 808,
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25 1522, 1524, 1526, 1528, 1530, 1532, 1534, 1536, 1538, 1540, 1542, 1544, 1546, 1548, 1550,
1552, 1554, and 1556;

- (c) a variant of any of the nucleotide sequences of (a) or (b) that has at least 70% sequence identity
to a sequence of (a) or (b);
- (d) an orthologous sequence of any of the nucleotide sequences of (a) or (b) that has at least 70%
30 identity to a sequence of (a) or (b);
- (e) a paralogous sequence of any of the nucleotide sequences of (a) or (b) that has at least 70%
identity to a sequence of (a) or (b);
- (f) a nucleotide sequence that hybridizes to any of the nucleotide sequence of (a) or (b) under
stringent conditions comprising 6x SSC and 65° C in two wash steps of 10 - 30 minutes;
- 35 (g) a nucleotide sequence encoding a polypeptide comprising a conserved domain that has at least
70% sequence homology with a conserved domain of a polypeptide encoded by any of the
nucleotide sequences of (a) - (f), wherein said conserved domain is required for the function of

the polypeptide encoded by any of the nucleotide sequences of (a) – (f) in regulating transcription and altering a trait in a transgenic plant.

2. The recombinant polynucleotide of Claim 1, wherein the recombinant polynucleotide is operably
5 linked to at least one regulatory element being effective in controlling expression of said recombinant polynucleotide when said recombinant polynucleotide is transformed into a plant.
3. The recombinant polynucleotide of Claim 2, wherein the recombinant polynucleotide is incorporated within an expression vector.
- 10 4. The recombinant polynucleotide of Claim 3, wherein the expression vector is incorporated into a cultured host cell.
5. A transgenic plant that overexpresses the recombinant polynucleotide according to Claim 1, wherein
15 said transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant.
6. The transgenic plant of Claim 5, wherein said altered trait is selected from the group consisting of:
increased tolerance to abiotic stress, increased tolerance to osmotic stress, increased tolerance to cold,
increased germination in cold, increased tolerance to heat, increased germination in heat, increased
20 tolerance to freezing conditions, increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to disease, increased tolerance to fungal disease, increased tolerance to *Erysiphe*, increased tolerance to *Fusarium*, increased tolerance to *Botrytis*, increased tolerance to multiple fungal pathogens, increased resistance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA, increased sensitivity to ACC, altered sugar sensing, increased tolerance to
25 sugars, altered C/N sensing, early flowering, late flowering, altered flower structure, loss of flower determinacy, reduced fertility, altered shoot meristem development, altered branching pattern, altered stem morphology, altered vascular tissue structure, reduced apical dominance, altered trichome density, altered trichome development, altered trichome structure, altered root development, altered shade avoidance, altered seed development, altered seed ripening, altered seed germination, slow growth, fast
30 growth, altered cell differentiation, altered cell proliferation, altered cell expansion, altered phase change, altered senescence, abnormal embryo development, altered programmed cell death, lethality when overexpressed, altered necrosis patterns, increased plant size, increased biomass, large seedlings, dwarfed plants, dark green leaves, change in leaf shape, increased leaf size and mass, light green or gray leaves, glossy leaves, altered abaxial/adaxial polarity, altered seed coloration, altered seed size, altered seed
35 shape, large seed, increased leaf wax, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seed prenyl content, altered leaf prenyl lipid content, increased anthocyanin levels, and decreased anthocyanin levels.

7. The transgenic plant of Claim 5, wherein the transgenic plant is selected from the group consisting of:
- 5 soybean, potato, cotton, oilseed rape, canola, sunflower, alfalfa, clover, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, pumpkin, spinach, squash, tobacco, tomato, tomatillo, watermelon, rosaceous fruits, fruit trees, brassicas, barley; wheat, corn, sweet corn, rice, rye; sugarcane, turf; millet; sorghum; currant; avocado; citrus fruits, oranges, lemons, grapefruit, tangerines, artichoke, cherries; walnut, peanut; endive; leek; arrowroot, beet,
- 10 cassava, turnip, radish, yam, sweet potato; beans, pine, poplar, eucalyptus, and mint.
8. The transgenic plant of Claim 5, wherein said recombinant polynucleotide comprises a constitutive, inducible, or tissue-specific promoter operably linked to said polynucleotide sequence.
- 15 9. A method for producing a transgenic plant having an altered trait as compared to a non-transgenic or wild-type plant, the method steps comprising:
- (a) providing an expression vector comprising:
- (i) a recombinant polynucleotide according to Claim 1; and
- (ii) at least one regulatory element flanking the polynucleotide sequence, said at least one
- 20 regulatory element being effective in controlling expression of said recombinant polynucleotide in a target plant;
- (b) introducing the expression vector into a plant cell, thereby producing a transgenic plant cell;
- (c) growing the transgenic plant cell into a transgenic plant and allowing the transgenic plant to overexpress a polypeptide encoded by the recombinant polynucleotide, said polypeptide having
- 25 the property of altering a trait in a plant as compared to a non-transgenic plant that does not overexpress the polypeptide; and
- (d) identifying at least one transgenic plant with an altered trait by comparing said transgenic plant with at least one non-transgenic plant that does not overexpress the polypeptide.
- 30 10. The method of Claim 9, the method steps further comprising:
- (e) selfing or crossing said at least one transgenic plant with an altered trait with itself or another plant, respectively; and
- (f) growing a progeny plant from seed that develops as a result of said selfing or crossing, thus producing a transgenic progeny plant having an altered trait.
- 35 11. The method of Claim 10, wherein:

said transgenic progeny plant expresses mRNA that encodes a DNA-binding protein having a region of a conserved domain that binds to a DNA molecule, regulates expression of said DNA molecule, and induces expression of a plant trait gene; and

5 said mRNA is expressed at a level greater than a non-transformed plant that does not overexpress said DNA-binding protein.

12. The method of Claim 9, wherein said altered trait is increased tolerance to an osmotic stress and said osmotic stress is selected from the group consisting of drought, heat and high salt concentration.

10 13. The method of Claim 12, wherein said recombinant polynucleotide comprises SEQ ID NO: 2105, 2108, 2110, 2112, 2113, or 2114, or encodes a polypeptide selected from the group consisting of SEQ ID NO: 10, 12, 80, 120, 154, 156, 162, 168, 170, 172, 190, 194, 208, 216, 226, 246, 256, 264, 268, 272, 278, 288, 296, 340, 342, 346, 372, 390, 392, 404, 406, 412, 418, 426, 488, 498, 506, 530, 558, 568, 604, 612, 618, 624, 626, 656, 658, 662, 1380, 1382, and 1496.

15

14. The method of Claim 9, wherein said altered trait is increased tolerance to low nitrogen conditions and said recombinant polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO: 44, 54, 116, 130, 146, 154, 166, 188, 194, 236, 244, 278, 288, 328, 380, 464, 508, 548, 590, and 610.

20

15. The method of Claim 9, wherein said altered trait is increased tolerance to low phosphorus conditions and said recombinant polynucleotide comprises SEQ ID NO: 2105 or encodes a polypeptide selected from the group consisting of SEQ ID NO: 80, 120, 328, 366, and 606.

25 16. The method of Claim 9, wherein said altered trait is increased size, growth rate or biomass and said recombinant polynucleotide comprises SEQ ID NO: 2103, 2105 or 2118, or encodes a polypeptide selected from the group consisting of SEQ ID NO: 10, 64, 70, 72, 74, 98, 120, 142, 150, 180, 188, 194, 200, 224, 228, 232, 394, 432, 468, 484, 490, 500, 502, 512, 526, 556, 608, and 632.

30 17. The method of Claim 9, wherein said altered trait is increased resistance or tolerance to disease and said recombinant polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO: 278.

35 18. The method of Claim 17, wherein said disease is a fungal disease selected from the group consisting of *Fusarium*, *Botrytis* and *Erysiphe*-mediated diseases.

19. The method of Claim 17, wherein overexpression of said polypeptide confers resistance or tolerance to more than one pathogen.
20. The method of Claim 9, wherein said altered trait is a reduction or elimination of shading responses and said recombinant polynucleotide comprises SEQ ID NO: 2219 or encodes a polypeptide selected from the group consisting of SEQ ID NO: 8, 60; 408; 484; 518, 528, 578, 620, 638, 1380, and 1382.

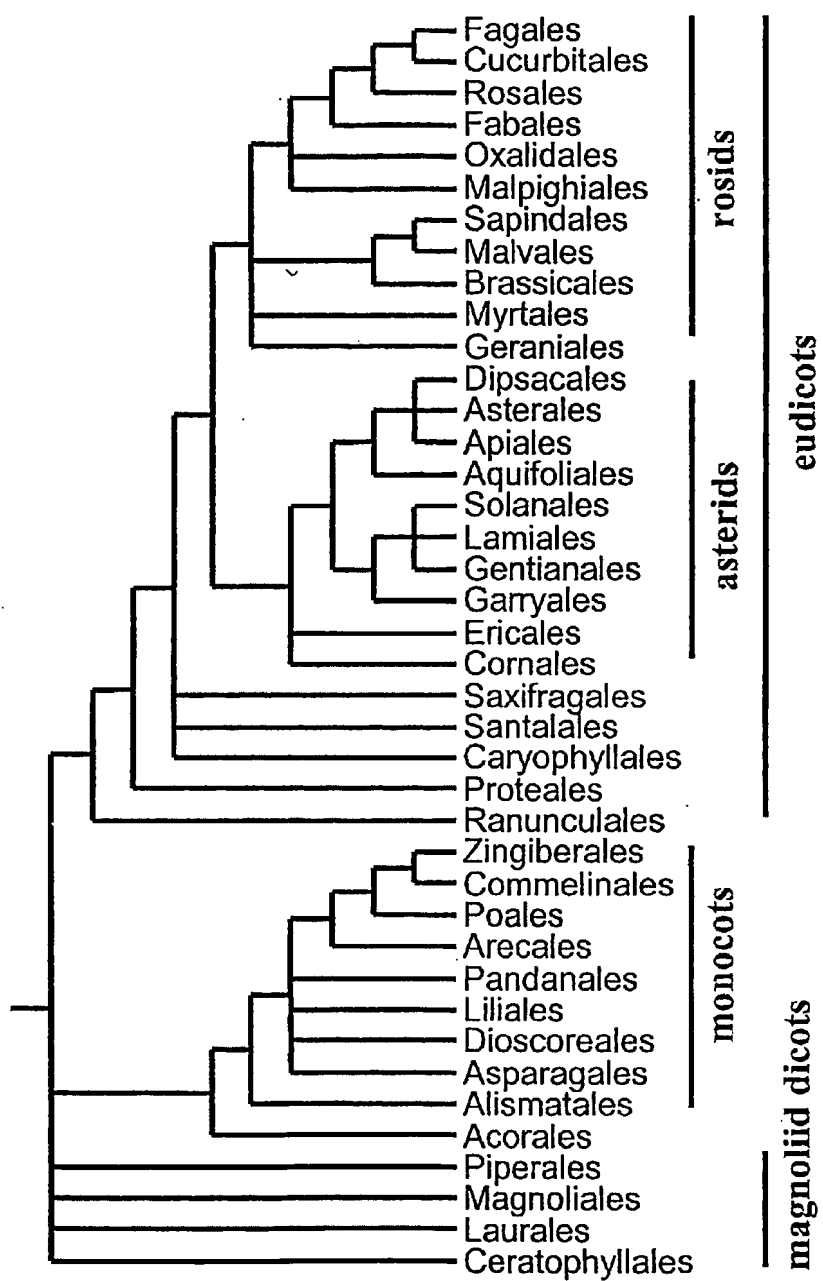


FIGURE 1

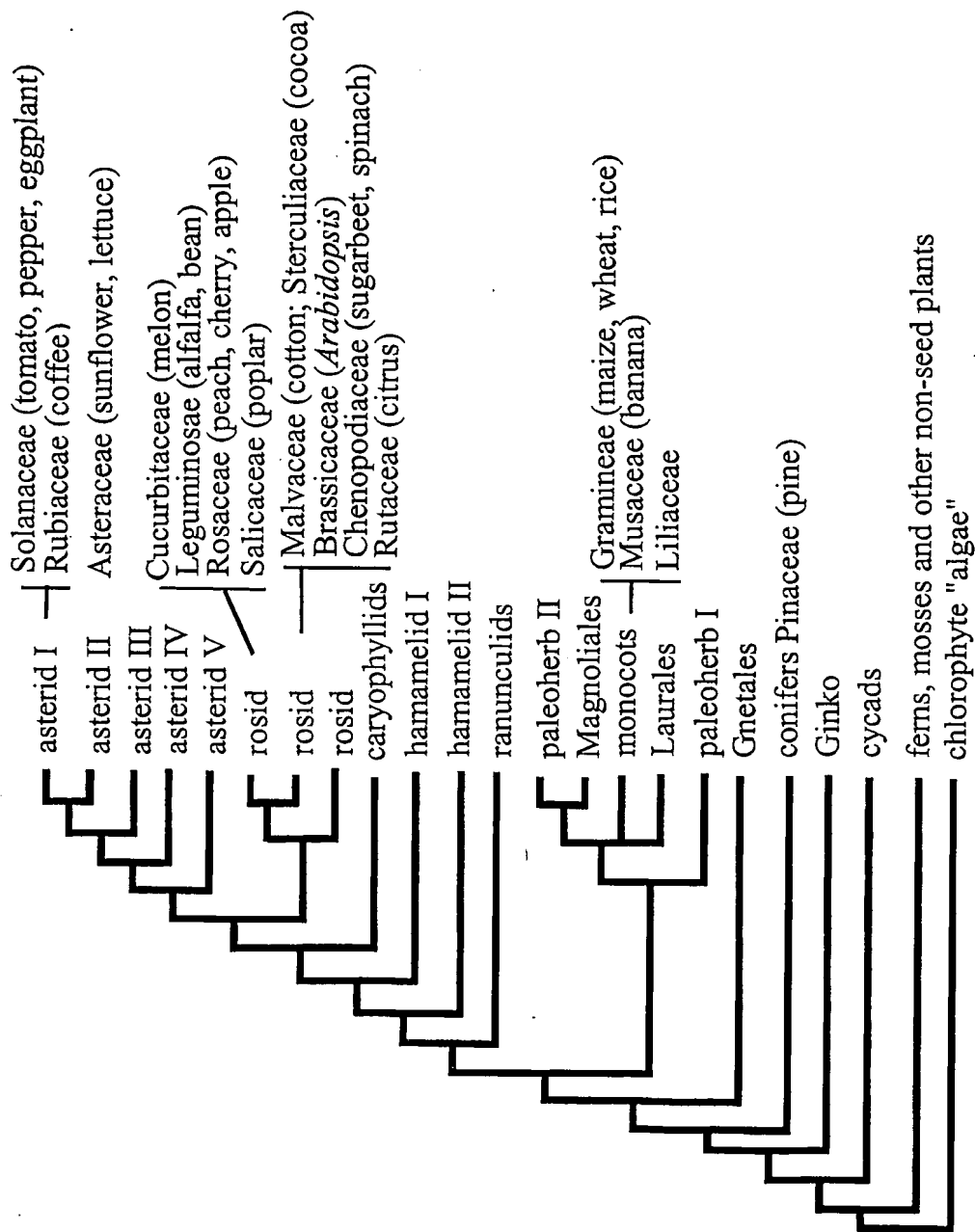


FIGURE 2

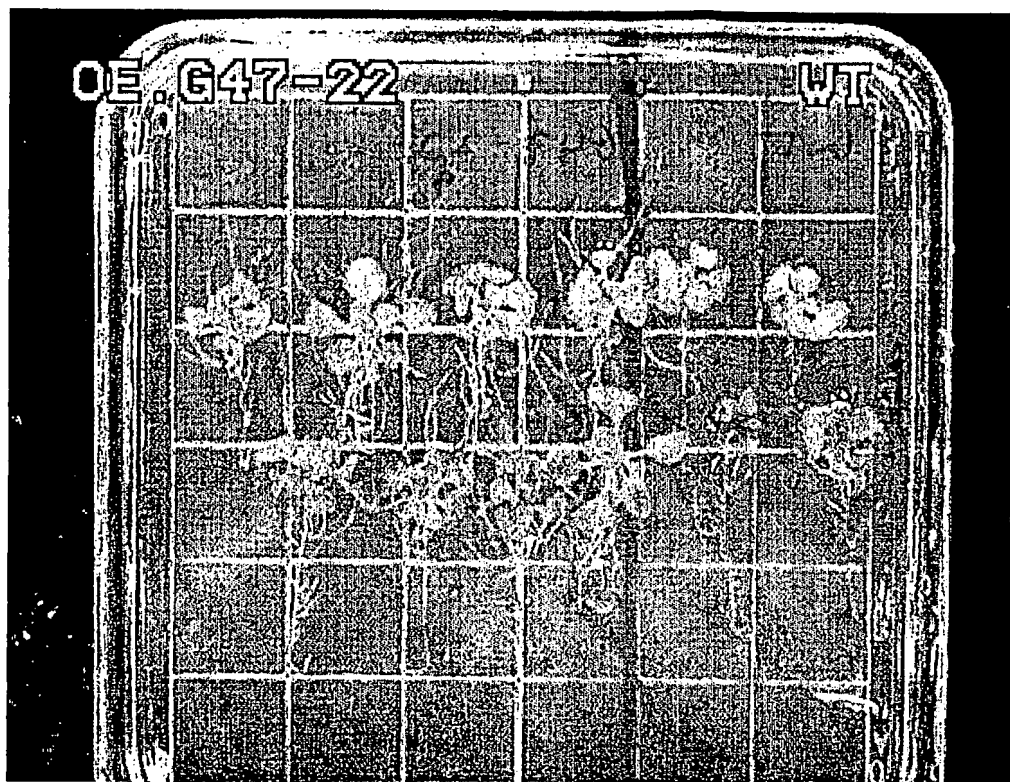


Figure 3A



Figure 3B

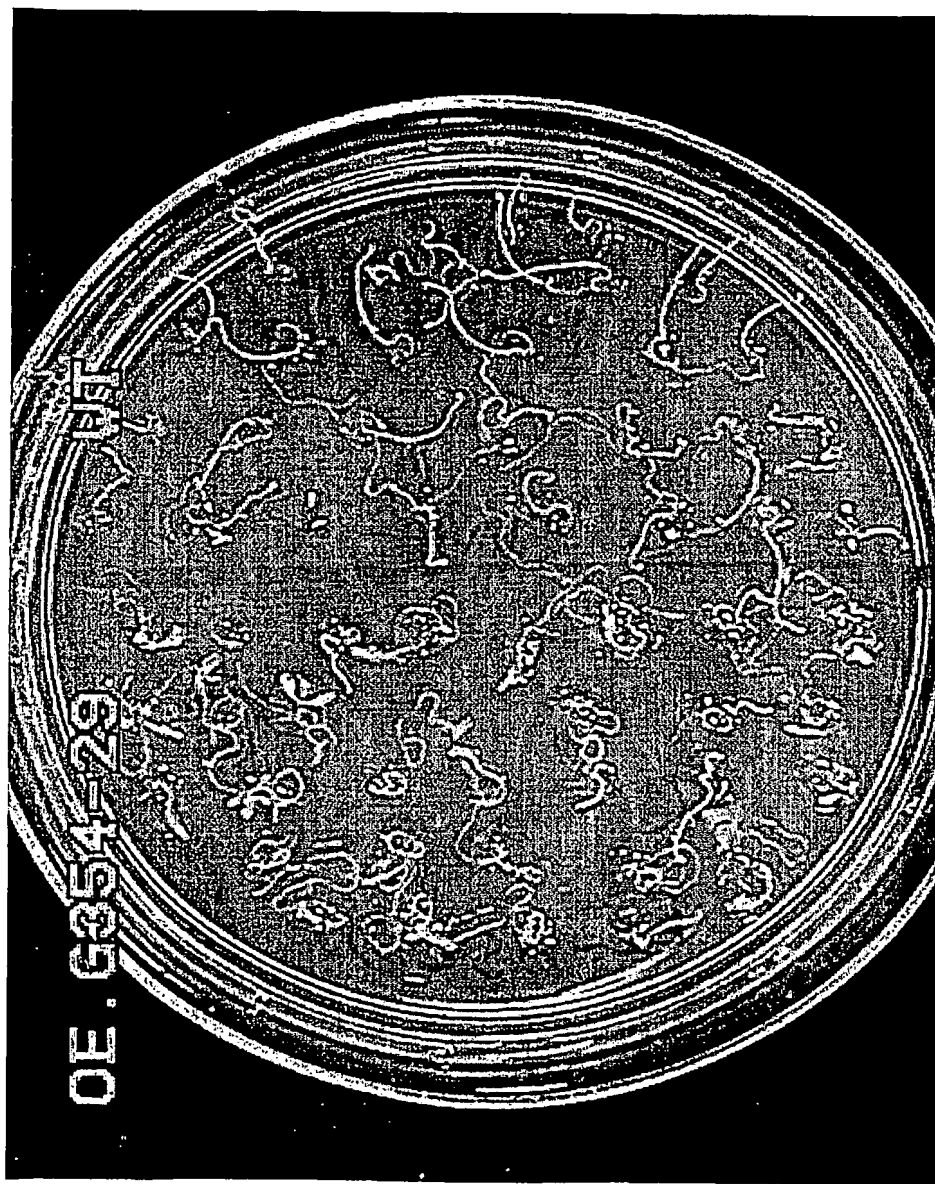


FIGURE 4



Figure 5B



Figure 5D



Figure 5A



Figure 5C

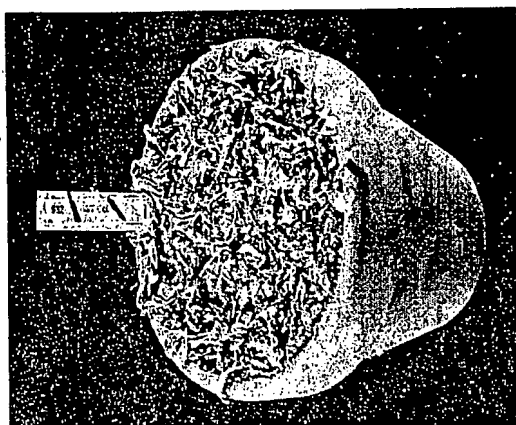


Figure 6A

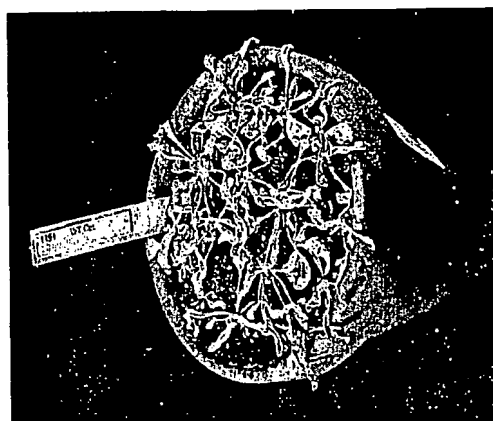


Figure 6B

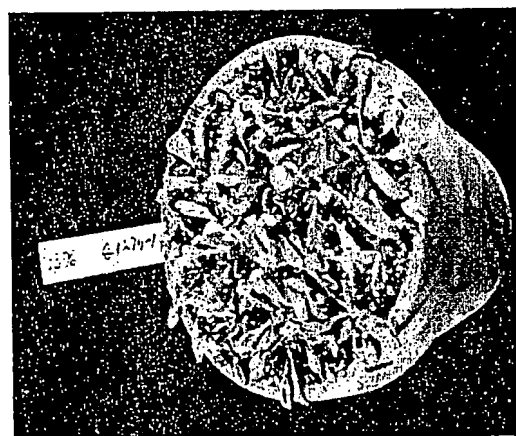


Figure 6C

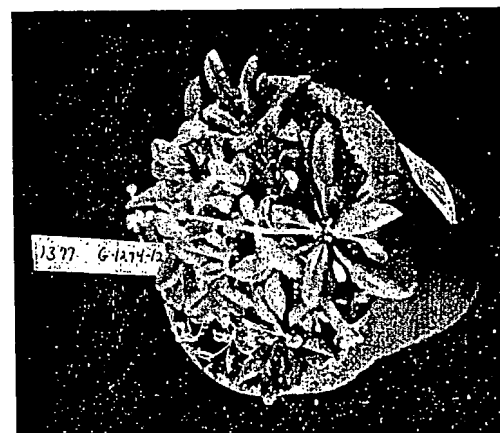


Figure 6D



Figure 7B

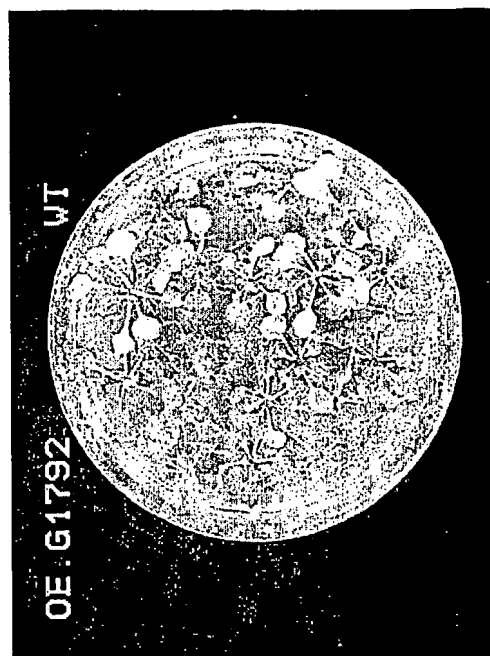


Figure 7D



Figure 7A



Figure 7C

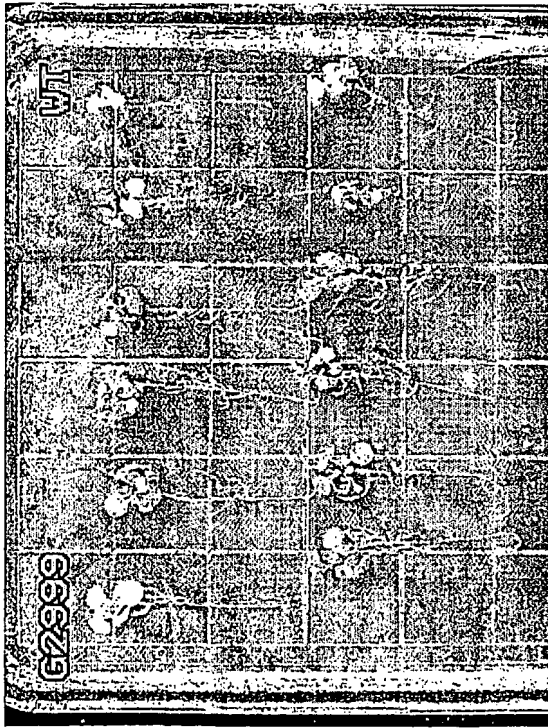


Figure 8A



Figure 8c



Figure 8B



Figure 9A

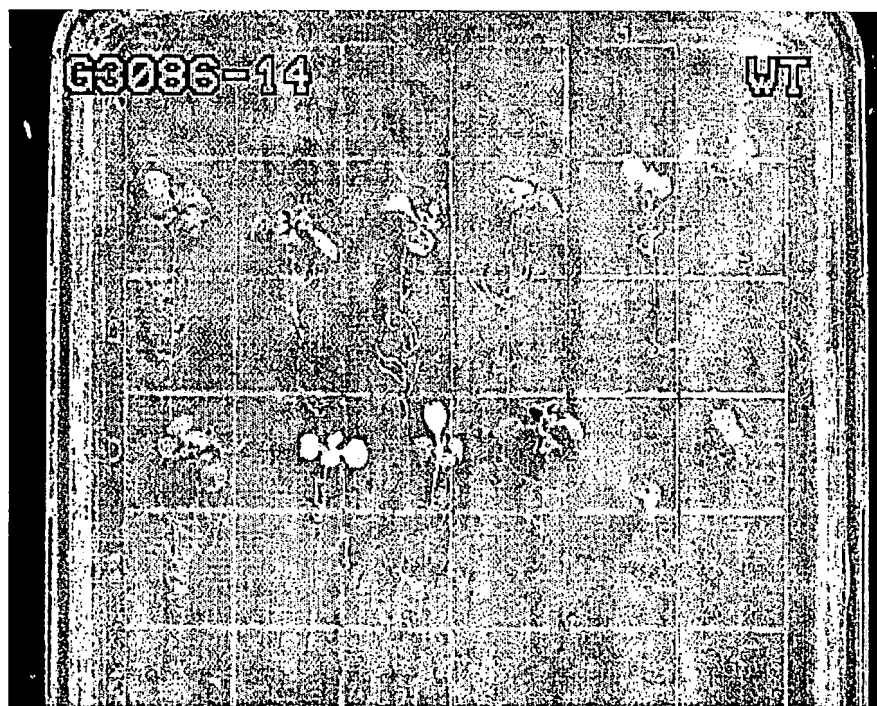


Figure 9B



Figure 10A

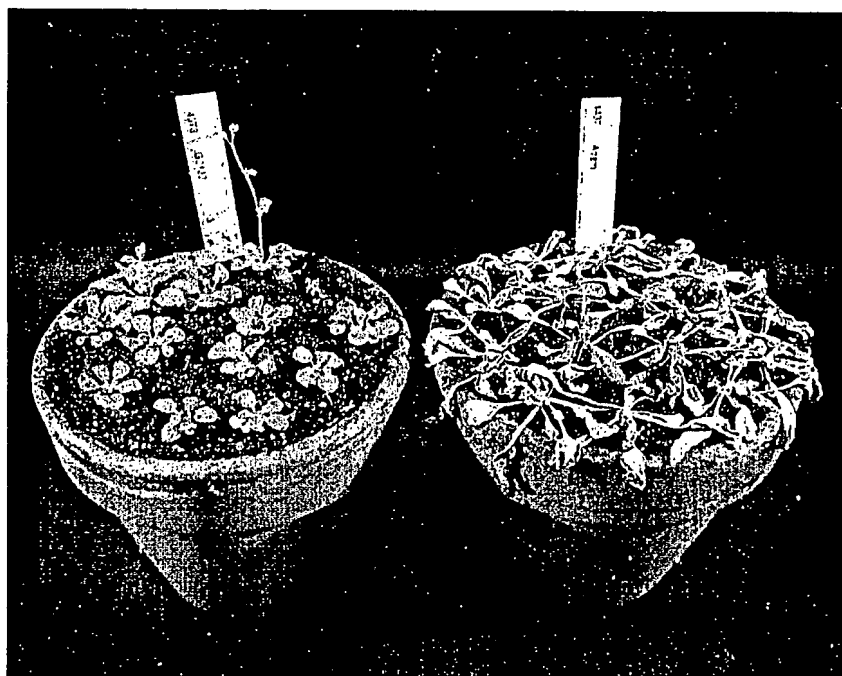


Figure 10B